

RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals."
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR InterPro: IPR002181; Fibrinogen C.
 DR PROSITE: P500514; FIBRIN AG C DOMAIN, PARTIAL.
 KW Blood coagulation; Plasma; Sulfation.
 FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
 FT MOD RES 5 20
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2338 MW; FCF5B6FF0DEC6627 CRC64;
 Query Match 27.3%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KLP 9
 DB 14 KLP 16
 RESULT 11
 ID M117 BOVIN STANDARD; PRT; 20 AA.
 AC P35451;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE 17 kDa milk glycoprotein (Fragment).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Milk;
 RX MEDLINE=93308294; PubMed=8320368;
 RA Soerensen E.S., Petersen T.E.;
 RT "Purification and characterization of three proteins isolated from
 RT the protease peptone fraction of bovine milk."
 RL J. Dairy Res. 60:189-197(1993).
 CC -!- FTM: N-GLYCOSYLATED.
 CC -!- SIMILARITY: TO CAMEL WHEY PROTEIN.
 KW Glycoprotein; Milk.
 FT NON TER 1 1
 FT NON TER 20 20
 SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;
 Query Match 27.3%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KLP 9
 DB 11 KLP 13
 RESULT 12
 ID FYRI ANTEL STANDARD; PRT; 4 AA.
 AC P58706;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Antho-Riamide I [Contains: Antho-Riamide II].
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 CC Nymanthea; Actiniidae; Anthopleura.
 CC NCBI_TaxID=6110;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE=92270459; PubMed=1821096;
 RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
 RA Gimmelikhuijzen C.J.P.;
 RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
 RT biologically active L-3-phenylacetyl-Tyr-Arg-Ile-NH2 and its
 RT des-phenylacetyl fragment Tyr-Arg-Ile-NH2."
 RL Peptides 12:1165-1173(1991).
 RN (2)
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Gimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two
 RT inhibitory neuropeptides, Antho-kaamide and Antho-Riamide."
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993)
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Neuron-specific.
 KW Neuropeptide; Amidation.
 FT CHAIN 1 4 ANTHO-RIAMIDE I.
 FT CHAIN 2 4 ANTHO-RIAMIDE II.
 FT MOD RES 1 1 L-3-PHENYLACTYL.
 FT MOD RES 4 4 AMIDATION.
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FY 6
 DB 1 FY 2
 RESULT 13
 ID PRCT PERAM STANDARD; PRT; 5 AA.
 AC P01373;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Proctolin.
 OS Periplaneta americana (American cockroach),
 OS Limulus polyphemus (Atlantic horseshoe crab), and
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 CC Blattidae; Periplaneta.
 CC NCBI_TaxID=6978, 6850, 6759;
 RN (1)
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=76074708; PubMed=576;
 RA Starratt A.N., Brown B.E.;
 RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 RT in insects."
 RL Life Sci. 17:1253-1256(1975).
 RN (2)
 RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;
 RX MEDLINE=81225865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron."
 RL Science 213:567-569(1981).
 RN (3)

```

RP SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RL horseshoe crab, Limulus polyphemus.";
RN Peptides 11:205-211(1990).
RN [4]
RP SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RL pericardial organs of the shore crab, Carcinus maenas.";
RN Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
DB 3 LP 4

RESULT 14
FARP MONEX ID FARP MONEX STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFRamide-like neuropeptide GNFRFP-amide.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28641;
RN [1]
RP SPECIES=
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRFRamide: a novel FMRFRamide-immunoreactive peptide isolated from
RT the sheep tapeworm, Moniezia expansa.";
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFRAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A43129;
DR PIR; A43129; A43129.
KW Neuropeptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 787 MW; 69D405C9C4481000 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 2 NF 3

RESULT 15
OVM LEPE ID OVM LEPE STANDARD; PRT; 6 AA.

```

```

AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (Lep-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SPECIES= AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=91271080; PubMed=2052497;
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
RT decemlineata";
RL Peptides 12:31-36(1991).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5D030000 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YK 7
DB 3 YK 4

RESULT 16
TRPI PSEPU ID TRPI PSEPU STANDARD; PRT; 6 AA.
AC P36474;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE TRPB operon transcriptional activator (fragment).
GN TRPI.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C1S;
RX MEDLINE=89335826; PubMed=2503057;
RA Berly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT putida";
RL Biochimie 71:521-531(1989).
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPB GENES ENCODING
CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
CC TRPB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; X13299; CAA31660.1; -.

```



```

DR InterPro: IPR000847; HTH_LYSR.
DR PROSITE: PS00044; HTH_LYSR FAMILY; PARTIAL.
KW Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
Db 5 LP 6

RESULT 17
CARP_MYTED
ID FARI_MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka I.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC RETRACTOR MUSCLE.
DR PIR; A29342; BCMUCR.
KW Hormone; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 831 MW; 6734072687669D80 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2
Db 2 MP 3

RESULT 18
FARI_MACRS
ID FARI_MACRS STANDARD; PRT; 7 AA.
AC P83274;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP1 (DNFLRP-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).

CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO: GO:0007218; P-neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540A20 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
Db 3 NF 4

RESULT 19
FARI_PROCL
ID FARI_PROCL STANDARD; PRT; 7 AA.
AC P38499;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Cardiac excitatory FMRamide homolog NPL.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Procambarus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183;
RA Mercier A.J., Orchard I., Tebruggge V., Skerrett M.;
RT "Isolation of two FMRamide-related peptides from crayfish
RT pericardial organs.";
RL Peptides 14:137-143(1993).
CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS INCREASES THE AMPLITUDE OF
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540A20 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
Db 3 NF 4

RESULT 20
FARI_PROCL
ID FARI_PROCL STANDARD; PRT; 7 AA.
AC P38499;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Cardiac excitatory FMRamide homolog DP2.
OS Procamburus clarkii (Red swamp crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidea; Cambaridae; Procambarus.
OX NCBI_TaxID=6728;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=93248032; PubMed=8387183;

```

```

RA Merrier A.J., Orchard I., Tebrugge V., Skerrett M.;
RT "Isolation of two FMRFamide-related peptides from crayfish
RL pericardial organs.";
CC -1- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
Db 3 NF 4

RESULT 21
FAR4 PANRE STANDARD; PRT; 7 AA.
AC P41675;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuroptide PP4 (KFNFRFP-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OC NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
RA Tim L., Kubiak T.M., Martin R.A., Geary T.G.;
RT "Isolation and preliminary biological characterization of
RT KPNFRFamide, a novel FMRFamide-related peptide from the free-living
RT nematode, Panagrellus redivivus.";
RL Peptides 16:87-93(1995).
CC -1- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
CC MUSCLE TENSION INCREASE.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
Db 3 NF 4

RESULT 22
FARB CALVO STANDARD; PRT; 7 AA.
AC F41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 11.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OC NCBI_TaxID=27454;

```

```

RN SEQUENCE.
RP TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.P., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; B44787; B44787.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 926 MW; 69D40699C44AB700 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
Db 3 NF 4

RESULT 23
HY7 PIG STANDARD; PRT; 7 AA.
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-I., Arimura A., Redding T.W., Coy D.H.,
RA Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. Res. 13:228-232(1981).
DR PIR; A01417; NYPG7.
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YK 7
Db 6 YK 7

RESULT 24
IGAO DACDE STANDARD; PRT; 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OC NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RA Avigad G., Markus Z.;

```

```

RT      "Identification of a peptide inhibitor of galactose oxidase from
RL      Dactylium dendroides."
CC      -|- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
CC      GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
CC      BINDING TO ITS PROSTHETIC COPPER GROUP.
DR      PIR; A01341; KEYDGO.
KW      Copper; Metalloenzyme inhibitor.
SQ      SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match      18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 QN 4
DB      3 QN 4

RESULT 25
UN06 PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins."
RL Electrophoresis 20:1098-1108(1999).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;

Query Match      18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LP 9
DB      5 LP 6

RESULT 26
WWA2 ACHFU
ID WWA2_ACHFU STANDARD; PRT; 7 AA.
AC P35920;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wamide-2
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RA "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from

```

```

RT      ganglia of the African giant snail, Achatina fulica."
RL      FEBS Lett. 323:104-108(1993).
DR      PIR; S33246; S33246.
KW      Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 964 MW; 7362DSB686D32310 CRC64;

Query Match      18.2%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 QM 11
DB      3 QM 4

RESULT 27
AKHG GRYBI
ID AKHG_GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (Lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88108553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus."
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera."
RL Peptides 9:681-688(1988).
CC -|- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC -|- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A28004; A28004.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match      18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 NF 5
DB      3 NF 4

RESULT 28
AKH LIBAU
ID AKH_LIBAU STANDARD; PRT; 8 AA.
AC P25418;

```

```

RESULT 30
ALL6_CVDPO
ID ALL6_CVDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Coddling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OC NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RX TISSUE=Larva;
RC MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RL "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1302-1309(1997)
CC 1-1 SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
CC Neuropeptide; Amidation.
KW MOD_RES 8
FT SEQUENCE 8 AA; 936 MW; 082879C45B573767 CRC64;
SQ
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB ||
5 NF 6

RESULT 31
CONW2_CONPU
ID CONW2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Negastropoda; Conoidea; Conidae; Conus.
OC NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999)
CC 1-1 SUBCELLULAR LOCATION: Secreted.
CC 1-1 TISSUE SPECIFICITY: Expressed by the venom duct.
CC 1-1 MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC 1-1 SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD_RES 2 4
FT SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
SQ
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
DB ||

```

```

Db          5 LP 6

RESULT 32
COXG RAT
ID COXG RAT STANDARD; PRT; 8 AA.
AC P80430;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIB (EC 1.9.3.1) (AED) (Fragment).
GN COX6B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; Tissue=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform.";
RL Bur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT. THIS PROTEIN MAY BE ONE OF THE
CC HEME-BINDING SUBUNITS OF THE OXIDASE.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanide c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIB FAMILY.
DR PIR; S65381; S65391.
KW Oxidoreductase; Mitochondrion.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4
Db 1 QN 2

RESULT 33
FAR1 PANRE
ID FAR1 PANRE STANDARD; PRT; 8 AA.
AC P41872;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide PF1 (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRFamide-like peptides from the free-living nematode
RT Panagrellus redivivus.";
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.

FT MOD_RES 8 AA; 995 MW; C6D40729C4576AB5 CRC64;
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
Db 4 NF 5

RESULT 34
FAR1 PENWO
ID FAR1 PENWO STANDARD; PRT; 8 AA.
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP1 (GDRNFLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupoen J., Krungkeasem C., Longyant S.,
RA Chaivachangkur P.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
Db 4 NF 5

RESULT 35
FAR2 MACRS
ID FAR2 MACRS STANDARD; PRT; 8 AA.
AC P83275;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP2 (ADKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Sathithongkum W., Jaidechoy S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.

```

```

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 4 NF 5

RESULT 36
FAR3_HOMAM ID FAR3_HOMAM STANDARD; PRT; 8 AA.
AC P41486;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=8616164; PubMed=3429714;
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT "Purification and characterization of FMRFamide-like immunoreactive
RT substances from the lobster nervous system: isolation and sequence
RT analysis of two closely related peptides."
RL J. Comp. Neurol. 266:16-26(1987).
CC -1- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM
CC POTASSIUM IN THE PRESENCE OF CALCIUM.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 4 NF 5

RESULT 37
FAR4_HOMAM ID FAR4_HOMAM STANDARD; PRT; 8 AA.
AC P41487;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=88116164; PubMed=3429714;
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;

```

```

RT "Purification and characterization of FMRFamide-like immunoreactive
RT substances from the lobster nervous system: isolation and sequence
RT analysis of two closely related peptides."
RL J. Comp. Neurol. 266:16-26(1987).
CC -1- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
CC NEUROMUSCULAR JUNCTIONS.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 4 NF 5

RESULT 38
HTF1_PERAM ID HTF1_PERAM STANDARD; PRT; 8 AA.
AC P04578;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor 1 (Neuropeptide M-I) (Periplanetin CC-I)
DE (Pea-CAH-1) (Ied-CC-1) (Hypertrehalosaemic neuropeptide 1).
OS Periplaneta americana (American cockroach).
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry."
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana."
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical."
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast

```

RT atom bombardment mass spectrometry."
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -!- FUNCTION: HYPERTREHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A44960; A44960.
 DR PIR; A49823; A49823.
 DR PIR; S08995; S08995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 DR Neuropeptide; Amidation; Pyrrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NF 5
 DB 3 NF 4
 RESULT 39
 HTF TENMO
 ID - HTF TENMO STANDARD; PRT; 8 AA.
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hypertrahalosemic factor (HOTH) (Hypertrahalosemic neuropeptide).
 OS Tenebrio molitor (Yellow mealworm), and
 OS Zophobas rugipes.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067, 7075;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=T. molitor, and Z. rugipes;
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90341091; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrahalosemic neuropeptide from
 RT tenebrionid beetles: a novel member of the AKH/RPCH family."
 RL Peptides 11:453-459(1990).
 CC -!- FUNCTION: HYPERTREHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A43976; A43976.
 DR PIR; B43976; B43976.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 DR Neuropeptide; Amidation; Pyrrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NF 5
 DB 3 NF 4
 RESULT 40
 LCK8 LEUWA
 ID - LCK8 LEUWA STANDARD; PRT; 8 AA.

AC P19990;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Leucokinin VIII (L-VIII).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 RT VIII: the final members of this new family of cephalomyotropic
 RT peptides isolated from head extracts of Leucophaea maderae."
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 DR PIR; JS0318; JS0318.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FY 6
 DB 4 FY 5
 RESULT 41
 NPB BOVIN
 ID - NPB BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PQ 3
 DB 5 PQ 6
 RESULT 42

```

RPCH_PANEO
ID _RPCH_PANEO STANDARD; PRT; 8 AA.
AC P08939;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Red pigment concentrating hormone (RPCH)
OS Pandanus borealis (Northern red shrimp)
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidae;
OC Pandalidae; Pandalus.
OX NCBI_TaxID=6703;
RN [1]
RP SEQUENCE.
RX MEDLINE=75054965; PubMed=4433569;
RA Fernlund P.;
RT "Structure of the red-pigment-concentrating hormone of the shrimp,
RT Pandanus borealis."
RL Biochim. Biophys. Acta 371:304-311(1974).
CC -1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY
CC -1- STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
CC CHROMATOPHORES.
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; A61348; A61348.
DR InterPro: IPR002047; AKH.
DR PROSITE; PS00256; AKH.1.
KW Pigment; Hormone; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 NF 5
DB 3 NF 4

RESULT 43
UPAA_HUMAN
ID _UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing."
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1 1
FT VARIANT 5 5 F -> P.
FT NON_TER 8 8 /FTID=VAR_000004.
FT SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 5 FY 6
DB 5 FY 6

RESULT 44
ALLO_CARMA
ID _ALLO_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUOTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9 9 AMIDATION.
FT SEQUENCE 9 AA; 963 MW; 372D79CDBA776C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PQ 3
DB 2 PQ 3

RESULT 45
FARI_CALVO
ID _FARI_CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Callipmrfamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callipmrfamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.

```


SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQ 3
 ||
 Db 2 PQ 3

RESULT 46
 FAR2 PANRE
 ID FAR2 PANRE STANDARD; PRT; 9 AA.
 AC P41873;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRamide-like neuropeptide P2 (SADPNFLRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93027659; PubMed=1408999;
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
 RA Garrison R.D., Williams J.F., Friedman A.R.;
 RT "Two FMRamide-like peptides from the free-living nematode
 Panagrellus redivivus";
 RL Peptides 13:209-214(1992).
 CC -!- FUNCTION: MTOACTIVE.
 CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
 CC -!- CAUDALLY TO THE BASE OF THE PHARYNX.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
 ||
 Db 5 NF 6

RESULT 47
 FAR3 MACRS
 ID FAR3 MACRS STANDARD; PRT; 9 AA.
 AC P83276;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE FMRamide-like neuropeptide FLP3 (NYDKNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sithigorngul P., Saraithongkum W., Jaidechoey S., Longyant S.,
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
 freshwater prawn Macrobrachium rosenbergii";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.

DR GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NF 5
 ||
 Db 5 NF 6

RESULT 48
 FAR5 PENMO
 ID FAR5 PENMO STANDARD; PRT; 9 AA.
 AC P83320;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE FMRamide-like neuropeptide FLP5 (SMPSLRFLRF-amide).
 OS Penaeus monodon (Pencoid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sithigorngul P., Pupiem J., Krungkarn C., Longyant S.,
 RA Chaivuthachakura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn Penaeus monodon";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MP 2
 ||
 Db 2 MP 3

RESULT 49
 FAR6 MACRS
 ID FAR6 MACRS STANDARD; PRT; 9 AA.
 AC P83279;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE FMRamide-like neuropeptide FLP6 (DGGNFLRF-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
 RA Sithigorngul W., Petsom A.;
 RT "Three more novel FMRamide-like neuropeptide sequences from the

```

RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1080.7; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1081 MW; 26800729C4540878 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 5 NF 6

RESULT 50
FARP MACRS STANDARD; PRT; 9 AA.
ID P83281;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE FMRFamide-like neuropeptide FL98 (VSHNNELSF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Decapoda; Decapoda; Fleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Saraihongkul W., Longyant S., Panchan N.,
RA Sithigorngul W., Petson A.;
RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 5 NF 6

RESULT 51
OXYT CVPCA STANDARD; PRT; 9 AA.
ID P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DE Vasotocin.
OS Cyprinus carpio (Common carp), and
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962, 7757;
RN [1]
RP SEQUENCE.
RC SPECIES=Carpio; TISSUE=Pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishes.";
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P. marinus; TISSUE=Pituitary;
RX MEDLINE=8825976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawachi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; B61364; B61364.
DR PIR; S06375; S06375.
DR InterPro; IPR000981; Neurhyp. horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4
DB 4 QN 5

RESULT 52
OXYT RABIT STANDARD; PRT; 9 AA.
AC P32878; P01188;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Oxytocin (Oxytocin).
OS Oryctolagus cuniculus (Rabbit),
OS Hippopotamus amphibius (Hippopotamus), (Common torqual),
OS Balanoptera physalus (Finback whale), and
OS Tachygllossus aculeatus aculeatus (Australian echidna), and
OS Hydroclagus collieri (Spotted ratfish) (Pacific ratfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
RN [1]
RP SEQUENCE.
RC SPECIES=Rabbit;
RX MEDLINE=72215060; PubMed=5150741;
RA Chauvet J., Chauvet M.-T., Acher R.;
RT "Evolution of neurohypophyseal hormones: isolation of active
RT principles from rabbits and rats.";
RL Biochimie 53:1099-1104(1971).
RN [2]
RP SEQUENCE.
RC SPECIES=H. amphibius;
RX MEDLINE=71232719; PubMed=5406007;
RA Ferguson D.R., Pickering B.T.;
RT "Arginine and lysine vasopressins in the hippopotamus
RT neurohypophysis.";
RL Gen. Comp. Endocrinol. 13:425-429(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=B. physalus;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Isolation of finback whale oxytocin and vasopressin.";

```


CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AF058451; AAC1294.1; -.
 DR HMAP; MF_00508; -; 1. Ribosomal S10.
 DR InterPro; IPR001848; Ribosomal_S10.
 DR PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
 KW Ribosomal protein.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1214 MW; DE3944004416D456 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4
 ||
 Db 2 QN 3

RESULT 56
 TKCL CALVO
 ID TKCL CALVO STANDARD; PRT; 9 AA.
 AC P41517;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin I.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE AND SYNTHESIS
 RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.F.; Clottens F.L.; Holman G.M.; Nichols R., Nachman R.J.,
 RA Maessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, Calliphora vomitoria, that have resemblances to
 RT tachykinins";
 RL Peptides 15:761-768(1994).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
 ||
 Db 5 FY 6

RESULT 57
 TKLI LOEMI
 ID TKLI LOEMI STANDARD; PRT; 9 AA.
 AC P16223;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Locustatachykinin I (TK-I).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Brain;
 RX MEDLINE=90194489; PubMed=2311766;
 RA Schoofs L.; Holman G.M.; Hayes T.K.; Nachman R.J.; de Loof A.;
 RA Locustatachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.;
 RL FEBS Lett. 261:397-401(1990).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
 CC OVIDUCT AND FOREGUT.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 9
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
 ||
 Db 5 FY 6

RESULT 58
 ANGL BOTJA
 ID ANGL BOTJA STANDARD; PRT; 10 AA.
 AC Q10581;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide I (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B.; Dalle Lucca J.; Carmona E.; Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca";
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 KW InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
 ||
 Db 8 FY 9

RESULT 59
 BPP2 BOTIN
 ID BPP2 BOTIN STANDARD; PRT; 10 AA.
 AC P30422;
 DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; B37196; B37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1213 MW; 30C53546C741773 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 QN 4
 DB 1 QN 2

 RESULT 60
 ID BPP2 BOTJA STANDARD; PRT; 10 AA.
 AC P01022;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
 DE inhibitor V-6-II). (Jararaca).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=72118526; PubMed=4334402;
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
 RA Kocy O.;
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
 RT jararaca. Isolation, elucidation of structure, and synthesis.";
 RL Biochemistry 10:4033-4039(1971).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01255; XAV168.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C741773 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 QN 4
 DB 1 QN 2

Db 1 QN 2

 RESULT 61
 CATB SHEEP STANDARD; PRT; 10 AA.
 ID AC P83205;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
 GN CTSB
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=22394055; PubMed=12506352;
 RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
 RA Mooko H.B., Beckers J.-F.M.P.;
 RT "Isolation and partial characterization of three pregnancy-associated
 RT glycoproteins from the ewe placenta.";
 RL Mol. Reprod. Dev. 64:199-206(2003).
 CC -!- FUNCTION: Thiol protease which is believed to participate in
 CC intracellular degradation and turnover of proteins. Has also been
 CC implicated in tumor invasion and metastasis.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
 CC for peptide bonds. Preferentially cleaves Arg-Arg-[Xaa bonds in
 CC small molecule substrates (thus differing from cathepsin L). In
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase
 CC activity, liberating C-terminal dipeptides.
 CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
 CC by a disulfide bond (By similarity).
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
 DR InterPro; IPR000169; SHProt acsite.
 DR PROSITE; PS00640; THIOLE PROTEASE ASN; PARTIAL.
 DR PROSITE; PS00139; THIOLE PROTEASE CYS; PARTIAL.
 DR PROSITE; PS00639; THIOLE PROTEASE HIS; PARTIAL.
 KW Hydrolase; Thiol protease; Lysosome.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9DSBA CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 8 LP 9
 DB 1 LP 2

 RESULT 62
 COXK ONCMV STANDARD; PRT; 10 AA.
 ID AC P80332;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIa-heart (EC 1.9.3.1) (Fragment).
 OS Onchornchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=94237150; PubMed=8181469;
 RA Freund R., Kadenbach B.;

RT "Identification of tissue-specific isoforms for subunits Vb and VIa
 RT of cytochrome c oxidase isolated from rainbow trout."
 RL Eur. J. Biochem. 221:1111-1116(1994).
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferrocyclochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIaA FAMILY.
 DR PIR; S43631; 943631.
 KW Oxidoreductase; inner membrane; Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KL 8
 ||
 DB 9 KL 10

RESULT 63
 FAR6 PANRE
 ID FAR6 PANRE STANDARD; PRT; 10 AA.
 AC P82660;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRPamide-like neuropeptide PF6 (NGAPQFVRP-amide).
 OS Panagrellus redivivus.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 CC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OC NCBI_TaxID=6233;
 OX [1]
 RN SEQUENCE, FUNCTION, AND AMIDATION.
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRPamide-related
 RT peptides (FARPs) from free-living nematode, Panagrellus redivivus."
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1132 MW; C813E4C9D776C76D CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PQ 3
 ||
 DB 4 PQ 5

RESULT 64
 FAR7 MACRS
 ID FAR7 MACRS STANDARD; PRT; 10 AA.
 AC P83280;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRPamide-like neuropeptide Flp7 (GIGRNFRLR-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Malacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 CC Palaemonoidea; Palaemonidae; Macrobrachium.
 OC NCBI_TaxID=79674;
 OX [1]
 RN

RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=eyestalk;
 RX MEDLINE=21107394; PubMed=11179812;
 RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
 RA Sithigorngul W., Petsom A.;
 RT "Three more novel FMRPamide-like neuropeptide sequences from the
 RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii."
 RL Peptides 22:191-197(2001).
 CC -!- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC GO: GO:0007218; P-neuropeptide signaling pathway; IDA.
 DR Neuropeptide; Amidation.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540A8 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NF 5
 ||
 DB 6 NF 7

RESULT 65
 FAR6 CALVO
 ID FAR6 CALVO STANDARD; PRT; 10 AA.
 AC P41867;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRPamide 12.
 OS Calliphora vomitoria (Blue blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Calliphoridae; Calliphora.
 OC NCBI_TaxID=27454;
 OX [1]
 RN SEQUENCE.
 RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRPamides) from the blowfly
 RT Calliphora vomitoria".
 RL Proc Natl Acad Sci U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; C44787; C44787.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1156 MW; 22810399C44AB6D8 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NF 5
 ||
 DB 6 NF 7

RESULT 66
 GOR3 ONCKE
 ID GOR3 ONCKE STANDARD; PRT; 10 AA.
 AC P20367; P81751;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin III (Gonadotropin-releasing hormone III) (LH-
 DE RH III) (Luliberin III).

```

DR PFam; PF00446; GNRH; 1.
DR PROSITE; PS00473; GNRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
  ||
DB 8 LP 9

RESULT 68
HTF1 ROMMI STANDARD; PRT; 10 AA.
AC P181I0;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RO 1 (Hypertrehalosaemic factor)
DE Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
  the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
RC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
  ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
  THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR INTERPRO; IP002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1163 MW; 05623674571A9C4 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
  ||
DB 3 NF 4

RESULT 69
HTF1 NAUCI STANDARD; PRT; 10 AA.
AC F10939;
DT 01-JUN-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic hormone (HTH) (Hypertrehalosaemic neuropeptide).
OS Nauphoeta cinerea (Cinereous cockroach)
OS Leucophaea maderae (Madeira cockroach),
OS Blattella germanica (German cockroach), and
OS Gromphadorina portoricensis (Madagascan hissing cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Nauphoeta.
OX NCBI_TaxID=6290. 6988. 6973. 36953.

```

[1]
 RN SEQUENCE.
 RP SPECIES=N.cinerea; TISSUE=Corpoxa cardiaca;
 RC MEDLINE=87100208; PubMed=3801028;
 RX Gaede G., Rinehart K.L. Jr.;
 RT "Amino acid sequence of a hypertrihaloasemic neuropeptide from the
 corpus cardiacum of the cockroach, Nauphoeta cinerea";
 RL Biochem. Biophys. Res. Commun. 141:774-781(1986).
 RN [2]
 RN SEQUENCE.
 RP SPECIES=L.maderae; G.portentosa, and B.germanica;
 RC MEDLINE=90253659; PubMed=2340112;
 RX Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrihaloasemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches Leucophaea maderae,
 Gryllodes sp. and Blattella germanica and Blatta orientalis
 and of the stick insect Extatosoma tiaratum assigned by tandem fast
 atom bombardment mass spectrometry";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 RN [3]
 RN SEQUENCE.
 RP SPECIES=B.germanica;
 RC MEDLINE=91179584; PubMed=2080017;
 RX Veenstra J.A., Camps F.;
 RT "Structure of the hypertrihaloasemic neuropeptide of the German
 cockroach, Blattella germanica";
 RL Neuropeptides 15:107-109(1990).
 CC -1- FUNCTION: HYPERTRIHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 DR PIR; A26381; A26381.
 DR PIR; A60421; A60421.
 DR PIR; S08997; S08997.
 DR PIR; S08998; S08998.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1092 MW; 05623678675B9C4 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 NF 5
 Db 3 NF 4
 RESULT 70
 MOSQ CLYJA STANDARD; PRT; 10 AA.
 AC P19962;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE [Gln]-mosacc.
 OS Clypeaster japonicus (Sand dollar).
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 CC Echinoidea; Euechinozoa; Echinozoa; Clypeasteroidea;
 CC Clypeasteridae; Clypeaster.
 CC NCBI_TaxID=7644;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Egg jelly;
 RC Suzuki N., Kurita M., Yoshino K., Kajitara H., Nomura K., Yamaguchi M.;
 RA "Purification and structure of mosacc and its derivatives from the
 egg jelly of the sea urchin Clypeaster japonicus";
 RL Zool. Sci. 4:649-656(1987)
 CC -1- FUNCTION: Stimulates sperm respiration and motility.
 DR PIR; JN0025; JN0025.

SQ SEQUENCE 10 AA; 1019 MW; 9AFB032456DDCSBA CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 QN 4
 Db 6 QN 7
 RESULT 71
 PNEU HUMAN STANDARD; PRT; 10 AA.
 ID PNEU HUMAN
 AC P22103;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pneumadin (PNM).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Lung;
 RC MEDLINE=91110910; PubMed=2274681;
 RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
 RT "Pneumadin: a new lung peptide which triggers antidiuresis";
 RL Regul. Pept. 30:77-87(1990).
 CC -1- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
 DR PIR; B33143; B33143.
 DR GO; GO:0030103; P:vasopressin secretion; NAS.
 FT MOD.RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 KL 8
 Db 5 KL 6
 RESULT 72
 PNEU RAT STANDARD; PRT; 10 AA.
 ID PNEU RAT
 AC P21996;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pneumadin (PNM).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE, AND SYNTHESIS.
 RP TISSUE=Lung;
 RC MEDLINE=91110910; PubMed=2274681;
 RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
 RT "Pneumadin: a new lung peptide which triggers antidiuresis";
 RL Regul. Pept. 30:77-87(1990).
 CC -1- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
 DR PIR; A33143; A33143.
 FT MOD.RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;

Matches: 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
||
Db 5 KL 6

RESULT 73

RL16_ACHLA STANDARD; PRT; 10 AA.
AC P292J;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 508 ribosomal protein L16 (fragment).
GN RPLP.
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92210505; PubMed=1556079;
RA Lim P.O.; Sears B.B.;
RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
organism and Acholeplasma laidlawii deduced from two ribosomal protein
gene sequences".
RL J. Bacteriol. 174:2606-2611(1992).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
(BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC
CC EMBL: M74771; AAA21914.1; --
CC PIR: F41839; F41839.
CC InterPro: IPR000114; Ribosomal_L16.
CC PROSITE: PS00586; RIBOSOMAL_L16_1; PARTIAL.
CC PROSITE: PS00701; RIBOSOMAL_L16_2; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 10
FT SEQUENCE 10 AA; 1324 MW; B3386A21B4032766 CRC64;
SQ

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2
||
Db 3 MP 4

RESULT 74

TEMK_RANTE STANDARD; PRT; 10 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.

RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M.; Mignogna G.; Canofeni S.; Miele R.; Mangoni M.L.;
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
temporaria".
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the breviniin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD_RES 10
FT SEQUENCE 10 AA; 1123 MW; 390549B37272457 CRC64;
SQ

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
||
Db 2 LP 3

RESULT 75

TKL2_LOCM STANDARD; PRT; 10 AA.
AC P16224; TKL2_LOCM
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin II (TK-II).
OS Locustatachykinin II (TK-II).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L.; Holman G.M.; Hayes T.K.; Nachman R.J.; de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuro-peptides with
homology to peptides of the vertebrate tachykinin family".
RL FEBS Lett. 261:397-401(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
OVIDUCT AND FOREGUT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
FT SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C665B7 CRC64;
SQ

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 8.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
||
Db 6 FY 7

Search completed: November 25, 2003, 18:17:26
Job time : 6.32447 secs

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 26.5053 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-6

Perfect score: 11

Sequence: 1 MPONFYKLPQM 11

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL_23.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	36.4	19	8 Q9ZY76	Q9ZY76 macroteleia
2	3	27.3	8	2 Q45615	Q45615 bacillus su
3	3	27.3	8	2 Q9RQ49	Q9RQ49 buchnera ap
4	3	27.3	8	11 Q99B40	Q99B40 mus musculus
5	3	27.3	8	11 Q62527	Q62527 mus spretus
6	3	27.3	9	4 Q14715	Q14715 homo sapien
7	3	27.3	9	8 P92072	P92072 euhadra her
8	3	27.3	9	8 Q94VG2	Q94VG2 varanus ind
9	3	27.3	9	11 Q8CG13	Q8CG13 mus musculus
10	3	27.3	10	2 Q9XBH3	Q9XBH3 bacillus ce
11	3	27.3	11	3 Q9URGL	Q9URGL neurospora
12	3	27.3	12	2 Q53579	Q53579 rhodobacter
13	3	27.3	13	2 Q9R889	Q9R889 streptococc
14	3	27.3	13	11 Q9QVL4	Q9QVL4 rattus sp.
15	3	27.3	14	13 Q91777	Q91777 xenopus lae
16	3	27.3	15	2 Q53580	Q53580 rhodobacter

17	3	27.3	15	2 Q9X637	Q9X637 klebsiella
18	3	27.3	15	2 Q9X635	Q9X635 escherichia
19	3	27.3	15	10 P82331	P82331 piusm sativ
20	3	27.3	15	12 Q66174	Q66174 human coron
21	3	27.3	16	2 Q9F9S4	Q9F9S4 pseudomonas
22	3	27.3	16	2 Q9R4X4	Q9R4X4 helicobacte
23	3	27.3	16	2 Q10748	Q10748 clostridium
24	3	27.3	16	6 Q28324	Q28324 capra hircu
25	3	27.3	16	8 Q34699	Q34699 helianthus
26	3	27.3	17	2 Q9ETL3	Q9ETL3 helicobacte
27	3	27.3	17	6 Q46667	Q46667 mactopus ro
28	3	27.3	17	11 Q9QUY6	Q9QUY6 rattus sp.
29	3	27.3	18	2 Q9ZG42	Q9ZG42 chlamydia t
30	3	27.3	18	4 Q9UC58	Q9UC58 homo sapien
31	3	27.3	18	4 Q16167	Q16167 homo sapien
32	3	27.3	18	10 Q8LNN9	Q8LNN9 oryza sativ
33	3	27.3	18	11 P70649	P70649 mus sp. syn
34	3	27.3	18	11 Q9QV11	Q9QV11 rattus sp.
35	3	27.3	18	11 P70650	P70650 mus sp. syn
36	3	27.3	18	13 Q9PRR7	Q9PRR7 gallus gall
37	3	27.3	19	4 Q8NFL2	Q8NFL2 homo sapien
38	3	27.3	19	4 Q9UDB7	Q9UDB7 homo sapien
39	3	27.3	19	5 Q9TWD0	Q9TWD0 sphaerechin
40	3	27.3	19	8 Q31687	Q31687 artemia par
41	3	27.3	19	8 Q9XMB5	Q9XMB5 aegilops ta
42	3	27.3	19	13 Q9DPN3	Q9DPN3 gillichthys
43	3	27.3	20	2 Q5X629	Q5X629 unidentified
44	3	27.3	20	2 Q9X632	Q9X632 pseudomonas
45	3	27.3	20	2 Q9X634	Q9X634 serratia na
46	3	27.3	20	2 Q9WU7	Q9WU7 ischerichia
47	3	27.3	20	2 Q9X630	Q9X630 ischericia a
48	3	27.3	20	2 Q46499	Q46499 desulfovibr
49	3	27.3	20	4 Q8NFW3	Q8NFW3 homo sapien
50	3	27.3	20	4 Q81Z13	Q81Z13 homo sapien
51	3	27.3	20	5 Q9TWR8	Q9TWR8 ceratilis c
52	3	27.3	20	10 Q9S8A8	Q9S8A8 secale cere
53	3	27.3	20	5 P83308	P83308 gallus gall
54	2	18.2	7	2 Q50556	Q50556 actinobacil
55	2	18.2	7	2 Q8GL00	Q8GL00 borrelia bu
56	2	18.2	7	8 Q98866	Q98866 spinacia ol
57	2	18.2	7	8 Q95945	Q95945 saccharomyc
58	2	18.2	7	11 Q63668	Q63668 rattus norv
59	2	18.2	7	12 Q62005	Q62005 transmissib
60	2	18.2	7	12 Q66113	Q66113 cherry leaf
61	2	18.2	7	15 Q8UE81	Q8UE81 human immun
62	2	18.2	8	2 Q09258	Q09258 synechococc
63	2	18.2	8	2 Q87471	Q87471 haemophilus
64	2	18.2	8	2 Q9Z1B9	Q9Z1B9 neisseria m
65	2	18.2	8	2 Q9R5R0	Q9R5R0 shigella dy
66	2	18.2	8	3 P87225	P87225 saccharomyc
67	2	18.2	8	4 Q15889	Q15889 homo sapien
68	2	18.2	8	4 Q15895	Q15895 homo sapien
69	2	18.2	8	4 Q15901	Q15901 homo sapien
70	2	18.2	8	4 Q15893	Q15893 homo sapien
71	2	18.2	8	4 Q9HCQ0	Q9HCQ0 homo sapien
72	2	18.2	8	4 Q9P0K3	Q9P0K3 homo sapien
73	2	18.2	8	5 Q9TWH6	Q9TWH6 perineris
74	2	18.2	8	5 Q02032	Q02032 lytechinus
75	2	18.2	8	6 Q9TRX8	Q9TRX8 bos taurus
76	2	18.2	8	6 Q9XSV1	Q9XSV1 canis famil
77	2	18.2	8	8 Q9T2Y3	Q9T2Y3 begonia for
78	2	18.2	8	8 Q94V82	Q94V82 varanus yuw
79	2	18.2	8	8 Q9TNN4	Q9TNN4 begonia for
80	2	18.2	8	8 Q94909	Q94909 locusta mig
81	2	18.2	8	8 Q94VE2	Q94VE2 varanus sal
82	2	18.2	8	8 Q9T2Y2	Q9T2Y2 begonia tai
83	2	18.2	8	8 Q94VA7	Q94VA7 varanus sal
84	2	18.2	8	8 Q94VB5	Q94VB5 varanus sal
85	2	18.2	8	10 Q9T2Y1	Q9T2Y1 begonia apt
86	2	18.2	8	10 Q9XGL9	Q9XGL9 begonia nan
87	2	18.2	8	10 Q9XGL8	Q9XGL8 begonia chi
88	2	18.2	8	10 Q9STD5	Q9STD5 begonia pal
89	2	18.2	8	11 Q9QV15	Q9QV15 rattus sp.

90 2 18.2 8 11 Q99NX9 Q99nx9 hydrochoeru
 91 2 18.2 8 11 Q9ET21 Q9et21 mus musculus
 92 2 18.2 8 11 Q9QVK5 Q9qvk5 rattus sp.
 93 2 18.2 8 12 Q83349 Q83349 murine coro
 94 2 18.2 8 12 Q89498 Q89498 murine hepa
 95 2 18.2 8 13 P87488 P87488 oncorhynch
 96 2 18.2 8 13 Q8J335 Q8j335 ficedula hy
 97 2 18.2 9 2 Q47556 Q47556 escherichia
 98 2 18.2 9 2 P72345 P72345 pseudomonas
 99 2 18.2 9 2 Q9R5R1 Q9r5r1 shigella dy
 100 2 18.2 9 2 Q46179 Q46179 clostridium

ALIGNMENTS

RESULT 1
 Q92Y76 ID Q92Y76 PRELIMINARY; PRT; 19 AA.
 AC Q92Y76; 19 AA.
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Macroteleia sp.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Pterygasteroidea;
 OC Scellionidae; Macroteleia.
 OC NCBI_TaxID=81090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99152621; PubMed=10028295;
 RA Dowdon M., Austin A.D.;
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
 RT the hymenoptera."
 RL Mcl. Biol. Evol. 16:298-309(1999).
 DR EMBL; AF082925; AAD17785.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2365 MW; 78C4D5D3A7ABCA1 CRC64;

Query Match 36.4%; Score 4; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0;

QY 4 NFKY 7
 DB 10 NFKY 13

RESULT 2
 Q4S615 ID Q4S615 PRELIMINARY; PRT; 8 AA.
 AC Q4S615;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE GntB protein (Fragment).
 GN GntB.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RC MEDLINE=94253000; PubMed=8195086;
 RA Ye R., Wong S.L.;
 RT "Transcriptional regulation of the Bacillus subtilis glucitol
 RT dehydrogenase gene."
 RL J. Bacteriol. 176:3314-3320(1994).
 DR EMBL; I16626; AAA20875.1; -.
 FT NON_TER 8

SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;
 Query Match 27.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0;

QY 2 PQN 4
 DB 6 PQN 8

RESULT 3
 Q9RQ49 ID Q9RQ49 PRELIMINARY; PRT; 8 AA.
 AC Q9RQ49; 8 AA.
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
 DE Nifs protein homolog (Fragment).
 GN NIFS.
 OS Buchnera aphidicola.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OC NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20022990; PubMed=1055290;
 RA Clark M.A., Moran N.A., Baumann P.;
 RT "Sequence evolution in bacterial endosymbionts having extreme base
 RT compositions."
 RL Mcl. Biol. Evol. 16:1586-1598(1999).
 DR EMBL; AF130814; AAF13805.1; -.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 992 MW; F3A73B5047672336 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0;

QY 7 KLP 9
 DB 2 KLP 4

RESULT 4
 Q99P40 ID Q99P40 PRELIMINARY; PRT; 8 AA.
 AC Q99P40;
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE Repressor of GATA (Fragment).
 GN ROG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57B6;
 RA Miao S., Ho I.;
 RT "ROG is a NF-AT target gene that partly rescues the phenotype of NF-
 RT ATC2/NF-ATc3 deficient th cells."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF335542; AAG59843.1; -.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 943 MW; FE3411B771B6C766 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0;

QY 1 MPQ 3

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
|||
Db 7 FYK 9

RESULT 9
Q8CG13 PRELIMINARY; PRT; 9 AA.
AC Q8CG13;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A (Fragment).
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Wyder K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;
RT "The mouse orthologue of the human ionotropic glutamate receptor-like gene (GRIN11A) maps to mouse chromosome 9.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDJ databases.
DR EMBL: AF462417; AA015648.1; -;
DR EMBL: AF462416; AA015648.1; JOINED.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;

Query Match 27.3%; Score 3; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 7 KLP 9

RESULT 10
Q9XBH3 PRELIMINARY; PRT; 10 AA.
AC Q9XBH3;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Calf-like protein (Fragment).
GN CLEP
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Oktad O.A., Hegna I., Lindbaeck T., Rishovd A.I., Kolsto A.B.;
RT "Genome organisation is not conserved between Bacillus cereus and Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL: AJ000394; CAB40625.1; -;
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1264 MW; D3757EC33339C9D6 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10

Db 1 LPQ 3
|||

RESULT 11
Q9URG1 PRELIMINARY; PRT; 11 AA.
AC Q9URG1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cytochrome c oxidase subunit 2 (fragment).
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92035059; PubMed=1657411;
RA Lemire E.G., Percy J.A., Correia J.M., Crowther B.M., Nargang F.E.;
RT "Alteration of the cytochrome c oxidase subunit 2 gene in the [exn-5] mutant of Neurospora crassa.";
RL Curr. Genet. 20:121-127(1991).
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1222 MW; 936B1558C7605DC5 CRC64;

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PQM 11
|||
Db 7 PQM 9

RESULT 12
Q53579 PRELIMINARY; PRT; 12 AA.
AC Q53579;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (fragment).
GN PUFA.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufa mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL: S97551; AAC60405.1; -;
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1627 MW; 0F92F6E8A70532B CRC64;

Query Match 27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
|||
Db 4 FYK 6

RESULT 13
Q9R8R9 PRELIMINARY; PRT; 13 AA.
AC Q9R8R9;

```

DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE C5a peptidase (Fragment).
OS SCPA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
ON NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=API.
RX MEDLINE=98398075; PubMed=9632622;
RA Berge A.; Rasmussen M.; Eijck L.;
RT "Identification of an insertion sequence located in a region encoding
RL virulence factors of Streptococcus pyogenes.";
DR EMBL; AF064540; AAC38768.1; -.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1603 MW; 5EDADCDAGCEEG723 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 6 KLP 8

RESULT 14
Q9QVL4 PRELIMINARY; PRT; 13 AA.
AC Q9QVL4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 90 kDa advanced glycosylation ENDPRODUCT binding protein
DE (Fragment).
DE Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=91341412; PubMed=1651976;
RA Yang Z.; Makita Z.; Horii Y.; Brunelle S.; Cerani A.; Sehajpal P.;
RA Suthanthiran M.; Viassara H.;
RT "Two novel rat liver membrane proteins that bind advanced
RT glycosylation endproducts: relationship to macrophage receptor for
RT glucose-modified proteins.";
RL J. Exp. Med. 174:515-524(1991).
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1466 MW; 349E02EEFCFE9AB7 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 4 KLP 6

RESULT 15
Q91777 PRELIMINARY; PRT; 14 AA.
AC Q91777;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Hypothetical 1.6 kDa protein.

```

```

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TIGSUE=Liver;
RX MEDLINE=90231335; PubMed=2330002;
RA Kajimoto Y.; Rotwein P.;
RT "Evolution of insulin-like growth factor I (IGF-I): structure and
RT expression of an IGF-I precursor from Xenopus laevis.";
RL Mol. Endocrinol. 4:217-226(1990).
DR EMBL; M29857; AAA70329.1; -.
KW Hypothetical protein.
SQ SEQUENCE 14 AA; 1627 MW; 3002F6B29B887BD7 CRC64;

Query Match 27.3%; Score 3; DB 13; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
DB 2 LPQ 4

RESULT 16
Q53580 PRELIMINARY; PRT; 15 AA.
AC Q53580;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
DE PUFA.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P.; Brand M.; Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufla
RT mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97552; AAC60406.1; -.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 2054 MW; 3561FE413591D31A CRC64;

Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
DB 4 FYK 6

RESULT 17
Q9X637 PRELIMINARY; PRT; 15 AA.
AC Q9X637;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Mert (Fragment).
DE MERT.
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=571;
RN [1]

```

```

DR EMBL AF131271; AAD37139.1; -.
DR InterPro:IPR003457; Transprt_MerT.
DR Pfam:PF02411; MerT; 1.
DR SMART:SM00015; MerT; 1.
DR TrEMBL:Q15155; MerT; 1.
SQ SEQUENCE 15 AA; 1492 MW; 65BFQCF9827A95D CRC64;
Query Match 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PQN 4
DB 4 PQN 6
RESULT 19
P82331 PRELIMINARY; PRT; 15 AA.
ID P82331
AC P82331;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT114) (Fragment).
DE Pisum sativum (Garden pea)
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OC NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=CV, DE GRACE, TISSUE=LEAF.
RX MEDLINE=20181728; PubMed=10715320;
RA Feltner J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341 (2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.7, ITS MW IS: 24.7 KDA.
KW Chloroplast; Thylakoid membrane.
FT DOMAIN 2 9 POLY-GLN.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 2000 MW; 2F1518C5051556D6 CRC64;
Query Match 27.3%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PQN 4
DB 8 PQN 10
RESULT 20
Q66174 PRELIMINARY; PRT; 15 AA.
ID Q66174
AC Q66174;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Surface protein (Fragment).
DE Human coronavirus (strain 229E).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OC NCBI_TaxID=11137;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=229E;
RX MEDLINE=89366667; PubMed=2701946;
RA Raabe T., Siddell S.J.

```

RT "Nucleotide sequence of the human coronavirus HCV 229E mRNA 4 and mRNA
 RT 5 unique regions.";
 RL Nucleic Acids Res. 17:6387-6387 (1989).
 DR EMBL; X15654; CAA33680.1; -;
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1834 MW; 8CE369AE77DC4015 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
 Db 3 KLP 5

RESULT 21
 ID Q9F9S4 PRELIMINARY; PRT; 16 AA.
 AC Q9F9S4;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Methylase HpyI (Fragment).
 GN M.HPYI
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Finland 9496;
 RA Van Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,
 RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;
 RT "Subtypes of the H. pylori iceA gene in Finnish pediatric patients.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF176822; AAG13123.1; -;
 DR InterPro; IPR002294; D12N5_mtfase.
 DR Pfam; PF02086; MethyltransfD12; 1.
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1944 MW; 7306DD11603768A CRC64;

Query Match 27.3%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKL 8
 Db 8 YKL 10

RESULT 22
 ID Q9R4X4 PRELIMINARY; PRT; 16 AA.
 AC Q9R4X4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Exotoxin A (Fragment).
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=94356232; PubMed=8075811;
 RA Wolz C., Lehmann R., Vasil M.L., Bischoff R., Doring G.;
 RT "A new extracellular protein of Pseudomonas aeruginosa PA103 regulated
 RT by regA".
 RL Microbiology 140:1755-1761 (1994).
 SQ SEQUENCE 16 AA; 1828 MW; D6C94C87E56823274 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
 Db 6 KLP 8

RESULT 23
 ID Q10748 PRELIMINARY; PRT; 16 AA.
 AC Q10748;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE 98 kDa cellulosomal protein (Fragment).
 OS Clostridium thermocellum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1515;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=JM20;
 RX MEDLINE=96267082; PubMed=8664281;
 RA Choi S.K., Ljungdahl L.G.;
 RT "Dissociation of the cellulosome of Clostridium thermocellum in the
 RT presence of ethylenediaminetetraacetic acid occurs with the formation
 RT of truncated polypeptides.";
 RL Biochemistry 35:4897-4905 (1996).
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1970 MW; D00573CE23802A15 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
 Db 6 KLP 8

RESULT 24
 ID Q28324 PRELIMINARY; PRT; 16 AA.
 AC Q28324;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Beta-x-globin (Fragment).
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=80227766; PubMed=6248519;
 RA Haynes J.R., Rostock P.R.Jr., Schon E.A., Gallagher P.M., Burks D.J.,
 RA Smith K., Lingrel J.B.;
 RT "The isolation of the beta-a-, beta-c-, and gamma-globin genes and a
 RT presumptive embryonic globin gene from a goat dna recombinant
 RT library".
 RL J. Biol. Chem. 255:6355-6367 (1980).
 DR EMBL; K00659; AAA30919.1; -;
 FT NON TER 1
 FT NON TER 16
 SQ SEQUENCE 16 AA; 1784 MW; D027A9E223320213 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNF 5


```

Db      12 QNF 14
||||
RESULT 25
Q34699 PRELIMINARY; PRT; 16 AA.
AC Q34699;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DSC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cob protein (Fragment).
GN COB
OS Helianthus annuus (Common sunflower).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Asterales; Asteraceae; Asteroidae;
OC Heliantheae; Helianthus.
OX NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMSBASO;
RA Koehler R.H.;
RL Submitted (OCT-1991) to the EMBL/GenBank/DBJ databases.
DR EMBL; X62592; CAA44477.1; -.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 16 AA; 1950 MW; A2980BEE7E26B700 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NPY 6
|||
DB 3 NPY 5

RESULT 26
Q9ETL3 PRELIMINARY; PRT; 17 AA.
ID Q9ETL3;
AC Q9ETL3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Methylase HpyI (Fragment).
GN M.HpyI OR HpyI.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Finland 18696;
RA Yan Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,
RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;
RT "Subtypes of the H. pylori iCEA gene in Finnish pediatric patients.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=7796;
RA Yan Y., Karhukorpi J., Lahti M., Sirvio A., Riipinen K., Kolho K.-L.,
RA Lindahl H., Verkasalo M., Fagerholm R., Rautelin H., Karttunen R.;
RT "the subtype of Helicobacter pylori iCEA gene in the Finnish pediatric
patients.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF176823; AAG13125.1; -.
DR EMBL; AF176090; AAG09227.1; -.
DR InterPro; IPR002294; D12N6_mtfase.
DR Pfam; PF02086; MethyltransfD12; 1.
FT NON_TER
SQ SEQUENCE 17 AA; 2058 MW; B2B306D1D1160376 CRC64;

```

```

Query Match 27.3%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
|||
DB 8 YKL 10

RESULT 27
Q46667 PRELIMINARY; PRT; 17 AA.
ID Q46667;
AC Q46667;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (fragment).
GN G6PD.
OS Macropus robustus robustus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=35580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97224585; PubMed=9060417;
RA Loebel D.A., Johnston P.G.;
RT "Analysis of the intron-exon structure of the G6PD gene of the
RT wallaroo (Macropus robustus) by polymerase chain reaction.";
RL Mamm. Genome 8:146-147(1997).
DR EMBL; U53779; AAC48792.2; -.
DR EMBL; U53778; AAC48792.2; JOINED.
DR InterPro; IPR001282; G6PD.
DR Pfam; PF02781; G6PD_C; 1.
FT NON_TER
SQ SEQUENCE 17 AA; 2039 MW; 3A5B76F61F908B21 CRC64;

Query Match 27.3%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
DB 14 KLP 16

RESULT 28
Q9QUY6 PRELIMINARY; PRT; 17 AA.
ID Q9QUY6;
AC Q9QUY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Oligodendrocyte-specific UDP-galactose:ceramide galactosyltransferase
DE (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE
RX MEDLINE=96085162; PubMed=8521863;
RA Schulte S., Stoffel W.;
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate
RT transporter. Copurification, separation and characterization of the two
RT glycoproteins.";
RL Eur. J. Biochem. 233:947-953(1995).
RN [2]
RP SEQUENCE 17 AA; 2017 MW; 0F92A645FFD7F828 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 LPQ 10
DB      5 LPQ 7

RESULT 29
Q9ZG42
ID Q9ZG42 PRELIMINARY; PRT; 18 AA.
AC Q9ZG42
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE Proline transport protein (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12 434E;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RT "Gene identification of Chlamydia trachomatis by random DNA
RT sequencing."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF087325; AAD04100.1; -.
FT NON TER 1
FT NON TER 18
SQ SEQUENCE 18 AA; 2236 MW; 55C4N82FD42CC261 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 FYK 7
DB      10 FYK 12

RESULT 30
Q9UC58
ID Q9UC58 PRELIMINARY; PRT; 18 AA.
AC Q9UC58
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Uronic-acid-rich protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95406991; PubMed=7676539;
RA Atmani F., Khan S.R.;
RT "Characterization of uronic-acid-rich inhibitor of calcium oxalate
RT crystallization isolated from rat urine."
RL Urol. Res. 23:95-101(1995).
SQ SEQUENCE 18 AA; 1867 MW; 15DE1BF37294B836 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LPQ 10
DB      3 LPQ 5

RESULT 31
Q16167
ID Q16167 PRELIMINARY; PRT; 18 AA.
AC Q16167
DT 01-NOV-1996 (TRENBLrel. 01, Created)

```

```

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE SERUM ALBUMIN (Fragment).
GN SERUM ALBUMIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94294404; PubMed=8022807;
RA Madison J., Galliano M., Watkins S., Minchiotti L., Porta F.,
RA Rossi A., Putnam F.W.;
RT "Genetic variants of human serum albumin in Italy: point mutants and a
RT carboxyl-terminal variant."
RL Proc. Natl. Acad. Sci. U.S.A. 91:6476-6480(1994).
DR EMBL: S70799; AAB31177.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 18 AA; 2089 MW; 2CCF6CSB0B08690B CRC64;

Query Match 27.3%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLP 9
DB      16 KLP 18

RESULT 32
Q8LNN9
ID Q8LNN9 PRELIMINARY; PRT; 18 AA.
AC Q8LNN9
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OSJNBA0040D23.8.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.H., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feidblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSJNBA0040D23 genomic sequence."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC074196; AAM76354.1; -.
DR Gramene; Q8LNN9; -.
KW Hypothetical protein.
SQ SEQUENCE 18 AA; 2005 MW; 23DBF28FF63C1608 CRC64;

Query Match 27.3%; Score 3; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLP 9
DB      9 KLP 11

RESULT 33
P70649
ID P70649 PRELIMINARY; PRT; 18 AA.
AC P70649;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)

```

```

DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Syntaxin 3 isoform D-1 (Fragment).
GN STX3 OR SYN3D.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=95321968; PubMed=7598732;
RA Ibaraki K., Horioka H.P., Morita T., Mori H., Sakimura K.,
RA Mishina M., Saisu H., Abe T.;
RT "Identification of four different forms of syntaxin 3.";
RL Biochem. Biophys. Res. Commun. 211:997-1005(1995).
DR EMBL; S78675; AAC17463.1; -.
DR MGD; MGI:103077; Stx3.
FT NON TER 1
SQ SEQUENCE 18 AA; 2073 MW; 289FBCA5D5495155 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 4 KLP 6

RESULT 34
ID Q9QV11 PRELIMINARY; PRT; 18 AA.
AC Q9QV11;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92031479; PubMed=1931964;
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
RT "Structural and functional correlates of sucrase-alpha-dextrinase in
RT intact brush border membranes.";
RL Biochemistry 30:10399-10408(1991).
FT NON TER 1
FT NON TER 18
SQ SEQUENCE 18 AA; 2122 MW; 68FFIABA87B24E49 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 2 KLP 4

RESULT 35
ID P70650 PRELIMINARY; PRT; 18 AA.
AC P70650;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Syntaxin 3 isoform D-2 (Fragment).
GN STX3 OR SYN3D.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=95321968; PubMed=7598732;
RA Ibaraki K., Horioka H.P., Morita T., Mori H., Sakimura K.,
RA Mishina M., Saisu H., Abe T.;
RT "Identification of four different forms of syntaxin 3.";
RL Biochem. Biophys. Res. Commun. 211:997-1005(1995).
DR EMBL; S78677; AAC17462.1; -.
DR MGD; MGI:103077; Stx3.
FT NON TER 1
SQ SEQUENCE 18 AA; 2043 MW; 289FBCA184495155 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 4 KLP 6

RESULT 36
ID Q9PRR7 PRELIMINARY; PRT; 18 AA.
AC Q9PRR7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE OVOFACTOR-1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=96068942; PubMed=8534988;
RA Nakamura T., Saico T., Kitazawa H., Takeuchi S., Itoh T.;
RT "Isolation of a new minor protein (ovofactor-1), which has a cell
RT growth promoting activity, from hen's egg white by heparin affinity
RT chromatography.";
RL Biochem. Biotechnol. Biochem. 59:1946-1948(1995).
SQ SEQUENCE 18 AA; 2056 MW; 56EE4AEED17C174 CRC64;

Query Match 27.3%; Score 3; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 5 KLP 7

RESULT 37
ID Q8NFL2 PRELIMINARY; PRT; 19 AA.
AC Q8NFL2;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Prolyl isomerase (Fragment).
OS Homo sapiens (Human).
ON Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22095969; PubMed=12101225;
RA Ryo A., Liou Y.C., Wulf G., Nakamura M., Lee S.W., Lu K.P.;

```

RT "PIN1 Is an E2F Target Gene Essential for Neu/Ras-Induced
 RT Transformation of Mammary Epithelial Cells.";
 RL Mol. Cell. Biol. 22:5281-5295(2002).
 DR EMBL; AF501321; AAM81970.1; -.
 KW Isomerase.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2235 MW; 1C4FC381C8A0F17F CRC64;

Query Match 27.3%; Score 3; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
 DB 6 KLP 8

RESULT 38
 Q9UDB7 PRELIMINARY; PRT; 19 AA.
 AC Q9UDB7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE CD8 B2TA chain isoform S BEVA1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93170376; PubMed=8436166;
 RA DiSanto J.P., Smith D., de Bruin D., Lacy E., Flomenberg N.; loci."
 RT "Transcriptional diversity at the duplicated human CD8 beta loci."
 RL Eur. J. Immunol. 23:320-326(1993).
 SQ SEQUENCE 19 AA; 2527 MW; D1405FE2CEEBA419 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
 DB 17 FYK 19

RESULT 39
 Q9TWD0 PRELIMINARY; PRT; 19 AA.
 AC Q9TWD0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Sialoprotein I (Fragment).
 OS Sphaerecthinus granulatus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
 OC Sphaerecthinus.
 OX NCBI_TaxID=39374;
 RN [1]_TaxID=39374;
 RP SEQUENCE
 RX MEDLINE=96428846; PubMed=8831948;
 RA Karananos N.K., Manouras A., Anagnostides S., Makatsori E.,
 RA Tsengidis T., Antonopoulos C.A.;
 RT "Isolation, biochemical and immunological characterisation of two sea
 RT urchin glycoproteins bearing sulphated poly(sialic acid)
 RT polysaccharides rich in N-glycolyl neuraminic acid."
 RL Biochimie 78:171-182(1996).
 SQ SEQUENCE 19 AA; 2265 MW; 38FFDEB1A033E850 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFY 6
 DB 5 NFY 7

RESULT 40
 Q31687 PRELIMINARY; PRT; 19 AA.
 ID Q31687;
 AC Q31687;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ATPase subunit 8 (Fragment).
 GN ATP8.
 GN Artemia parthenogenetica.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
 OC Artemiidae; Artemia.
 OX NCBI_TaxID=6663;
 RN [1]_TaxID=6663;
 RP SEQUENCE FROM N.A.
 RX STRAIN=La Mata;
 RX MEDLINE=94223692; PubMed=8169960;
 RA Perez M.L., Valverde J.R., Batuecas B., Amat F., Marco R., Garesse R.;
 RT "Speciation in the artemia genus: mitochondrial DNA analysis of
 RT bisexual and parthenogenetic brine shrimps.";
 RL J. Mol. Evol. 38:156-168(1994).
 DR EMBL; X67263; CAA47685.1; -.
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 19 AA; 2246 MW; 41922AD313E087E3 CRC64;
 Query Match 27.3%; Score 3; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PQM 11
 DB 2 PQM 4

RESULT 41
 Q9XMB5 PRELIMINARY; PRT; 19 AA.
 ID Q9XMB5;
 AC Q9XMB5;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ORF165 (Fragment).
 OS Aegilops tauschii (Aegilops squarrosa).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Aegilops.
 OX NCBI_TaxID=37682;
 RN [1]_TaxID=37682;
 RP SEQUENCE FROM N.A.
 RC STRAIN=KU29;
 RA Tsukamoto N., Asakura N., Takumi S., Mori N., Nakamura C.;
 RT "The presence of paternal sub-genomic mitochondrial DNA copies in the
 RT nucleus-cytoplasm hybrids of tetraploid wheat with the cytoplasm of
 RT Aegilops squarrosa.";
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF142479; AAD3734.1; -.
 DR InterPro; IPR003319; YMF19.
 DR Pfam; PF02326; YMF19; 1.
 KW Mitochondrion.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2394 MW; F435DB3B595D3ADC CRC64;
 Query Match 27.3%; Score 3; DB 8; Length 19;

Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQP 3
|||
Db 1 MQP 3

RESULT 42

Q9DFN3 PRELIMINARY; PRT; 19 AA.

AC Q9DFN3;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Glycogen myosphosphorylase (Fragment).
OS Gallichthys mirabilis (Long-jawed mudsucker).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidae;
OC Gobiidae; Gallichthys.
OX NCBI_TaxID=8222;
RN [1]
RP SEQUENCE FROM N.A.
RX Tissue=Skeletal white muscle;
RX MEDLINE=21117151; PubMed=1172064;
RA Gracey A.Y., Troll J.V., Somero G.N.;
RT "Hypoxia-induced gene expression profiling in the euryoxic fish
RT Gallichthys mirabilis.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1993-1998(2001).
DR EMBL; AF266202; AAG13322.1; -.
FT NON TER 1
SQ SEQUENCE 19 AA; 2215 MW; 3554ECD38909FBAA CRC64;

Query Match 27.3%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 13 KLP 15

RESULT 43

Q9X629 PRELIMINARY; PRT; 20 AA.

AC Q9X629;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE MerT (Fragment).
GN MERT.
OS unidentified enterobacterium 2705A.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae;
OX NCBI_TaxID=93168;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=2705A;
RX MEDLINE=9708220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RT bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=2705A;
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RT gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]

RP SEQUENCE FROM N.A.
RC STRAIN=2705A;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
RT mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131264; AAD37125.1; -.
FT NON TER 20
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
|||
Db 9 PQN 11

RESULT 44

Q9X632 PRELIMINARY; PRT; 20 AA.

AC Q9X632;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE MERT (Fragment).
GN MERT.
OS Pseudomonas aeruginosa.
OG Plasmid pCER100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9708220; PubMed=9055422;
RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
RT "Phylogeny of mercury resistance (mer) operons of gram-negative
RT bacteria isolated from the fecal flora of primates.";
RL Appl. Environ. Microbiol. 63:1066-1076(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98027386; PubMed=9361435;
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "Association of mercury resistance with antibiotic resistance in the
RT gram-negative fecal bacteria of primates.";
RL Appl. Environ. Microbiol. 63:4494-4503(1997).
RN [3]

RP SEQUENCE FROM N.A.
RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
RT "15-bp tandem repeats occur at a sharp transition in gc content in the
RT mer operon.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131269; AAD37135.1; -.
FT NON TER 20
SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
|||
Db 9 PQN 11

RESULT 45

Q9X634 PRELIMINARY; PRT; 20 AA.

AC Q9X634;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE MerT (Fragment).
 GN MERT.
 OS Serratia marcescens.
 OG Plasmid pR831b.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97208220; PubMed=9055422;
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative
 RT bacteria isolated from the fecal flora of primates.";
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98027386; PubMed=9361435;
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "Association of mercury resistance with antibiotic resistance in the
 RT gram-negative fecal bacteria of primates.";
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the
 RT mer operon.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF131270; AAD37137.1; -.
 KW Plasmid.
 FT NON-TER 20 20
 SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;
 Query Match 27.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PQN 4
 Db 9 PQN 11
 RESULT 46
 Q9WVU7 PRELIMINARY; PRT; 20 AA.
 AC Q9WVU7
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE MerT (Fragment).
 GN MERT.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=92H, 2701, 343, and 47H;
 RC MEDLINE=97208220; PubMed=9055422;
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative
 RT bacteria isolated from the fecal flora of primates.";
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=92H, 2701, 343, and 47H;
 RC MEDLINE=98027386; PubMed=9361435;
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "Association of mercury resistance with antibiotic resistance in the
 RT gram-negative fecal bacteria of primates.";
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the
 RT mer operon.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF131267; AAD37131.1; -.
 FT NON-TER 20 20
 SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;
 Query Match 27.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PQN 4
 Db 9 PQN 11
 RESULT 48
 Q46499 PRELIMINARY; PRT; 20 AA.
 ID Q46499

RC STRAIN=92H, 2701, 343, and 47H;
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the
 RT mer operon.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF131268; AAD37133.1; -.
 DR EMBL; AF131263; AAD37124.1; -.
 DR EMBL; AF131265; AAD37127.1; -.
 DR EMBL; AF131266; AAD37129.1; -.
 FT NON-TER 20 20
 SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;
 Query Match 27.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PQN 4
 Db 9 PQN 11
 RESULT 47
 Q9X630 PRELIMINARY; PRT; 20 AA.
 ID Q9X630
 AC Q9X630
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE MerT (Fragment).
 GN MERT.
 OS Lacteria adcarboxylata.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Lactercia.
 OX NCBI_TaxID=83655;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=533H;
 RC MEDLINE=97208220; PubMed=9055422;
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;
 RT "Phylogeny of mercury resistance (mer) operons of gram-negative
 RT bacteria isolated from the fecal flora of primates.";
 RL Appl. Environ. Microbiol. 63:1066-1076(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=533H;
 RC MEDLINE=98027386; PubMed=9361435;
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "Association of mercury resistance with antibiotic resistance in the
 RT gram-negative fecal bacteria of primates.";
 RL Appl. Environ. Microbiol. 63:4494-4503(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=533H;
 RA Wireman J., Liebert C.A., Smith T., Summers A.O.;
 RT "15-bp tandem repeats occur at a sharp transition in gc content in the
 RT mer operon.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF131267; AAD37131.1; -.
 FT NON-TER 20 20
 SQ SEQUENCE 20 AA; 2061 MW; 7ED4CC01A34A5F87 CRC64;
 Query Match 27.3%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 PQN 4
 Db 9 PQN 11
 RESULT 48
 Q46499 PRELIMINARY; PRT; 20 AA.
 ID Q46499

```

AC Q46499;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TRENBLrel. 01, Last annotation update)
DE Periplasmic (Fragment).
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobivibrionales;
OC Desulfobivibrionaceae; Desulfobivibrio.
OX NCBI_TaxID=876;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Me;
RA Lim S.K., Lee S.J., Kim B.H.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U49192; AAA91808.1; -.
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 20 AA; 1996 MW; E93207D26C22999B CRC64;

Query Match 27.3%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
DB 9 LPQ 11

RESULT 49
Q8NFW3 PRELIMINARY; PRT; 20 AA.
ID Q8NFW3
AC Q8NFW3
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Synovial sarcoma SVT/SSX1 fusion protein (Fragment).
GN SVT/SSX1 FUSION.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tamborini E., Agus V., Pierotti M.A., Pilotti S., Rosai J.;
RT "Diversity of both fusion transcripts and rearrangement type in
RT synovial sarcoma.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402619; AAM95901.1; -.
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2377 MW; F1534C73F9108E83 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
DB 12 PQN 14

RESULT 50
Q8IZ13 PRELIMINARY; PRT; 20 AA.
ID Q8IZ13
AC Q8IZ13
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE LEF1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RA Filali M., Cheng N., Abbot D., Leontiev V., Engelhardt J.F.;
RT "Wnt-3A/b-Catenin Signaling Induces Transcription from the LEF-1
RT promoter.";
RL J. Biol. Chem. 0:0-0(2002).
DR EMBL; AV129650; AAN06089.1; -.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 1761 MW; E4F1891E56FBA675 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQ 3
DB 1 MPQ 3

RESULT 51
Q9TW18 PRELIMINARY; PRT; 20 AA.
ID Q9TW18
AC Q9TW18
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Major cuticular protein (Fragment).
OS Ceratitis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritoidea; Tephritidae; Ceratitis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE.
RX MEDLINE=95279142; PubMed=7759285;
RX Tsiliras A., Koromantzou E., Allen G., Dimitriadis G.;
RT "Partial N-terminal sequences of larval cuticular proteins from the
RT dipteran Ceratitis capitata.";
RL Hereditas 122:79-83(1995).
SQ SEQUENCE 20 AA; 2408 MW; 2BC25E2F9ECL5A80 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFY 6
DB 17 NFY 19

RESULT 52
Q9S8A8 PRELIMINARY; PRT; 20 AA.
ID Q9S8A8
AC Q9S8A8
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE Gamma-35 SECALIN isoform P9-12 (COELIAC immunoreactive protein)
DE (Fragment)
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE.
RX MEDLINE=96283789; PubMed=8679669;
RX Rocher A., Calero M., Soriano F., Mendez E.;
RT "Identification of major rye secalins as coeliac immunoreactive
RT proteins.";
RL Biochim. Biophys. Acta 1295:13-22(1996).
SQ SEQUENCE 20 AA; 2249 MW; 96D3DA4098BB5C80 CRC64;

```

Query Match 27.3%; Score 3; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 ||
 Db 18 LPQ 20

RESULT 53
 P83308 PRELIMINARY; PRT; 5 AA.
 AC P83308; 2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE FMRamide-like neuropeptide (LPLRF-amide).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=Brain;
 RX PubMed=6137771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FMRamide."
 RL Nature 305:328-330(1983).
 CC -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 18.2%; Score 2; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 ||
 Db 1 LP 2

RESULT 54
 O50556 PRELIMINARY; PRT; 7 AA.
 AC O50556;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE GLYA (Fragment).
 GN GLYA.
 OS Actinobacillus actinomycetomycitans (Haemophilus
 OS actinomycetomycitans).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Actinobacillus.
 OX NCBI_TaxID=714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33384;
 RX MEDLINE=96355846; PubMed=8751884;
 RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
 RA Kraig E.;
 RT "cis Elements and trans factors are both important in strain-specific
 RT regulation of the leukotoxin gene in Actinobacillus
 RT actinomycetomycitans."
 RL Infect. Immun. 64:3451-3460(1996).
 DR EMBL; U51862; AAB88721.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 ||
 Db 3 LP 4

RESULT 55
 O8GL00 PRELIMINARY; PRT; 7 AA.
 AC O8GL00; 2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE PF-50 protein (Fragment).
 GN PF-50.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OG Plasmid group cp32-13.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CA15;
 RA Stevenson B., Miller J.C.;
 RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
 RT prophages: conservation amidst diversity.";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY142106; AANI7857.1; -.
 KW Plasmid.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
 ||
 Db 5 KL 6

RESULT 56
 O98866 PRELIMINARY; PRT; 7 AA.
 AC O98866;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DE Cytochrome b/f subunit IV (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86120353; PubMed=3003688;
 RA Siljeh-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
 RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
 RT protein S11 and RNA polymerase alpha-subunit.";
 RL Nucleic Acids Res. 14:1029-1044(1986).
 DR EMBL; X03496; CAA27215.1; -.
 KW Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
 Db 1 NF 2

RESULT 57

Q95945 PRELIMINARY; PRT; 7 AA.
 AC Q95945;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DE Inside intron 5 (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OG Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D273-10B;
 RX MEDLINE=8106985; PubMed=6254986;
 PA Bonitz S.G., Coruzzi G., Thallentfeld B., Tzagoloff A., Macino G.;
 PT "Assembly of the mitochondrial membrane system: Structure and
 RT nucleotide sequence of the gene coding for subunit 1 of yeast
 RT cytochrome oxidase.";
 RL J. Biol. Chem. 255:11927-11941(1980).
 DR EMBL; V00694; CAA24066.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 859 MW; 75E7232362CDC460 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
 Db 5 KL 6

RESULT 58

Q63668 PRELIMINARY; PRT; 7 AA.
 AC Q63668;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE ORF2 protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 EX MEDLINE=95396550; PubMed=7667072;
 PA Mandon B., Bellanger A.C., Elalouf J.M.;
 RT "Inverse-PCR-mediated cloning of the promoter for the rat vasopressin
 RT V2 receptor gene.";
 RL Fliugers Arch. 430:112-18(1995).
 DR EMBL; X83264; CAA58237.1; -.
 SQ SEQUENCE 7 AA; 703 MW; 75A767287DC6D6F0 CRC64;

Query Match 18.2%; Score 2; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 Db 5 LP 6

RESULT 59

Q66205 PRELIMINARY; PRT; 7 AA.
 AC Q66205;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE Membrane protein (1 is 3rd base in codon) (Fragment).
 OS Transmissible gastroenteritis virus
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID=11149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FS772/70;
 RX MEDLINE=8216185; PubMed=2835592;
 PA Britton P., Carmenes R.S., Page K.W., Garwes D.J., Parra F.;
 RT "Sequence of the Nucleoprotein Gene from a Virulent British Field
 RT Isolate of Transmissible Gastroenteritis Virus and its Expression in
 RT Saccharomyces Cerevisiae.";
 RL Mol. Microbiol. 2:89-99(1988).
 DR EMBL; Y00542; CAA68606.1; -.
 KW NON_TER 1
 SQ SEQUENCE 7 AA; 869 MW; 72C691E727233B70 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
 Db 2 KL 3

RESULT 60

Q66113 PRELIMINARY; PRT; 7 AA.
 AC Q66113;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE C-terminus of the viral replicase (Fragment).
 OS Cherry leaf roll virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
 OC Nepovirus.
 OX NCBI_TaxID=12615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Walnut;
 RA Borja M.;
 RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Walnut;
 RX MEDLINE=96124520; PubMed=8560786;
 RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
 RT "Long, nearly identical untranslated sequences at the 3' terminal
 RT regions of the genomic RNAs of cherry leafroll virus (walnut
 RT strain).";
 RL Virus Genes 10:245-252(1995).
 DR EMBL; Z34365; CAA84019.1; -.
 KW NON_TER 1
 SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 18.2%; Score 2; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
 Db 5 LP 6

```

RESULT 61
QJUE81 PRELIMINARY; PRT; 7 AA.
ID Q8UE81
AC Q8UE81
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=487;
RX MEDLINE=22056123; PubMed=12060770;
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics
approach to predicting phenotype from genotype.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAC32344.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 18.2%; Score 2; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3
Db 1 PQ 2

RESULT 62
O09258 PRELIMINARY; PRT; 8 AA.
ID O09258
AC O09258
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NifH (Fragment).
GN NIFH.
OS Synechococcus sp. (strain PCC 8801 / RP-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RP-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
RP-1.";
RT Microbiology 145:743-753(1999).
DR EMBL; AF001780; AAC33369.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 985 MW; F16B59CDD046C406 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FY 6
Db 6 FY 7

RESULT 63
O87471 PRELIMINARY; PRT; 8 AA.
ID O87471
AC O87471
DT 01-NOV-1998 (TREMBlrel. 08, Created)

```

```

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE H1FA (Fragment).
GN H1FA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bagan;
RX MEDLINE=98389689; PubMed=9721313;
RA Mhlanga-Mutagadura T., Morlin G., Smith A.L., Eisenstark A.,
Golomb M.;
RT "Evolution of the major pilus gene cluster of haemophilus
RT influenzae.";
RT J. Bacteriol. 180:4693-4703(1998).
DR EMBL; AF071762; AAC35830.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 876 MW; DAB44451A7272325 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
Db 2 KL 3

RESULT 64
Q9ZIE9 PRELIMINARY; PRT; 8 AA.
ID Q9ZIE9
AC Q9ZIE9
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE Carbamoyl-phosphate synthase subunit B (Fragment).
GN CARB.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1527;
RX MEDLINE=95291461; PubMed=7773412;
RA Lawson F.S., Billows F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RL Microbiology 141:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1527;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029363; AAC78449.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 988 MW; FA372AB1B4032766 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MP 2
Db 1 MP 2

RESULT 65

```

```

Q9R5R0
ID Q9R5R0 PRELIMINARY; PRT; 8 AA.
AC Q9R5R0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 11,500 DA product of ORF4 (Fragment).
OS Shigella dysenteriae
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=622;
RN [1]_
RP SEQUENCE.
RX MEDLINE=9208268; PubMed=1660923;
RA Polard P., Prere M.F., Chandler M., Fayet O.;
RT "Programmed translational frameshifting and initiation at an A/U codon
RT in gene expression of bacterial insertion sequence IS911.";
RL J. Mol. Biol. 222:465-477(1991).
FT NON_TER 8
SQ SEQUENCE 8 AA; 935 MW; F4C5B9C45AE33336 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 5 NF 6

RESULT 66
P87225 PRELIMINARY; PRT; 8 AA.
ID P87225;
AC P87225;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GINII protein (Fragment).
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]_
RP SEQUENCE FROM N.A.
RA Wedler H., Wedler E., Scharfe M., Wambutt R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]_
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z73169; CAA97518.2; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1019 MW; 4E21A9C449D5B73B CRC64;

Query Match 18.2%; Score 2; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NF 5
DB 5 NF 6

RESULT 67
Q15889 PRELIMINARY; PRT; 8 AA.
ID Q15889;
AC Q15889;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP15H8) (Fragment).
OS Homo sapiens (Human).
OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.;
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32070; AAA73879.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 865 MW; 0474472325A761E7 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
DB 5 KL 6

RESULT 68
Q15895 PRELIMINARY; PRT; 8 AA.
ID Q15895;
AC Q15895;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A10A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.;
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32075; AAA73885.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
DB 3 QM 4

RESULT 69
Q15901 PRELIMINARY; PRT; 8 AA.
ID Q15901;
AC Q15901;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP7B11B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.;
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32075; AAA73885.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
DB 3 QM 4

```

```

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.;
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32070; AAA73879.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 865 MW; 0474472325A761E7 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KL 8
DB 5 KL 6

RESULT 68
Q15895 PRELIMINARY; PRT; 8 AA.
ID Q15895;
AC Q15895;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A10A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.;
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32075; AAA73885.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
DB 3 QM 4

RESULT 69
Q15901 PRELIMINARY; PRT; 8 AA.
ID Q15901;
AC Q15901;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP7B11B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.;
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32075; AAA73885.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QM 11
DB 3 QM 4

```

```

RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32080; AAA73891.1; -.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 860 MW; 37D72878676729CB CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
DB 3 LP 4

RESULT 70
Q15893 PRELIMINARY; PRT; 8 AA.
AC Q15893;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32073; AAA73883.1; -.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QN 4
DB 2 QN 3

RESULT 71
Q9HCO0 PRELIMINARY; PRT; 8 AA.
AC Q9HCO0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphodiesterase 10A7 (PDE10A7) (Fragment).
GN HSPDE10A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20453115; PubMed=10998054;

RA Fujishige K., Kotera J., Yuasa K., Omori K.;
RT "The human phosphodiesterase PDE10A gene. Genomic organization and
RT evolutionary relatedness with other PDEs containing GAP domains.";
RL Eur. J. Biochem. 267:5943-5951(2000).
DR EMBL; AB041779; BAB16368.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 966 MW; FD4B19D5A6C76446 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQ 3
DB 3 PQ 4

RESULT 72
Q9P0K3 PRELIMINARY; PRT; 8 AA.
AC Q9P0K3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE cGMP-specific phosphodiesterase PDE5A2 (Fragment).
GN PDE5A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20145478; PubMed=10679249;
RA Lin C.S., Lau A., Tu R., Lue T.F.;
RT "Identification of three alternative first exons and an intronic
RT promoter of human PDE5A gene.";
RL Biochem. Biophys. Res. Commun. 268:596-602(2000).
DR EMBL; AF151195; AAF40302.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 908 MW; E8A33AA879D76726 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LP 9
DB 2 LP 3

RESULT 73
Q9TWH6 PRELIMINARY; PRT; 8 AA.
AC Q9TWH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE BIOACTIVE peptide P4=PUTATIVE ESOPHAGEAL NEUROREGULATOR.
OS Perinereis vancaurica.
OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
OC Phyllocorida; Nereididae; Perinereis.
OX NCBI_TaxID=6355;
RN [1]
RP SEQUENCE
RC MEDLINE=95323338; PubMed=7599979;
RA Takahashi T., Furukawa Y., Muneoka Y., Matsushima O., Ikeda T.,
RA Fujita T., Minakata H., Nomoto K.;
RT "Isolation and characterization of four novel bioactive peptides from
RT a polychaete annelid, Perinereis vancaurica.";
RL Comp. Biochem. Physiol. C, Pharmacol. Toxicol. Endocrinol. 110:297-
RL 304(1995).
SQ SEQUENCE 8 AA; 989 MW; 954772CAA87B0B59 CRC64;

```

Query Match 18.2%; Score 2; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FY 6
 ||
 Db 1 FY 2

RESULT 74

002032 PRELIMINARY; PRT; 8 AA.

AC 002032;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Metallothionein (Fragment).
 GN LPM2.
 OS Lytechinus pictus (Painted sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
 OC Lytechinus.
 OX NCBI_TaxID=7653;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97264487; PubMed=9110313;
 RA Cserjesi P., Fang H., Brandhorst B.P.;
 RT "Metallothionein gene expression in embryos of the sea urchin
 Lytechinus pictus.";
 RL Mol. Reprod. Dev. 47:39-46(1997).
 DR EMBL; U83400; AAB58320.1; -.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 823 MW; EBD5A2C1F7686766 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MP 2
 ||
 Db 1 MP 2

RESULT 75

Q9TRX8 PRELIMINARY; PRT; 8 AA.

AC Q9TRX8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Osteopontin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91282766; PubMed=1676261;
 RA Prince C.W., Dickie D., Krundieck C.L.;
 RT "Osteopontin, a substrate for transglutaminase and factor XIII
 activity.";
 RL Biochem. Biophys. Res. Commun. 177:1205-1210 (1991).
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LP 9
 |||

Db 1 LP 2

Search completed: November 25, 2003, 18:25:21
 Job time : 28.5553 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 35.633 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-6
Perfect score: 11
Sequence: 1 MPQNFYKLPQM 11

Scoring table: OLLGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	11	100.0	11	22	AA1982.DAT
2	11	100.0	11	22	AA1983.DAT
3	11	100.0	11	22	AA1984.DAT
4	11	100.0	11	22	AA1985.DAT
5	11	100.0	11	22	AA1986.DAT
6	11	100.0	11	22	AA1987.DAT
7	11	100.0	11	22	AA1988.DAT
8	11	100.0	11	22	AA1989.DAT
9	5	45.5	20	23	AA1990.DAT

10	4	36.4	4	24	ABJ36686	G protein coupled
11	4	36.4	5	18	AAW12496	Interleukin-6 anta
12	4	36.4	7	19	AAW48024	AE114 analogue eff
13	4	36.4	7	19	AAW47992	AE114 analogue eff
14	4	36.4	7	23	ABH80641	Clostridium botuli
15	4	36.4	8	20	AAV53386	E6 protein epitope
16	4	36.4	8	20	AAV40373	Amino acid sequenc
17	4	36.4	8	20	AAV426724	HPV-derived lipope
18	4	36.4	8	20	AAV10348	T cell epitope/MHC
19	4	36.4	8	22	ABP11965	HIV A02 super moti
20	4	36.4	8	22	ABP18445	HIV B62 super moti
21	4	36.4	8	23	ABG90030	MHC class I molecu
22	4	36.4	9	14	AAE43729	MHC class I allele
23	4	36.4	9	15	AAE59196	Peptide fragment (
24	4	36.4	9	17	AAW49468	Human leucocyte an
25	4	36.4	9	18	AAW39312	HPV16 E6-encoded C
26	4	36.4	9	19	AAW78890	Human papillomavir
27	4	36.4	9	19	AAW54754	Peptide from HPV 1
28	4	36.4	9	19	AAW54509	Synthetic polypept
29	4	36.4	9	20	AAV53385	E6 protein epitope
30	4	36.4	9	20	AAV40372	Amino acid sequenc
31	4	36.4	9	20	AAV26723	HPV-derived lipope
32	4	36.4	9	20	AAV10560	HLA class I motif
33	4	36.4	9	21	AAE33702	MHC class I associ
34	4	36.4	9	21	AAE66471	HLA-A2-binding HPV
35	4	36.4	9	22	AAE07583	Human PUMP-1 pepti
36	4	36.4	9	22	AAE23452	HIV peptide SEQ ID
37	4	36.4	9	22	AAE23484	HIV peptide SEQ ID
38	4	36.4	9	22	AAE93798	Human papilloma vi
39	4	36.4	9	22	AAE95948	MHC class-I associ
40	4	36.4	9	23	ABG80243	MHC class I molecu
41	4	36.4	9	23	ABG80674	Human tumour-associ
42	4	36.4	9	24	AAQ22817	HPV-16 E6 peptide,
43	4	36.4	9	24	AAJ20153	MHC binding peptid
44	4	36.4	9	24	ABU03246	Human expressed pr
45	4	36.4	9	24	ABE99353	Peptide derived fr
46	4	36.4	10	14	AAE43305	HIV-1 IIB gp120 m
47	4	36.4	10	19	AAW76930	Fusion immunoglob
48	4	36.4	10	20	AAE52988	Human papillomavir
49	4	36.4	10	22	AAU70117	Human calcitonin D
50	4	36.4	11	13	AAE28392	Bradykinin recepto
51	4	36.4	11	19	AAW76927	Fusion immunoglob
52	4	36.4	12	18	AAW15379	Salmonella secrete
53	4	36.4	12	23	ABP46973	Human BlyS binding
54	4	36.4	12	24	ABE97425	HAB186/CD147 prote
55	4	36.4	14	20	ABE88428	Human guanine nucl
56	4	36.4	14	22	AAE97223	Human peptide #498
57	4	36.4	14	23	AAU69635	Cell death protect
58	4	36.4	15	9	AAE81956	Peptide immunogen
59	4	36.4	15	14	AAE43901	HIV-1 IIB gp120 m
60	4	36.4	15	14	AAE43907	HIV-1 RF gp120 mon
61	4	36.4	15	16	AAE72007	Biologically activ
62	4	36.4	15	20	AAW99862	HIV-1 gp120 V1/V2
63	4	36.4	15	20	AAW87621	Epitope of HIV-1 g
64	4	36.4	15	20	AAW72822	HIV-1 gp120 monocl
65	4	36.4	15	23	ABE98878	Proline rich gamma
66	4	36.4	15	24	ABE98946	Translation initia
67	4	36.4	16	20	AAV29841	HIV HXB2 V3 fusion
68	4	36.4	17	19	AAW47339	Apolipoprotein B t
69	4	36.4	17	20	AAE55381	Apolipoprotein fra
70	4	36.4	17	20	AAV23106	Alipoprotein B try
71	4	36.4	18	19	AAW23967	Peptide GFS2. Syn
72	4	36.4	18	23	ABU00634	B lymphocyte stimu
73	4	36.4	18	23	ABG33495	B lymphocyte stimu
74	4	36.4	19	21	AAW79176	Fusion immunoglob
75	4	36.4	19	21	AAE85068	Immunogenic peptid
76	4	36.4	19	22	ABE53432	Human liver peptid
77	4	36.4	19	22	ABE38586	Peptide #6092 enco
78	4	36.4	19	22	AAE59212	Human brain expres
79	4	36.4	19	22	AAW71747	Human bone marrow
80	4	36.4	19	22	AAW32039	Peptide #6076 enco
81	4	36.4	19	23	ABG41561	Human peptide enco
82	4	36.4	19	23	AAU69634	Cell death protect

83 C108G epitopic pep
84 Fusion immunoglobu
85 Fusion immunoglobu
86 Human HIV-1 Th-CTL
87 Human HIV-1 Th-CTL
88 Human HIV-1 Th-CTL
89 HPV 16 E6 protein
90 Cell death protect
91 Peptide substrate
92 Peptide component
93 Peptide component
94 Ketone analogue pr
95 Human tumour suppr
96 Peptide intermedia
97 Protected oligopep
98 Oxirane compound w
99 Geminivirus Rep pe
100

ALIGNMENTS

RESULT 1
ID AAB72251 standard; peptide; 11 AA.
XX AC AAB72251;
XX DT 14-MAY-2001 (first entry)
XX DE Colostrinin derived cytokine inducing peptide SEQ ID 6.
XX KW Colostrinin; immune response; cytokine; blood cell proliferation;
XX KW central nervous system disorder; neurological disorder; mental disorder;
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
XX KW neurosis; infection.
XX OS Synthetic.
XX PN WO200111937-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US22818.
XX PR 17-AUG-1999; 99US-0149311.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PA (REGE-) REGEN THERAPEUTICS PLC.
XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX PT Inducing a cytokine and modulating an immune response, useful for
XX PT treating central nervous system diseases and bacterial and viral
XX PT infections, comprises administering colostrinin as an immunological
XX PT regulator -
XX PS Claim 1; Page 34; 50pp; English.
XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
XX CC a proline rich polypeptide aggregate contained in colostrum. The
XX CC peptides have immune response modulatory activity, and are capable of
XX CC inducing cytokines. Colostrinin and its derived peptides are useful for
XX CC inducing cytokine production, for modulating an immunological response
XX CC and for inducing blood cell proliferation. The peptides are useful in the
XX CC treatment of disorders of the central nervous system, neurological
XX CC disorders, mental disorders, dementia, neurodegenerative diseases,
XX CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
XX CC disorders of the immune system, bacterial and viral infections and
XX CC acquired immunological deficiencies.

XX SQ Sequence 11 AA;
XX Query Match 100.0%; Score 11; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 6.9e-06;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 MPQNFYKLPQM 11
XX DB 1 MPQNFYKLPQM 11
XX
XX RESULT 2
XX AAB72505
XX ID AAB72505 standard; Peptide; 11 AA.
XX AC AAB72505;
XX DT 09-MAY-2001 (first entry)
XX DE Colostrinin peptide #6.
XX KW Dermatological; oxidative stress regulator; colostrinin.
XX OS Unidentified.
XX PN WO200112650-A2.
XX PD 22-FEB-2001.
XX PF 17-AUG-2000; 2000WO-US22665.
XX PR 17-AUG-1999; 99US-0149310.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX PT Modulating oxidative stress level in a cell, involves contacting the
XX PT cell with an oxidative stress regulator selected from colostrinin, its
XX PT constituent peptide, analog or their combinations -
XX PS Claim 6; Page 25; 48pp; English.
XX CC The present invention relates to a method for modulating the oxidative
XX CC stress level in a cell or a patient, comprising contacting the cell with,
XX CC or administering to the patient, an oxidative stress regulator selected
XX CC from colostrinin, or its constituent peptide (e.g. the present peptide),
XX CC to change the level of an oxidising species in the cell. The method can
XX CC be used to treat oxidative damage to skin, by decreasing or preventing an
XX CC increase in the level of damage to a biomolecule of the patient.
XX SQ Sequence 11 AA;
XX Query Match 100.0%; Score 11; DB 22; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 6.9e-06;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 MPQNFYKLPQM 11
XX DB 1 MPQNFYKLPQM 11
XX
XX RESULT 3
XX AAB72537
XX ID AAB72537 standard; Peptide; 11 AA.
XX AC AAB72537;
XX DT 09-MAY-2001 (first entry)
XX

DE Colostrinin peptide #6.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 OS
 XX WO200112651-A2.
 PN
 XX 22-FEB-2001.
 PD
 XX 17-AUG-2000; 2000WO-US22774.
 PF
 XX 17-AUG-1999; 99US-0149633.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I;
 XX
 XX WPI; 2001-226545/23.
 DR
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 XX Claim 6; Page 21; 35pp; English.
 PS
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 CC
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 11; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPQNFYKLPQM 11
 DB |||||
 1 MPQNFYKLPQM 11

RESULT 4
 AAB59311
 ID AAB59311 standard; Peptide; 11 AA.
 XX
 XX AAB59311;
 AC
 XX 21-MAR-2001 (first entry)
 DT
 XX Ewe colostrinin peptide fragment A-2.
 DE
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 KW
 XX Ovis sp.
 OS
 XX WO200075173-A2.
 PN
 XX 14-DEC-2000.
 PD
 XX 02-JUN-2000; 2000WO-GB02128.
 PF
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX (REGG-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 XX characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis, and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 11; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPQNFYKLPQM 11
 DB |||||
 1 MPQNFYKLPQM 11

RESULT 5
 AAE20233
 ID AAE20233 standard; peptide; 11 AA.
 XX
 XX AAE20233;
 AC
 XX 18-JUN-2002 (first entry)
 DT
 XX Colostrinin constituent peptide #6.
 DE
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 11
 FT /note= "Optionally C-terminal amide"
 FT
 XX WO200213850-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22776.
 PF
 XX 17-AUG-2000; 2000WO-US22776.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boldogh I;
 PI
 XX WPI; 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 XX Claim 6; Page 25; 51pp; English.
 PS
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs) as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 11 AA;
 Query Match 100.0%; Score 11; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11
 |||||
 Db 1 MPQNFYKLPQM 11

RESULT 6

AAW51041
 ID AAW51041 standard; Peptide; 11 AA.

AC AAW51041;

XX 30-MAY-2002 (first entry)

DT Colostrinin constituent peptide.

DE Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; human.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 11 /note= "Optional C-terminal amidation"

FT WO200213849-A1.

PN 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

PI WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, where the
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide. Cytokines induced by this peptide in human
 CC leucocyte cultures include interferon-gamma, tumour necrosis
 CC factor-alpha, interleukin-6 and interleukin-10.

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11
 |||||
 Db 1 MPQNFYKLPQM 11

RESULT 7

AAO14582
 ID AAO14582 standard; peptide; 11 AA.

AC AAO14582;

XX 27-MAY-2002 (first entry)

DT Neural cell regulatory colostrinin peptide 6.

DE Neural cell differentiation; neural cell regulator; colostrinin peptide;
 XX neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

OS Unidentified.

XX Key Location/Qualifiers

FT Modified-site 11 /note= "Optional C-terminal amide"

FT WO200213851-A1.

PN 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

PA Boldogh I, Stanton JG, Hughes TK;

PI WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrin peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 11; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPQNFYKLPQM 11
 |||||
 Db 1 MPQNFYKLPQM 11
 RESULT 8
 ID AAB59342 standard; Peptide; 12 AA.
 XX
 AC AAB59342;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrin peptide fragment derived sequence #2.
 XX
 KW Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB02128.
 XX
 PR 02-JUN-1999; 99GB-0012852.
 XX
 PA (REG-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-071058/08.
 XX
 PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 8; Page 27; 63pp; English.
 CC
 CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 11; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.4e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPQNFYKLPQM 11
 |||||
 Db 2 MPQNFYKLPQM 12
 RESULT 9
 ID AAU88197 standard; Peptide; 20 AA.
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE G protein coupled receptor related peptide SEQ ID No 9.

XX AAU88197;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Insulin/insulin-like growth factor receptor-binding peptide #161.
 XX
 KW Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
 KW ophthalmological; insulin; receptor; gene therapy; diabetes;
 KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;
 KW diabetic retinopathy; neurological diseases; stroke;
 KW diabetic neuropathy.
 XX
 OS Synthetic.
 XX
 PN WO200172771-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 29-MAR-2000; 2000WO-US08528.
 XX
 PR 29-MAR-2000; 2000WO-US08528.
 XX
 PA (DGIB-) DGI BIOTECHNOLOGIES LLC.
 XX (NOVO) NOVO NORDISK AS.
 PA
 PI Beasley J, Blume AJ, Schaeffer L, Pillutla R, Brandt J;
 PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandeckl WS;
 PI Hansen PH, Ravera M, Hsiao K;
 XX
 DR WPI; 2002-025774/03.
 XX
 PT Modulating insulin activity in mammalian cells, for treating e.g.
 PT diabetes and tumours, comprises using peptides that bind to insulin or
 PT insulin-like growth factor receptors -
 XX
 PS Disclosure; Page 44; 390pp; English.
 XX
 CC The invention relates to a method of modulating insulin activity in
 CC mammalian cells by administering a peptide that binds the insulin
 CC receptor (IR). A composition containing a peptide, optionally expressed
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin
 CC agonist are useful for treating diabetes. Also, peptides that are
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are
 CC useful for treating insulin-like growth factor (IGF)-sensitive tumours
 CC (e.g. of prostate and breast) and diabetic retinopathy. While IGF-1
 CC receptor agonists are useful for treating neurological diseases,
 CC including stroke and diabetic neuropathy. The peptides are also useful in
 CC screening for compounds that bind to IR or IGF-1 receptor, potential
 CC therapeutics and research reagents. AAU88034-AAU90957 represent IR
 CC and/or IGF-1 receptor-binding peptides and related amino acid sequences
 CC of the invention.
 XX
 SQ Sequence 20 AA;
 Query Match 45.5%; Score 5; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PONYF 6
 |||||
 Db 8 PONYF 12
 RESULT 10
 ID ABU36686 standard; Peptide; 4 AA.
 XX
 AC ABU36686;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE G protein coupled receptor related peptide SEQ ID No 9.

XX Nootropic; cardiant; antiarteriosclerotic; hypotensive; cytostatic;
 KW antibacterial; analgesic; anti-allergic; antiasthmatic; anti-inflammatory;
 KW osteoprotective; neuroprotective; anxiolytic; anorectic; lead compound;
 KW G protein coupled receptor signaling inhibitor; GPCR; library;
 KW high throughput screening assay; stroke; myocardial infarction;
 KW restenosis; atherosclerosis; hypotension; cancer; infection; asthma;
 KW septic shock; pain; allergic disorder; inflammatory bowel disease;
 KW osteoporosis; obesity; psychotic; neurological disorder; anxiety;
 KW schizophrenia; Alzheimer's disease.
 XX Mammalia sp.
 OS WO200272778-A2.
 PN 19-SEP-2002.
 PD 14-MAR-2002; 2002WO-US07561.
 PF 14-MAR-2001; 2001US-275472P.
 PR 11-MAY-2001; 2001US-0852910.
 XX (CUEB-) CUE BIOTECH.
 PA Gilchrist A, Hamm HE;
 PI WPI; 2003-247841/24.
 DR Identifying G protein coupled receptor (GPCR) signaling inhibitors,
 PT useful in screening drugs for treating stroke, cancers or pain, by
 FT identifying compounds that block GPCR mediated signaling with high
 PT affinity and specificity -
 PS Disclosure; Page 12; 94pp; English.
 XX The invention relates to a novel method for identifying a G protein
 CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises
 CC selecting or identifying a member of a library of peptides and/or
 CC candidate compounds, having binding to a GPCR of higher affinity than
 CC that of the native peptide. The peptide library is based on a native GPCR
 CC binding peptide. The method is useful for identifying inhibitors of a G
 CC protein coupled receptor (GPCR) signaling. The method is particularly
 CC useful for identifying drugs that antagonise the binding between a GPCR
 CC and its extracellular ligand(s). The method is especially useful in
 CC modern high throughput screening assays for identifying potent lead
 CC compounds. The compounds, peptides or inhibitors identified by the method
 CC are useful for preventing, ameliorating or treating diseases in which
 CC GPCR signaling is a causative factor or in which a specific class of G
 CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,
 CC atherosclerosis, hypotension, cancers, infections, septic shock, pain,
 CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,
 CC obesity, or psychotic and neurological disorders (e.g. anxiety,
 CC schizophrenia or Alzheimer's disease). This sequence represents a peptide
 CC relating to the G protein coupled receptors of the invention.
 XX
 SQ Sequence 4 AA;
 Query Match 36.4%; Score 4; DB 24; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 QY 8 LPQM 11
 DB 1 LPQM 4
 RESULT 11
 AAW12496
 ID AAW12496 standard; peptide; 5 AA.
 XX
 AC AAW12496;
 XX
 XX 22-APR-1997 (first entry)
 DT

XX Interleukin-6 antagonist 61.
 DE Interleukin-6; IL-6; antagonist; inhibitor; autoimmune disease;
 KW skin; intestine; systemic lupus erythematosus; chronic rheumatism.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 5
 FT /note= "amidated"
 XX JP08311098-A.
 PN 26-NOV-1996.
 PD 22-MAY-1995; 95JP-0146742.
 PF 22-MAY-1995; 95JP-0146742.
 PR (DAIL) DAICEL CHEM IND LTD.
 XX (FUJI) FUJISAWA PHARM CO LTD.
 PA WPI; 1997-061811/06.
 DR Interleukin-6 antagonistic peptide(s) comprising arginine - useful
 PT for treating autoimmune, renal, skin and intestinal diseases
 PS Example 61; Page 12; 20pp; Japanese.
 XX The present peptide is a specific example of new interleukin-6
 CC antagonists of the general formula X-A-B-D-Y, where X is 1-10 amino
 CC acids or an amino group protecting group; Y is 1-5 amino acids, a
 CC carboxyl group protecting group or an amide; A is preferably Arg
 CC having an opt. protected guanidino group but can be any amino acid;
 CC D is Arg having an opt. protected guanidino group and B is preferably
 CC a Leu residue but can be any amino acid, including non-natural
 CC amino acids, opt. having a protected side-chain. The peptides are
 CC useful for treating autoimmune diseases (e.g. systemic lupus
 CC erythematosus or chronic rheumatism), renal, skin and intestinal
 CC diseases.
 XX
 SQ Sequence 5 AA;
 Query Match 36.4%; Score 4; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 QY 5 FYKL 8
 DB 1 FYKL 4
 RESULT 12
 AAW48024
 ID AAW48024 standard; peptide; 7 AA.
 XX
 AC AAW48024;
 XX 12-JUN-1998 (first entry)
 DT AE114 analogue effector compound SEQ ID NO:102.
 DE Mammalian II key peptide; mammalian invariant chain protein; allergy;
 KW immune response; MHC class II; antigenic; autoimmune disease.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Acylated"
 FT Modified-site 7
 FT /note= "Amidated"

```

XX PN WO9749430-A1.
XX PD 31-DEC-1997.
XX PF 09-JUN-1997; 97WO-US09993.
XX PR 26-JUN-1996; 96US-0670605.
XX PA (ANTI-) ANTIGEN EXPRESS INC.
XX PI Adams S, Humphreys RE, Xu M;
XX PI WPI; 1998-076917/07.
XX DR
XX CC The present sequence represents an AEl14 analogue effector compound
XX CC used in the present invention. The present invention describes
XX CC a mammalian invariant chain protein (ii) key peptide of sequence
XX CC LRMKLPPKPKVSKMR and modifications with the exclusion of peptide
XX CC YRMKLPPKPKVSKMR. MHC class II molecules are synthesised in the
XX CC endoplasmic reticulum with their antigenic peptide sites blocked by the
XX CC invariant chain protein (ii). The products and method can be used for
XX CC the modulation of an immune response for therapeutic or diagnostic
XX CC purposes. The enhancement of immunity can be used in the treatment of
XX CC e.g. malignant or allergic disease. The immunosuppression can be used
XX CC for the treatment of autoimmune disease, e.g. rheumatoid arthritis,
XX CC multiple sclerosis, diabetes mellitus, lupus erythematosus, and
XX CC psoriasis or allograft rejection.
XX SQ Sequence 7 AA;
XX
Query Match 36.4%; Score 4; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
DB 4 KLPQ 7
|||||
|

RESULT 13
AAW47992
ID AAW47992 standard; peptide; 7 AA.
XX AC AAW47992;
XX DT 12-JUN-1998 (first entry)
XX DE AEl14 analogue effector compound SEQ ID NO:69.
XX KW Mammalian ii key peptide; mammalian invariant chain protein; allergy;
XX KW immune response; MHC class II; antigenic; autoimmune disease.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Acylated"
XX FT Modified-site 7 /note= "Amidated"
XX FT
XX PN WO9749430-A1.
XX PD 31-DEC-1997.
XX PF 09-JUN-1997; 97WO-US09993.
XX PT

```

```

PR 26-JUN-1996; 96US-0670605.
XX PA (ANTI-) ANTIGEN EXPRESS INC.
XX PI Adams S, Humphreys RE, Xu M;
XX PI WPI; 1998-076917/07.
XX DR
XX CC New mammalian invariant chain protein (ii) key peptide(s) - used for
XX CC modulation of immune response, e.g. for treating malignant, allergic
XX CC or autoimmune disease or allograft rejection
XX PS Example 2; Page 34; 149pp; English.
XX CC The present sequence represents an AEl14 analogue effector compound
XX CC used in the present invention. The present invention describes
XX CC a mammalian invariant chain protein (ii) key peptide of sequence
XX CC LRMKLPPKPKVSKMR and modifications with the exclusion of peptide
XX CC YRMKLPPKPKVSKMR. MHC class II molecules are synthesised in the
XX CC endoplasmic reticulum with their antigenic peptide sites blocked by the
XX CC invariant chain protein (ii). The products and method can be used for
XX CC the modulation of an immune response for therapeutic or diagnostic
XX CC purposes. The enhancement of immunity can be used in the treatment of
XX CC e.g. malignant or allergic disease. The immunosuppression can be used
XX CC for the treatment of autoimmune disease, e.g. rheumatoid arthritis,
XX CC multiple sclerosis, diabetes mellitus, lupus erythematosus, and
XX CC psoriasis or allograft rejection.
XX SQ Sequence 7 AA;
XX
Query Match 36.4%; Score 4; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKLP 9
DB 3 YKLP 6
|||||
|

RESULT 14
ABB80641
ID ABB80641 standard; peptide; 7 AA.
XX AC ABB80641;
XX DT 15-JUL-2002 (first entry)
XX DE Clostridium botulinum toxin type A leucine based motif.
XX KW Neurotoxin; biological persistence; dysphonia; strabismus; muscle spasm;
XX KW dystonia; pain; blepharospasm; hemifacial spasm; excessive salivation;
XX KW eyelid disorder; cerebral palsy; focal spasticity; spasmodic colitis;
XX KW neurogenic bladder; anismus; limb spasticity; tic; tremor; bruxism;
XX KW anal fissure; achalasia; dysphagia; lacrimation; hyperhidrosis; headache;
XX KW excessive gastrointestinal secretion; leucine-based motif; botulinum.
XX OS Clostridium botulinum.
XX PN WO200208268-A2.
XX PD 31-JAN-2002.
XX PF 20-JUL-2001; 2001WO-US23122.
XX PR 21-JUL-2000; 2000US-0620840.
XX PA (ALLR ) ALLERGAN SALES INC.
XX PI Steward LE, Fernandez-salas E, Herrington TM, Roki KR;
XX PI WPI; 2002-241566/29.
XX DR
XX PT Novel modified neurotoxin comprising structural modification which

```

PT alters the biological persistence and/or biological activity of a
 PT neurotoxin, useful for treating neuromuscular or autonomic disorder, or
 PT pain
 XX
 PS Claim 28; Page 76; 102pp; English.
 XX
 CC The sequence represents a leucine based motif from Clostridium botulinum,
 CC botulinum toxin type A, which may act as a biological persistence
 CC enhancing component in a neurotoxin. The invention relates to a novel
 CC modified neurotoxin including a structural modification, where the
 CC structural modification is effective to alter the biological persistence,
 CC or biological activity. The modified neurotoxin is useful for treating
 CC spasmodic dysphonia, laryngeal dystonia, oromandibular dysphonia, lingual
 CC dystonia, cervical dystonia, focal hand dystonia, blepharospasm,
 CC strabismus, hemifacial spasm, eyelid disorder, cerebral palsy, focal
 CC spasticity, spasmodic colitis, neurogenic bladder, anismus, limb
 CC spasticity, tics, tremors, bruxism, anal fissure, achalasia, dysphagia,
 CC lacticrimation, hyperhidrosis, excessive salivation, excessive
 CC gastrointestinal secretions, pain from muscle spasms, headache pain, brow
 CC furrows or skin wrinkles.
 XX
 SQ Sequence 7 AA;

Query Match 36.4%; Score 4; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8
 Db 3 FYKL 6

RESULT 15

AAV53386
 ID AAV53386 standard; Protein; 8 AA.

AC AAV53386;

DT 18-JAN-2000 (first entry)

DE E6 protein epitope (aa 8-15) binds HLA.

XX Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
 KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
 KW human immunodeficiency virus; hepatitis B virus; papilloma virus;
 KW melanoma; malaria; parasite.

XX Synthetic.

OS Homo sapiens.

XX FR2776926-A1.

XX 08-OCT-1999.

XX 07-APR-1998; 98FR-0004323.

XX 07-APR-1998; 98FR-0004323.

XX (INERM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (CNRS) CNRS CENT NAT RECH SCI.

PA (INSP) INST PASTEUR LILLE.

XX Le Gal FA, Guillet JG, Gahery SH, Gras MH, Melnyk O, Tartar A;
 XX WPI; 1999-583113/50.

XX New lipopeptide containing lipid regions and two epitopes, all
 PT separated by peptide spacers that impart hydrophilicity, useful in
 PT vaccines -

XX Disclosure; Page 19; 35pp; French.

XX The invention relates to the generation of a lipopeptide comprising at

CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
 CC epitope and at least one lipid residue with (i) the epitopes and lipid
 CC portion and (ii) the epitopes, being separated independently by peptide
 CC spacers. These spacers comprise sequences of amino acids which carry an
 CC overall electrical charge in neutral media to ensure that the
 CC lipopeptide is hydrophilic. The peptides AAV53301-Y53549 represents
 CC examples of peptide epitopes used to generate the lipopeptides. These are
 CC used in therapeutic or prophylactic compositions and vaccines to induce
 CC specific immune responses against human immunodeficiency, hepatitis B or
 CC papilloma viruses; p53 of melanoma or the malaria parasite.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
 Db 4 KLPQ 7

RESULT 16

AAV40373

ID AAV40373 standard; Peptide; 8 AA.

XX AAV40373;

XX 19-NOV-1999 (first entry)

DE Amino acid sequence of an E6 and E7 protein epitope.

XX Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
 KW vaccine; tumor; infection; immune response; cytokine profile;
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
 KW autoimmune disease.

XX Human papillomavirus.

XX FR2774687-A1.

XX 13-AUG-1999.

XX 06-FEB-1998; 98FR-0001439.

XX 06-FEB-1998; 98FR-0001439.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PA (INSP) INST PASTEUR LILLE.

XX Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;
 XX WPI; 1999-510734/43.

XX New lipopeptide comprising C-terminal interferon-gamma fragment with
 PT attached lipophilic groups, used as interferon mimic, e.g. for treating
 PT cancer or virus infection

XX Disclosure; Page 42; 53pp; French.

XX AAV40123-Y40379 represent epitopes that are able to activate cytotoxic
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
 CC B epitopes recognized by corresponding antibodies. The epitopes may be
 CC used in the composition of the invention. The specification describes a
 CC lipopeptide that has a peptide part derived from mammalian interferon
 CC gamma (IFN γ) and one or more lipophilic parts comprising a linear or
 CC branched, (un)saturated 4-20C hydrocarbon chain or a steroid. The
 CC lipopeptide mimics the activity of IFN γ . Compositions comprising the
 CC lipopeptide are used to treat or prevent any condition that responds
 CC to IFN γ , and as adjuvant for vaccines (particularly those directed
 CC against tumors, viral or parasitic infections), to stimulate or
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.

CC Particular applications are treatment of infections (particularly
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers
 CC (particularly of kidney, cutaneous T cells or ovary, chronic
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune
 CC diseases.
 XX
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
 ||||
 Db 4 KLPQ 7

RESULT 17

AA26724
 ID AAY26724 standard; peptide; 8 AA.

AC AAY26724;

DT 14-SEP-1999 (first entry)

DE HPV-derived lipopeptide epitope (E6 aa8-15) for mixed micelles.

KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
 KW melanoma; Plasmodium falciparum; malaria.

OS Synthetic.

OS Human papillomavirus.

XX FR2771640-A1.

XX 04-JUN-1999.

XX 03-DEC-1997; 97FR-0015246.

XX 03-DEC-1997; 97FR-0015246.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX (INSP) INST PASTEUR LILLE.

XX Bossus M, Bourgault VI, Gras-Kasse H, Guillet JG, Lippens G;

XX Tartar A, Wieruszski JM;

XX WPI; 1999-349509/30.

XX Immunogenic lipopeptide micelles - comprising lipopeptides
 PT containing cytotoxic and helper T-lymphocyte epitopes

XX Disclosure; Page 32; 60pp; French.

XX The invention relates to the generation of mixed micelles or
 CC microaggregates for inducing an immune response comprising: (a) a first
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at
 CC least one HNL (helper T-lymphocyte) epitope and at least one lipid unit
 CC different from that of the first lipopeptide. This peptide represents
 CC an example of a lipopeptide epitope used in the invention and is derived
 CC from the human papilloma virus 56 protein. The immunogenic lipopeptide
 CC micelles are used in vaccines, especially against HIV, hepatitis B virus
 CC (HBV), papilloma viruses, p53, melanoma or Plasmodium falciparum malaria.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 KLPQ 10
 ||||
 Db 4 KLPQ 7

RESULT 18

AA10348

ID AAY10348 standard; Peptide; 8 AA.

XX AC AAY10348;

XX DT 12-MAY-1999 (first entry)

XX T cell epitope/MHC ligand SEQ ID NO:278.

XX Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;
 KW immunisation; tumour; infectious disease; immunotherapy; cancer;
 KW malignant melanoma; viral disease; hepatitis; AIDS.

OS Synthetic.

OS Human papillomavirus.

XX WO9902183-A2.

XX PD 21-JAN-1999.

XX PF 10-JUL-1998; 98WO-US14289.

XX PR 10-DEC-1997; 97US-0988320.

XX PR 10-JUL-1997; 97CA-2209815.

XX PA (CTL-) CTL IMMUNOTHERAPIES CORP.

XX PI Kuendig TW, Simard JUL;

XX WPI; 1999-120514/10.

XX Inducing a cytotoxic T lymphocyte response - by maintaining a level
 PT of antigen in the lymphatic system of a mammal so as to provide a
 PT sustained CTL response, used to treat, e.g. AIDS

XX Disclosure; Page 34; 199pp; English.

XX The present invention describes a method of inducing and/or sustaining
 CC an immunological cytotoxic T lymphocyte (CTL) response in a mammal. The
 CC method comprises: (a) delivering an antigen to the mammal at a level to
 CC induce an immunological CTL response in the mammal; and (b) maintaining
 CC the level of the antigen in the mammal's lymphatic system to maintain
 CC the immunologic CTL response. The method can be used for the delivery of
 CC e.g. a differentiation antigen, a tumour-specific multinease antigen,
 CC an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor
 CC gene antigen, or a viral antigen. They can be used for the treatment of
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery
 CC to the lymphatic system provides for potent CTL stimulation that takes
 CC place in the milieu of the lymphoid organ, and it sustains stimulation
 CC that is necessary to keep CTL active, cytotoxic and recirculating
 CC through the body. AA10071 to AA10639 represent examples of peptide
 CC antigens given in the present invention.

XX Sequence 8 AA;

Query Match 36.4%; Score 4; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
 ||||
 Db 4 KLPQ 7

```

RESULT 19
ABP11965
ID ABP11965 standard; Peptide; 8 AA.
XX
AC ABP11965;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif env peptide #22.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
FN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 114; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
XX
Query Match 36.4%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FYKL 8
DB 3 FYKL 6
RESULT 20
ABP18445
ID ABP18445 standard; Peptide; 8 AA.

```

```

XX
AC ABP18445;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV B62 super motif env peptide #20.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
FN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 247; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
XX
Query Match 36.4%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FYKL 8
DB 3 FYKL 6
RESULT 21
ABG80030
ID ABG80030 standard; Peptide; 8 AA.
XX
AC ABG80030;
XX

```



```

PR 04-JUN-1993; 93US-0073205.
XX 29-NOV-1993; 93US-0159184.
XX (CVTE-) CYTEL CORP.
XX Grey HM, Kast WM, Sette A, Sidney J;
XX WPI; 1994-302678/37.
XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
PT for treatment or prophylaxis of cancer, virus infection or
XX autoimmune diseases.
XX Example 5; Page 103; 138pp; English.
XX AAR59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1
CC binding motif. These peptides bind HLA-A2.1 and have a binding affinity
CC of at least 1% as compared to a reference peptide (AAR71293). AAR59196
CC has an IC50 of 0.0006 and the sequence occurs at position 18 in the HPV
CC E7 protein. The peptides of the invention can induce cytotoxic T
CC lymphocytes which can react with target cells. They can be used for the
CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma,
CC etc.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 9 AA;
XX Query Match 36.4%; Score 4; DB 15; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 KLPQ 10
XX DB 1 KLPQ 4
XX
XX RESULT 24
XX ID AAW49468 standard; peptide; 9 AA.
XX AC AAW49468;
XX DT 05-JUN-1998 (first entry)
XX DE Human leucocyte antigen DQ4 binding peptide #359.
XX KW Human leucocyte antigen; HLA-DQ4; combinatorial library;
XX autoimmune disease; chronic articular rheumatism.
XX OS Synthetic.
XX PN JP08151396-A.
XX PD 11-JUN-1996.
XX PF 28-NOV-1994; 9AJP-0292657.
XX PR 28-NOV-1994; 9AJP-0292657.
XX PA (TEIJ ) TEIJIN LTD.
XX DR WPI; 1996-329479/33.
XX HLA-binding oligopeptide and an immuno:regulator contg it - used in
PT the treatment of auto:immune disease
XX Claim 4; Page 42; 61pp; Japanese.
XX This peptide is an example of a peptide which binds to a human leucocyte
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
CC combinatorial library comprising the sequence AAV05953, by screening
CC with an HLA-DQ4 molecule. The peptide is used for the treatment of
CC autoimmune disease, or especially for treatment of viral diseases.

```

```

XX SQ Sequence 9 AA;
XX Query Match 36.4%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 FYKL 8
XX DB 3 FYKL 6
XX
XX RESULT 25
XX ID AAW39512 standard; peptide; 9 AA.
XX AC AAW39512;
XX DT 11-JUN-1998 (first entry)
XX DE HPV16 E6-encoded CTL epitope 5.
XX KW T cell epitope; immune response; human leukocyte antigen; HLA Class I;
XX vaccine; immunogenic; major histocompatibility complex; MHC; B cell;
XX disease; anti-tumour; anti-viral; HPV16 E6.
XX OS Synthetic.
XX OS Human Papillomavirus.
XX PN W09741440-A1.
XX PD 06-NOV-1997.
XX PF 28-APR-1997; 97WO-NL00229.
XX PR 23-DEC-1996; 96EP-0203670.
XX PR 26-APR-1996; 96EP-0201145.
XX PA (UYLE-) RIJCSUNIV LEIDEN.
XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
XX PI Kast WM, Melief CJM, Offringa R, Toes REM, Van Der Burg SH;
XX DR WPI; 1997-549891/50.
XX PT Method of selecting T cell peptide epitope(s) - by measuring the
XX stability of HLA class I-peptide complexes on intact B cells
XX Example 2; Page 59; 109pp; English.
XX Peptides AAW39430-W39734 are used in a novel method for the selection of
CC immunogenic T-cell peptide epitopes present in polypeptide antigens. The
CC method involves the identification of peptide sequences capable of
CC binding to an HLA (human leukocyte antigen) class I molecule and
CC measuring the binding of this epitope peptide to the HLA class I
CC peptide. The stability of binding of the peptide and MHC (major
CC histocompatibility complex) class I molecule is measured on intact human
CC B cells carrying the MHC molecule at their cell surfaces. The method can
CC be used to select peptide epitopes for generating vaccines against a
CC disease associated with the polypeptide, e.g. cancers or AIDS. The
CC peptide epitopes are especially T-cell peptide epitopes with strong
CC anti-tumour and anti-viral immune responses. Peptide AAW39512 is a HPV16
CC E6 encoded cytotoxic T lymphocyte (CTL) epitope used in a binding assay
CC to test for binding to HLA-A*0201 at different temperatures for different
CC incubation times.
XX SQ Sequence 9 AA;
XX Query Match 36.4%; Score 4; DB 18; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 KLPQ 10

```

```

Db      |||||
        1 KLPQ 4

RESULT 26
AAW78890
ID AAW78890 standard; peptide; 9 AA.
XX AC AAW78890;
XX DT 17-NOV-1998 (first entry)
XX DE Human papillomavirus 16 E6 protein fragment 18-26.
XX KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
XX class II associated peptide; pathogen; gene therapy; genetic disease;
XX infection; downregulation; immune response.
XX OS Human papillomavirus.
XX OS Synthetic.
XX PN WO9831398-A1.
XX PD 23-JUL-1998.
XX PF 22-JAN-1998; 98WO-US01499.
XX PR 06-JAN-1998; 98US-0003253.
XX PR 22-JAN-1997; 97US-0787547.
XX PA (PANG-) PANGAEA PHARM INC.
XX PI Curley JM, Hedley ML, Langer RS, Lunsford LB;
XX WPI; 1998-427556/36.
XX DR
XX FT New preparations of microparticles - comprising a synthetic polymer
XX matrix and nucleic acid comprising an expression vector for use in
XX gene therapy
XX PS Disclosure; Page 10; 101pp; English.
XX CC A microparticle preparation (MP) has been developed, consisting of
XX microparticles having a diameter of less than 100 nm. The MP
XX comprises: (a) a polymeric matrix (PM) consisting of one or more
XX synthetic polymers having a solubility in water of less than 1 mg/l; and
XX (b) an expression vector selected from RNA molecules (at least 50% of
XX which are closed circles) or circular plasmid DNA (at least 50% of which
XX are supercoiled). Also described is a MP of at most 20 microns in
XX diameter, comprising: (a) a PM; and (b) a NAM comprising an expression
XX control sequence operatively linked to a coding sequence, where the
XX coding sequence encodes an expression product selected from: (i) a
XX polypeptide at least 7 amino acids in length, having a sequence identical
XX to the sequence of: (i) a fragment of a naturally-occurring mammalian
XX protein; or (ii) a fragment of a naturally-occurring protein from an
XX infectious agent which infects a mammal; (2) a peptide having a length
XX and sequence which permits it to bind to an MHC class I or II molecule;
XX and (3) the polypeptide or the peptide linked to a trafficking sequence.
XX AA69763 to AA69765, and AAW7893 to AAW7897 are peptide fragments for
XX use in the present invention. The MPs are highly effective vehicles for
XX the delivery of polynucleotides into phagocytic cells. They can be used
XX for gene therapy, e.g. for treating genetic diseases, infections or
XX tumours or for downregulating an immune response.
XX SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 KLPQ 10
Db |||||
1 KLPQ 4

RESULT 28
AAW54509
ID AAW54509 standard; peptide; 9 AA.
XX AC AAW54509;
XX DT 01-SEP-1998 (first entry)
XX DE Synthetic polypeptide HPV 16 E6 18-26.
XX KW Carbohydrate-specific; cytolytic T cell; therapeutic; tumour;
XX major histocompatibility complex; vaccine; protective immune response;
XX pathogenic bacteria; virus; CTL response.
XX XX

```

OS Synthetic.
 XX WO9815286-A1.
 XX 16-APR-1998.
 XX 08-OCT-1997; 97WO-US18146.
 XX 08-OCT-1996; 96US-0028260.
 XX (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
 XX Grey H;
 XX WPI; 1998-240595/21.
 XX Composition for stimulating carbohydrate-specific cytotoxic T
 PT lymphocytes - comprises synthetic peptide with attached carbohydrate
 PT haptan, designed to bind to class I molecule, used in vaccines
 PT against cancer or infectious disease
 XX
 PS Disclosure; Page 18; 64pp; English.
 XX The peptides AAW54491-W54531 and AAW54533-W54534 are examples of
 CC polypeptides tested and used in the production of a synthetic
 CC polypeptide, for stimulating a carbohydrate-specific cytolytic T cell
 CC (CII) response. The polypeptide should be at least 8 amino acids, 2 of
 CC which are anchor residues. The polypeptide binds to the binding groove
 CC of a major histocompatibility complex class I molecule and a carbohydrate
 CC molecule which is linked to an internal amino acid of the polypeptide
 CC extends beyond the groove. This stimulates T cells which are able to
 CC lyse specifically cells that express carbohydrate residues on their
 CC surface. The polypeptides are used as vaccines to generate therapeutic
 CC or protective immune responses, particularly against tumours but also
 CC against pathogenic bacteria and viruses (e.g. mycobacteria that cause
 CC leprosy and tuberculosis).
 XX
 SQ Sequence 9 AA;
 Query Match 36.4%; Score 4; DB 19; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 7 KLPQ 10
 DB 1 KLPQ 4
 RESULT 29
 AAY53385
 ID AAY53385 standard; Protein; 9 AA.
 XX
 AC AAY53385;
 XX
 DT 18-JAN-2000 (first entry)
 XX
 DE B6 protein epitope (aa 18-26) binds HLA.
 XX
 KW Lipopeptide; epitope; cytotoxic T lymphocyte; CTL; lipid; spacer; p53;
 KW electrical charge; hydrophilicity; vaccine; immune response; HIV; HBV;
 KW human immunodeficiency virus; hepatitis B virus; papilloma virus;
 KW melanoma; malaria; parasite.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN FR2776926-A1.
 XX
 PD 08-OCT-1999.
 XX
 PF 07-APR-1998; 98FR-0004323.
 XX
 PR 07-APR-1998; 98FR-0004323.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA (INSP) INST PASTEUR LILLE.
 XX
 PI Le Gal FA, Guillet JG, Gabery SH, Gras MH, Melnyk O, Tartar A;
 XX WPI; 1999-583113/50.
 XX
 XX New lipopeptide containing lipid regions and two epitopes, all
 PT separated by peptide spacers that impart hydrophilicity, useful in
 PT vaccines -
 XX
 PS Disclosure; Page 19; 35pp; French.
 XX
 CC The invention relates to the generation of a lipopeptide comprising at
 CC least one auxiliary T epitope, at least one cytotoxic T lymphocyte (CTL)
 CC epitope and at least one lipid residue with (i) the epitopes and lipid
 CC portion and (ii) the epitopes, being separated independently by peptide
 CC spacers. These spacers comprise sequences of amino acids which carry an
 CC overall electrical charge in neutral media to ensure that the
 CC lipopeptide is hydrophilic. The peptides AAY53301-Y53549 represents
 CC examples of peptide epitopes used to generate the lipopeptides. These are
 CC used in therapeutic or prophylactic compositions and vaccines to induce
 CC specific immune responses against human immunodeficiency, hepatitis B or
 CC papilloma viruses; p53 of melanoma or the malaria parasite.
 XX
 SQ Sequence 9 AA;
 Query Match 36.4%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 7 KLPQ 10
 DB 1 KLPQ 4
 RESULT 30
 AAY40372
 ID AAY40372 standard; Peptide; 9 AA.
 XX
 AC AAY40372;
 XX
 DT 19-NOV-1999 (first entry)
 XX
 DE Amino acid sequence of an E6 and E7 protein epitope.
 XX
 KW Cytotoxic T cell; T lymphocyte; CD8+ epitope; T helper cell;
 KW CD4+ epitope; B epitope; lipopeptide; interferon gamma; adjuvant;
 KW vaccine; tumor; infection; immune response; cytokine profile;
 KW acquired immune deficiency syndrome; papilloma; cancer; hepatitis;
 KW autoimmune disease.
 XX
 OS Human papillomavirus.
 XX
 PN FR2774687-A1.
 XX
 PD 13-AUG-1999.
 XX
 PF 06-FEB-1998; 98FR-0001439.
 XX
 PR 06-FEB-1998; 98FR-0001439.
 XX
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INSP) INST PASTEUR LILLE.
 XX
 PI Thiam K, Guillet JG, Ver Waerde C, Auriault C, Gras MH, Loing E;
 XX WPI; 1999-510734/43.
 XX
 XX New lipopeptide comprising C-terminal interferon-gamma fragment with
 PT attached lipophilic groups, used as interferon mimic, e.g. for treating

CC place in the milieu of the lymphoid organ, and it sustains stimulation
CC that is necessary to keep CTL active, cytotoxic and recirculating
CC through the body. AAY10071 to AAY10639 represent examples of peptide
CC antigens given in the present invention.
XX
XX
SQ Sequence 9 AA;
Query Match 36.4%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
DB 1 KLPQ 4

RESULT 33
AAB33702
ID AAB33702 standard; Peptide; 9 AA.
XX
XX AAB33702;
AC
XX
XX 26-JAN-2001 (first entry)
DT
XX
XX MHC class I associated immunogenic peptide SEQ ID 101.
DE
XX
XX Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
KW major histocompatibility complex; vaginal tissue; mucosal tissue..
XX
XX Unidentified.
OS
XX WO200053161-A2.
PN
XX 14-SEP-2000.
PD
XX
XX 10-MAR-2000; 2000WO-US06578.
XX
XX 11-MAR-1999; 99US-0266463.
PR
XX 27-MAY-1999; 99US-0321346.
PR
XX (ZYCO-) ZYCO INC.
PA
XX
XX Lunsford LB, Putnam D, Hedley ML;
PI
XX WPI; 2000-638130/61.
DR
XX
XX Microparticles useful for administering a nucleic acid into the mucosal
PT tissue preferably vaginal tissue of an animal, comprises a polymeric
PT matrix, a lipid and a nucleic acid molecule -
XX
XX Disclosure; Page 16; 96pp; English.
PS
XX
XX The present invention relates to microparticles which are less than 20
CC microns in diameter, which comprise a polymeric matrix, a lipid and a
CC nucleic acid molecule. The microparticle is specifically not
CC encapsulated in a liposome and does not comprise a cell. The nucleotide
CC sequence encodes an expression product that binds to major
CC histocompatibility complex (MHC) type I or II molecules. Peptides
CC AAB33602-B33647 represent MHC class II associated immunogenic peptides,
CC and AAB33648-B33710 represent MHC class I associated immunogenic
CC peptides. The peptides are examples of the expression products of the
CC nucleotide sequences which can be included in the microparticles of the
CC invention. Sequences AAB33711-B33716 represent alternative expression
CC products and nuclear localisation signals also used in the invention. The
CC microparticles are useful for administering a nucleic acid into the
CC mucosal tissue preferably vaginal tissue of an animal.
XX
XX
SQ Sequence 9 AA;
Query Match 36.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
DB 1 KLPQ 4

RESULT 34
AAY66471
ID AAY66471 standard; Peptide; 9 AA.
XX
XX AAY66471;
AC
XX
XX 22-FEB-2000 (first entry)
DT
XX
XX HLA-A2-binding HPV type 16 B6 conserved peptide #273.
DE
XX
XX Human papillomavirus; HPV; MHC; major histocompatibility complex;
KW Class I; HLA-A2; human leukocyte antigen; epitope; allele; binding;
KW conserved; genome; peptide; targeting; toxic; drug; antibody; antigen;
KW antiviral; molecular conjugate therapeutic; diagnosis; treatment;
KW pathogen; localisation; quantification; detection; infection;
KW drug resistance; immune response.
XX
XX Human papillomavirus.
OS
XX WO9949893-A1.
PN
XX 07-OCT-1999.
PD
XX
XX 31-MAR-1999; 99WO-US07111.
PF
XX
XX 31-MAR-1998; 98US-0052530.
PR
XX (UYBO-) UNIV BOSTON.
PA
XX
XX Delisi C, Berzofsky J, Gulukota K, Vaccaro D, Weng Z, Zhang C;
PI WPI; 2000-038361/03.
DR
XX
XX Novel methods for designing molecular conjugate therapeutics which are
PT used for diagnosis, imaging and treatment against pathogens -
PT
XX
XX Example 4; Page 54; 62pp; English.
PS
XX
XX AAY66462-Y66474 are peptides derived from conserved portions of the
CC human papillomavirus genome (HPV) that are presented by HLA-A2 MHC
CC (major histocompatibility complex) Class I molecules. The peptides are
CC used to construct targeting antigens comprising one or more peptides
CC bound to the corresponding MHC Class I molecule, which can be used to
CC raise antibodies. The antibody may then be used as a targeting vehicle
CC to deliver a potentially toxic drug to its target site of action, rather
CC than administering it systemically, which may result in adverse side
CC effects. The invention relates to improved methods for the design
CC of molecular conjugate therapeutics for the diagnosis and treatment of
CC infections caused by pathogens with a high mutation rate (such as
CC HPV). This method involves identifying conserved peptide-encoding
CC regions among the genomes of multiple variants of a pathogen,
CC identifying the Class I MHC molecules which occur with greatest
CC frequency in a population of interest (e.g., human sub-populations),
CC and determining which of the peptides bind to the Class I MHC
CC molecules. The MHC-binding peptides and the corresponding Class
CC I MHC molecules are selected and used to construct targeting
CC antigens, which are in turn used to produce targeting antibodies.
CC The methods may be used in localisation, quantification and in situ
CC detection of specific peptide-MHC Class I complexes and also to
CC detect and treat viral infection. The methods of the invention
CC mitigate against the development of viral resistance to drugs and
CC to the immune response, as well as providing a solution for
CC targeting toxic compounds to destroy viruses sequestered in sites not
CC accessible to T cells. In addition, the methods eliminate the virus,
CC whereas current therapies only arrest viral replication.
XX
XX
SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
 ||||
 DB 1 KLPQ 4

RESULT 35
 AAEO7583
 ID AAE07583 standard; peptide; 9 AA.
 AC AAE07583;
 XX
 XX 06-NOV-2001 (first entry)
 DT
 XX Human PUMP-1 peptide (residues 238-246).
 DE
 XX PUMP-1 protease; cancer; neoplastic state; malignancy; ovary; lung;
 KW prostate; colon; cytostatic; gene therapy; vaccine; immunogen; human.
 XX
 XX Homo sapiens.
 OS
 XX WC200154712-A1.
 PN
 XX 02-AUG-2001.
 PD
 XX 26-JAN-2001; 2001WO-US02698.
 PF
 XX 27-JAN-2000; 2000US-0492543.
 PR
 XX (UYAR-) UNIV ARKANSAS.
 PA
 XX O'Brien TJ;
 PI
 XX WPI; 2001-496835/54.
 DR
 XX
 XX Diagnosing cancer in an individual, useful for early detection of
 PT ovarian cancer, lung cancer or prostate cancer, comprises determining
 FT the presence of PUMP-1 protease in biological sample obtained from
 PT individual -
 PS
 XX Example 20; Page 65; 145pp; English.

CC The patent discloses compositions and methods for the early diagnosis
 CC of ovarian cancer. The method involves obtaining a biological sample
 CC from an individual and detecting PUMP-1 protease in the sample, where
 CC the presence of PUMP-1 in the sample is indicative of the presence of
 CC cancer in the individual and the absence of PUMP-1 is indicative of
 CC the absence of cancer in the individual. The method is useful for the
 CC early detection or diagnosis of ovarian cancer and other neoplastic
 CC state or malignancies (e.g. lung cancer, prostate cancer, colon cancer
 CC or other cancers in which PUMP-1 is overexpressed). It is also useful
 CC for diagnosing whether an individual has cancer, is suspected of having
 CC cancer or is at risk of getting cancer. The method is also used to
 CC detect and treat malignant hyperplasia. The PUMP-1 proteins are also
 CC useful for vaccinating against neoplastic states. The oligonucleotide
 CC is useful for treating neoplastic states such as lung cancer, prostate
 CC cancer, colon cancer or other cancers in which PUMP-1 is overexpressed.
 CC The present sequence is PUMP-1 peptide (residues 238-246) from human.
 CC This peptide is a putative immunogen and binds strongly to HLA A1
 CC and is used to inoculate an individual against PUMP-1.

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQNF 5
 ||||
 DB 4 PQNF 7

RESULT 36
 AAM23452
 ID AAM23452 standard; Peptide; 9 AA.
 XX
 XX AAM23452;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 XX HIV peptide SEQ ID NO 1337.
 DE
 XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
 KW human immunodeficiency virus; vaccine.
 XX
 XX Human immunodeficiency virus.
 OS
 XX Synthetic.
 XX
 XX WO200155177-A2.
 PN
 XX 02-AUG-2001.
 PD
 XX 29-JAN-2001; 2001WO-DK00059.
 PF
 XX 28-JAN-2000; 2000EP-0610017.
 PR
 XX 31-JAN-2000; 2000US-0179333.
 XX
 XX (STAT-) STATENS SERUM INST.
 PA
 XX Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
 PI
 XX WPI; 2001-476184/51.
 DR
 XX
 XX The generation of cytotoxic T cell lymphocytes epitopes for use in
 PT anti-HIV vaccines -
 FT
 XX Example 4; Page 378; 383pp; English.

CC The invention relates to identification of cytotoxic T cell lymphocyte
 CC (CTL) epitopes (AAM23115-AAM23484) that generate anti-HIV activity. CTL
 CC are a major protective mechanism against viral diseases. Antibodies may
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
 CC prevent infection of cells in the host, but CTL will limit viral
 CC production by killing the cell. The CTL epitopes are useful in medicine,
 CC in the manufacture of vaccines or diagnostic agents.

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 ||||
 DB 3 FYKL 6

RESULT 37
 AAM23484
 ID AAM23484 standard; Peptide; 9 AA.
 XX
 XX AAM23484;
 AC
 XX 22-OCT-2001 (first entry)
 DT
 XX HIV peptide SEQ ID NO 1369.
 DE
 XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
 KW human immunodeficiency virus; vaccine.
 XX
 XX Human immunodeficiency virus.
 OS
 XX Synthetic.

PN WO200155177-A2.

XX PD 02-AUG-2001.

XX PF 29-JAN-2001; 2001WO-DK00059.

XX PR 28-JAN-2000; 2000EP-0610017.

XX PR 31-JAN-2000; 2000US-0179333.

XX PA (STAT-) STATENS SERUM INST.

XX PI Ponsgaard A, Brunak S, Buus S, Corbet S, Laemoller SL, Hansen J;

XX DX WPI; 2001-476184/51.

XX PT The generation of cytotoxic T cell lymphocytes epitopes for use in
anti-HIV vaccines -

XX PS Example 4; Page 383; 383pp; English.

XX CC The invention relates to identification of cytotoxic T cell lymphocyte
(CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
are a major protective mechanism against viral diseases. Antibodies may
neutralise extracellular human immunodeficiency virus (HIV) and limit or
prevent infection of cells in the host, but CTL will limit viral
production by killing the cell. The CTL epitopes are useful in medicine,
CC in the manufacture of vaccines or diagnostic agents.

XX SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8

DB 3 FYKL 6

RESULT 38

ID AAG93798 standard; Peptide; 9 AA.

AC AAG93798;

DT 17-SEP-2001 (first entry)

XX DE Human papilloma virus 16 E6 peptide 1.

XX KW Continuous flow production; microparticle; gene therapy;
antitense therapy; vaccination; treatment; autoimmune disease;
immune response modulation.

XX OS Human wart virus.

XX PN WO200136583-A1.

XX PD 25-MAY-2001.

XX PF 17-NOV-2000; 2000WO-US31770.

XX PR 19-NOV-1999; 99US-0443654.

XX PA (ZYCO-) ZYCOS INC.

XX PI Hedley ML, Hsu Y, Tyo M;

XX DX WPI; 2001-425203/45.

XX CC Continuous production of microparticles containing nucleic acid for
e.g. gene therapy, comprises mixing a solution of polymeric material
and nucleic acid with a surfactant solution, removing solvent and
drying -

XX PS Disclosure; Page 12; 47pp; English.

XX CC The present sequence is that of a peptide of the invention.
The invention relates to a method for scalable, continuous flow
production of a nucleic acid containing microparticle that maintains the
structural integrity of the associated nucleic acid and results in a
microparticle having purity suitable for introduction into an animal
host. Microparticles prepared according to the method can be used for
delivery of a nucleic acid for gene therapy, antisense therapy or
vaccination, treatment of autoimmune disease and either specific or
non-specific modulation of an immune response. The microparticles may
also be used to deliver nucleic acid encoding a protein or peptide useful
in any kind of therapy. The method is economical, aseptic and scalable.
The method also enables control over the size of microparticles. The
microparticles produced are free of impurities such as organic solvents
CC and are readily dispersed in a wide range of dispersing agents.

XX SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10

DB 1 KLPQ 4

RESULT 39

ID AAB95948 standard; Peptide; 9 AA.

AC AAB95948;

DT 25-JUN-2001 (first entry)

XX DE MHC class-I associated HPV epitope SEQ ID 55.

XX KW Epitope; tumour antigen; antiviral; immunostimulatory; cervical cancer;
human papillomavirus-associated disease; condyloma; cervical dysplasia;
cervical dysplasia; major histocompatibility complex; MHC I.

XX OS Human papillomavirus.

XX PN WO200119408-A1.

XX DX 22-MAR-2001.

XX PF 18-SEP-2000; 2000WO-US25559.

XX PR 16-SEP-1999; 99US-0154665.

XX PR 16-SEP-1999; 99US-0398534.

XX PR 09-DEC-1999; 99US-0169846.

XX PR 09-DEC-1999; 99US-0458173.

XX PA (ZYCO-) ZYCOS INC.

XX PI Hedley ML, Urban RC, Chicrz RM;

XX DX WPI; 2001-265996/27.

XX PT Novel nucleic acids encoding polypeptide polypeptides containing
multiple epitopes from one or more proteins, useful for treating tumors
and as vaccines against pathogenic agents -

XX PS Disclosure; Page 8; 64pp; English.

XX CC This invention relates to polynucleotides encoding a hybrid polypeptide
comprising a signal sequence and three segments that are either
contiguous or separated by a spacer amino acid or spacer peptide. The
invention specifically details polynucleotides encoding a polypeptide
peptide where the peptide segments are tumour antigens or a naturally

CC occurring protein of a pathogenic agent. The polypeptide peptides exhibit
 CC antiviral and immunostimulatory activity. The polynucleotide and
 CC polypeptide peptides are useful for eliciting an immune response in a
 CC mammal. The polynucleotide and protein are useful as vaccines for
 CC treating tumours and pathogenic infections. The polynucleotide is also
 CC useful for preventing or treating human papillomavirus (HPV)-associated
 CC diseases, particularly exophytic condyloma, flat condyloma, cervical
 CC cancer, respiratory papilloma, conjunctival papilloma, genital-tract HPV
 CC infection, cervical dysplasia, high grade squamous intraepithelial
 CC lesions, and anal HPV infection. The polynucleotide and polypeptide are
 CC useful for generating or enhancing prophylactic or therapeutic immune
 CC responses against pathogens, tumours or autoimmune diseases in a
 CC population of individuals having diverse MHC allotypes, as positive
 CC controls in cell stimulation assays in vitro, and as tools to
 CC understand processing of epitopes within cells. Peptides
 CC AAB95894 - AAB96037 and AAB96044 - AAB96048 represent major
 CC histocompatibility complex I (MHC I) associated tumour and pathogen
 CC antigens. The peptides can be used as part of the polypeptide proteins of
 CC the invention. Also included are examples of the polypeptide proteins
 CC represented by AAB96050 - AAB96052, and localisation signal peptides
 CC AAB96038 - AAB96043 and AAB96049 which can be used in the construction of
 CC the polypeptide peptides.

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
 Db 1 KLPQ 4

RESULT 41

ID AAG80243 standard; Peptide; 9 AA.

AC AAG80243;

DT 15-NOV-2002 (first entry)

DE MHC class I molecule, viral epitope #491.

KW Major histocompatibility complex; MHC; MHC class I molecule; virus;
 KW epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;
 KW antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;
 KW lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;
 KW acquired immune deficiency syndrome; AIDS.

OS Viridae.

FN WO200262368-A2.

PD 15-AUG-2002.

PF 22-JAN-2002; 2002WO-US02033.

PR 02-FEB-2001; 2001US-0776232.

FA (CTLI-) CTL IMMUNOTHERAPIES CORP.

F1 Kundig TM, Simard JUL;

DR WP1; 2002-657506/70.

XX Inducing or sustaining immunological cytotoxic T lymphocyte response in
 XX a mammal, useful for treating a mammal with malignant tumour or
 XX infectious disease, by directly administering an antigen to the
 XX lymphatic system of the mammal -

PS Disclosure; Page 40; 73pp; English.

CC The invention relates to a method of inducing and/or sustaining an
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal
 CC comprising administering directly to the lymphatic system of the mammal:
 CC (a) an antigen in the form of a polypeptide; (b) a vector comprising a
 CC nucleic acid encoding the antigen; or (c) a non-peptide antigen. The
 CC method is useful for inducing and/or sustaining CTL response in a mammal.
 CC This is particularly useful for treating a mammal having a malignant
 CC tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious
 CC disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),
 CC malaria, measles or tuberculosis), or in an animal having a
 CC predisposition to these diseases. The mammal may be dogs, cats, mice,
 CC cattle, sheep, pigs, goats, rabbits, or preferably humans.
 CC AAG97733-ABG8019 represent viral epitopes on major histocompatibility
 CC complex (MHC) class I molecules, used in the method of the invention.

XX Sequence 9 AA;

Query Match 36.4%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
 Db 1 KLPQ 4

RESULT 41

ID AAG80674 standard; Protein; 9 AA.

AC AAG80674;

DT 19-MAR-2002 (first entry)

DE Human tumour-associated antigen B132 immunogenic peptide SEQ ID 95.

KW Tumour-associated antigen B132; human; cytostatic; immunotherapy;
 KW cancer; kidney; lung; colon; breast; carcinoma; tumour proliferation;
 KW vaccine; diagnosis.

OS Homo sapiens.

FN WO200189281-A2.

PD 29-NOV-2001.

PF 21-MAY-2001; 2001WO-BP05787.

PR 23-MAY-2000; 2000DE-1025521.

FA (BOEH) BOEHRINGER INGELHEIM INT GMBH.

PI Adolf G, Heider K, Koenig U, Sommergruber W, Gruenfelder A;
 PI Abseher R;

DR WP1; 2002-083034/11.

PT New tumor-associated antigen B132, useful for immunotherapy of cancer
 PT and for identifying antitumour agents, also related nucleic acid and
 PT antibodies -

PS Claim 5; Page 105; 108pp; German.

XX This invention describes a novel human tumour-associated antigen (Ag),
 XX designated B132 which has cytostatic activity. The antigen and its
 XX immunogenic fragments or decomposition products, are useful in vivo
 XX or ex vivo immunotherapy of cancers, particularly kidney cell, lung,
 XX colon or breast carcinoma. DNA (I) that encodes antigen can be used
 XX similarly (also to detect tumour-related mutations), also as a
 XX therapeutic target to identify inhibitors of tumour proliferation, and
 XX for monitoring the response of patients, for optimisation of therapy.
 XX Cells that express B132 are useful in cancer vaccines. Antibodies (Ab)
 XX raised against the antigen can be used for diagnosis of B132-related

CC tumours, also therapeutically (by delivery of cytotoxic compounds or
 CC radioisotopes). This sequence represents an immunogenic peptide
 CC derived from the human tumour-associated antigen B132 described in the
 CC method of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFYK 7
 ||||
 5 NFYK 8

Db

RESULT 42
 AAO22617
 ID AAO22617 standard; Peptide; 9 AA.

XX AC AAO22617;

XX DT 15-MAY-2003 (first entry)

XX DE HPV-16 E6 peptide, SEQ ID No 1.

XX KW Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;
 KW cancer; human papilloma virus; cervix; cell-mediated immune response;
 KW HPV; HPV-16; E6 peptide.

XX OS Human papilloma virus.

XX PN WO2003008649-A1.

XX PD 30-JAN-2003.

XX PF 19-JUL-2002; 2002WO-US23198.

XX PR 20-JUL-2001; 2001US-306809P.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Sastry KJ, Tortolero-luna G, Follen M;

XX WPI; 2003-239363/23.

XX PT Determining a possible recurrence of a (pre-)cancerous growth in a
 PT patient infected with human papilloma virus (HPV), comprises incubating
 PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
 PT immune response -

XX PS Example 1; Page 96; 132pp; English.

XX CC The invention relates to a novel method for determining the possibility
 CC of recurrence of a (pre-)cancerous growth in a patient infected with
 CC human papilloma virus (HPV) or suspected of being infected with HPV, and
 CC has or had a (pre-)cancerous growth on or around the cervix. The novel
 CC method comprises incubating an E6 or E7 peptide of HPV with a sample from
 CC the patient, and assaying the sample for a cell-mediated immune response
 CC against the peptide. The method is useful for determining the possibility
 CC and preventing the recurrence of a (pre-)cancerous growth in a patient
 CC infected with HPV or suspected of being infected with HPV. The HPV E6 or
 CC E7 peptides are useful in immunotherapy for the preventing or reducing
 CC the risk of development of (pre-)cancerous growths. This sequence
 CC represents an HPV-16 E6 peptide of the invention.

XX SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10

Db 1 KLPQ 4
 ||||

RESULT 43
 ABJ20153

XX ID ABJ20153 standard; Peptide; 9 AA.

XX AC ABJ20153;

XX DT 10-APR-2003 (first entry)

XX DE MHC binding peptide SEQ ID No 318.

XX KW Antirheumatic; anti-allergic; antiarthritic; nootropic; neuroprotective;
 KW antiinflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 KW inflammation; gene therapy; MHC binding peptide.

XX OS Synthetic.

XX PN WO200294981-A2.

XX PD 28-NOV-2002.

XX PF 16-MAY-2002; 2002WO-IL00383.

XX PR 16-MAY-2001; 2001US-290958P.

XX PR 29-MAY-2001; 2001US-0865548.

XX PA (TECR) TECHNION RES & DEV FOUND LTD.

XX PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;

XX WPI; 2003-210043/20.

XX PT Identifying peptides that are capable of binding to major
 PT histocompatibility complex (MHC) molecules of a particular haplotype by
 PT analyzing peptides bound to the soluble and secreted form of the MHC
 PT molecules of the particular haplotype -

XX PS Claim 51; Page 225; 238pp; English.

XX CC The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The
 CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell, and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention.

XX SQ Sequence 9 AA;

Query Match 36.4%; Score 4; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 ||||

Db 6 FYKL 9

RESULT 44
 ABU03246

XX ID ABU03246 standard; Protein; 9 AA.

XX AC ABU03246;

```

XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #26.
XX KW Translational profiling; expressed protein tag; EPT; kinase;
XX KW phosphatase; protease; protease inhibitor; transporter;
XX KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer;
XX KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
XX KW leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US09671.
XX PR 28-MAR-2001; 2001US-279495P.
XX PR 21-MAY-2001; 2001US-292544P.
XX PR 08-AUG-2001; 2001US-310801P.
XX PR 01-OCT-2001; 2001US-326370P.
XX PR 04-DEC-2001; 2001US-336780P.
XX PR 20-FEB-2002; 2002US-358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PT Chicx RM, Tomlinson AJ, Urban RG;
XX PI WPI; 2003-040607/03.
XX PS Claim 10; SEQ ID No 26; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor.
XX CC The polypeptide is useful as an immunogenic composition for eliciting
XX CC in a mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to
XX CC this polypeptide, is useful for treating cancer. The polypeptide is
XX CC also useful for identifying compounds that binds to a naturally
XX CC processed class I or class II MHC-binding polypeptide. The polypeptides
XX CC and polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling.
XX CC Note: This sequence does not appear in the printed specification but was
XX CC obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 9 AA;
XX Query Match 36.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FYKL 8
DB 6 FYKL 9
RESULT 45
ABB99353
ID ABB99353 standard; peptide; 9 AA.

```

```

XX AC ABB99353;
XX DT 29-JAN-2003 (first entry)
XX DE Peptide derived from E6 protein of HPV18.
XX KW E6 protein; HPV; HPV18; human leukocyte antigen; HLA; HPV16;
XX KW immunogenic peptide; cytotoxic T lymphocyte; HPV16 infection; vaccine.
XX OS Human papillomavirus 18.
XX PN WO200277012-A2.
XX PD 03-OCT-2002.
XX PF 22-MAR-2002; 2002WO-US09261.
XX PR 23-MAR-2001; 2001US-278520P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Khleif SN, Berzofsky JA;
XX DR WPI; 2003-029912/02.
XX PT Inducing a cytotoxic T lymphocyte response against human papilloma
XX PT virus 16 (HPV 16), useful for preventing or treating HPV 16 infection,
XX PT comprises contacting the cytotoxic T cells with an immunogenic peptide
XX PT from E6 protein.
XX PS Example 1; Page 41; 61pp; English.
XX CC The present sequence represents a peptide which is derived from the E6
XX CC protein of human papilloma virus 16 (HPV16). The peptide has lower
XX CC affinity for the human leukocyte antigen (HLA)-A2.1 molecule than the
XX CC corresponding epitope from HPV18. The HPV18 immunogenic peptide is used
XX CC in the method of the invention. The specification describes a method for
XX CC inducing a cytotoxic T lymphocyte response against HPV16 in a patient.
XX CC The method comprises contacting cytotoxic T cells from the patient with
XX CC an immunogenic peptide (e.g. HPV18 E6 peptide) of 20 amino acid residues
XX CC or less, and returning the cytotoxic T cells to the patient to induce a
XX CC cytotoxic T cell response. The method is useful for preventing or
XX CC treating HPV16 infection. The HPV18 peptide is also useful as a vaccine.
XX SQ Sequence 9 AA;
XX Query Match 36.4%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 KLPQ 10
DB 1 KLPQ 4
RESULT 46
AAR43905
ID AAR43905 standard; peptide; 10 AA.
XX AC AAR43905;
XX DT 06-JUN-1994 (first entry)
XX DE HIV-1 IIB gp120 monoclonal antibody antigenic peptide A10P.
XX KW Human immunodeficiency virus; therapy; HIV-1 infection; diagnosis;
XX KW post-exposure prophylaxis; infection; cytotoxic agent targeting;
XX KW neutralisation domain; G3-136; BAT085.
XX OS Synthetic.
XX PN US5266478-A.

```

```

XX 30-NOV-1993.
XX
XX 25-NOV-1991; 91US-0797692.
XX
XX 29-MAY-1987; 87US-0057445.
XX
XX 24-DEC-1987; 87US-0137861.
XX
XX 26-APR-1991; 91US-0692259.
XX
XX 26-SEP-1991; 91US-0757533.
XX
XX 25-NOV-1991; 91US-0797692.
XX
XX (TANO-) TANOX BIOSYSTEMS INC.
XX
XX Chang TW, Fung WSC, Sun BNC, Sun CRY;
XX
XX WPI; 1993-395339/49.
XX
XX Monoclonal antibody to HIV-1 gp120 - used for therapy of HIV-1
XX infection or AIDS. post-exposure prophylaxis and diagnosis of HIV-1
XX HIV-1 infection
XX
XX Example; Page 8; 9pp; Japanese.
XX
XX The sequence is that of a synthetic peptide corresponding to a
XX unique neutralisation domain in the V2 region of HIV-1 gp120. It
XX showed no reaction with monoclonal antibodies (MAbs) BA1085 and
XX G3-136.
XX
XX Sequence 10 AA;
XX
XX Query Match 36.4%; Score 4; DB 14; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.7e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 FYKL 8
XX Db 3 FYKL 6
XX
XX RESULT 47
XX ID AAW76930 standard; peptide; 10 AA.
XX
XX AC AAW76930;
XX
XX DT 25-JAN-1999 (first entry)
XX
XX DE Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #70.
XX
XX B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;
XX human immune deficiency virus; HIV; tolerance; treatment; therapy;
XX prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;
XX microbial infection; autoimmune disease; antibody; apoptosis;
XX antiviral T cell immunity.
XX
XX Mus sp.
XX OS Homo sapiens.
XX
XX WO9836087-A1.
XX
XX 20-AUG-1998.
XX
XX 13-FEB-1998; 98WO-US02766.
XX
XX 13-FEB-1997; 97US-0040581.
XX
XX (AMNA-) AMERICAN NAT RED CROSS.
XX
XX Scott D, Zambidis E;
XX
XX WPI; 1998-506315/43.
XX
XX New fusion immunoglobulin heavy chain including gp120 epitopes and

```

```

PT related complete antibodies - DNA, vectors and transformed cells,
PT used to induce tolerance to the epitopes for treatment of human
PT immune deficiency virus infection
XX
XX Disclosure; Page 38; 154pp; English.
XX
XX This sequence is an epitope used in the construction of a novel fusion
XX immunoglobulin heavy chain (IgH) protein with a mammalian, especially
XX human, IgH chain fused in frame at its N-terminus to one or more human
XX immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
XX transfected cells are used to tolerate subjects to gp120 epitopes and to
XX maintain this tolerance, particularly for treatment of HIV infection,
XX optionally together with other therapeutic/prophylactic agents such as
XX vaccines, chemotherapeutic agents and immune response modifiers. Such
XX proteins can be used against other diseases where an immune response is
XX deleterious, e.g. microbial infection, tumours or autoimmune disease.
XX Induction of tolerance suppresses production of antibodies against gp120,
XX so prevents or inhibits 'bystander' apoptosis of uninfected T cells that
XX are bound to gp120 protein, maximising induction of protective antiviral
XX T cell immunity.
XX
XX Sequence 10 AA;
XX
XX Query Match 36.4%; Score 4; DB 19; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.7e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 FYKL 8
XX Db 5 FYKL 8
XX
XX RESULT 48
XX ID AAM52988 standard; peptide; 10 AA.
XX
XX AC AAM52988;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Human papillomavirus type 16 E6 protein peptide P1 (residues 18-27).
XX
XX HPV16; E6 protein; cytotoxic T-lymphocyte; CTL; MHC class I;
XX major histocompatibility complex; immunomodulator.
XX
XX Human papillomavirus type 16.
XX
XX KR98020034-A.
XX
XX 25-JUN-1998.
XX
XX 05-SEP-1996; 96KR-0038373.
XX
XX 05-SEP-1996; 96KR-0038373.
XX
XX (CHEI-) CHEIL FOODS & CHEM INC.
XX (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX
XX Kim HS, Yoo WD, Noh GS, Chung GT, Park SH, Kang BT, Yoon HS;
XX Jin SW;
XX
XX WPI; 1999-285579/24.
XX
XX Peptide for modulating immune response in a human against human
XX papilloma virus type 16 E6 protein -
XX
XX Example 1; Page 2; 5pp; Korean.
XX
XX The invention relates to peptides derived from the human papillomavirus
XX type 16 (HPV16) E6 protein (AAM52985-AAM52987). The peptides are
XX presented on major histocompatibility complex (MHC) class I molecules and
XX act as cytotoxic T-lymphocyte (CTL) epitopes. The peptides of the
XX invention may be used for modulating an immune response against HPV16 in

```

CC a human (e.g., in a vaccine). Sequences AAM52988-AAM52994 represent HPV16
 CC E6 protein-derived peptides used in an exemplification of the invention.

XX
 SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred.No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
 ||||
 Db 1 KLPQ 4

RESULT 49

AAU70117
 ID AAU70117 standard; Peptide; 10 AA.

XX
 AC AAU70117;

XX
 DT 29-JAN-2002 (first entry)

XX
 DE Human calcitonin DNA encoded HLA-B35 binding peptide #4.

XX Human; tumour rejection antigen precursor; preprocalcitonin; HLA;
 KW cytolytic T lymphocyte; major histocompatibility complex; alpha-CGRP;
 KW calcitonin; cellular abnormality; cell lysis; immune responsive cell;
 KW lung cancer; human leukocyte antigen binding peptide; HLA; CGRP.

XX
 OS Homo sapiens.

XX
 PN WO200175179-A2.

XX
 PD 11-OCT-2001.

XX
 DP 14-MAR-2001; 2001WO-US40288.

XX
 PR 31-MAR-2000; 2000US-0539567.

XX
 PA (LUDW-) LUDWIG INST CANCER RES.

XX
 PA (INSR) INST ROUSSY GUSTAVE.

XX
 PA (INRM) INST NAT SANTE & RECH MEDICALE.

XX
 PI Echchakir H, Mami-Chouaib F, Vergnon I, Chouaib S, Baurain JF;

XX
 PI Coulie PG, Boon-Falleur T;

XX
 DR WPI; 2001-648564/74.

XX
 PT Determining the presence of a transformed cell by assaying for the
 PT expression of tumour rejection antigen precursors or for the presence of
 PT T cells specific for a complex between major histocompatibility complex
 PT and cell surface antigen

XX
 PS Example 7; Page 16; 33pp; English.

XX
 CC The invention relates to a method for detecting the presence of a
 CC transformed cell by assaying a cell sample for expression of nucleotides
 CC 292-403 of DNA encoding the tumour rejection antigen precursor,
 CC preprocalcitonin or for the presence of cytolytic T lymphocytes specific
 CC for a complex between a major histocompatibility complex and a peptide
 CC sequence found in alpha-CGRP, calcitonin, or preprocalcitonin. The
 CC sequences of the invention are useful for identifying those individuals
 CC diagnosed with conditions characterised by cellular abnormalities. A
 CC subject afflicted with a disorder characterised by inappropriate or
 CC abnormal amounts of a polypeptide encoded by nucleotides 292-403 of
 CC preprocalcitonin (such as lung cancer) can be treated by removing an
 CC immune responsive cell, contacting it with a cell line transfected with a
 CC nucleic acid molecule coding for the protein expressed by the abnormal
 CC cells, under conditions favouring the production of cytolytic T cells
 CC against a peptide derived from the protein, and introducing the T cells
 CC back to the subject, to lyse the abnormal cells. Sequences
 CC AAU69966-AAU70143 represent the polypeptides calcitonin and CGRP, a
 CC fragment of the preprocalcitonin polypeptide and human leukocyte antigen

CC (HLA) binding peptides of the invention.

XX
 SQ Sequence 10 AA;

Query Match 36.4%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred.No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQN 4
 ||||
 Db 6 MPQN 9

RESULT 50

AAU70117

ID AAR28392 standard; peptide; 11 AA.

XX

AC AAR28392;

XX

DT 25-MAR-2003 (updated)

DT 18-MAR-1993 (first entry)

XX

DE Bradykinin receptor antagonist CT-0008.

XX

KW Bradykinin receptor antagonist; heterodimer; higher oligomer;
 KW potency; duration; CP-0088; burns; migraine; shock CNS injury; asthma;
 KW rhinitis; premature labour; inflammatory arthritis; homodimer;
 KW inflammatory bowel disease.

XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "D-form residue"

FT /label= Nle

XX
 PN WO9217201-A1.

XX
 PD 15-OCT-1992.

XX
 PP 30-MAR-1992; 92WO-US02431.

XX
 PR 01-APR-1991; 91US-0677391.

XX
 PR 27-MAR-1992; 92US-0859582.

XX
 PA (CORT-) CORTECH INC.

XX
 PI Allen LG, Blodgett JK, Cheronis JC, Eubanks SR, Nguyen KT;

XX
 PI Whalley ET;

XX
 DR WPI; 1992-365995/44.

XX
 PT Bradykinin antagonists comprising linked bradykinin antagonist
 PT chains - are for treatment of post-operative pain, asthma and
 PT aseptic shock

XX
 PS Disclosure; Page 76; 109pp; English.

XX
 CC The sequence given is a bradykinin receptor antagonist which can form
 CC homo- or heterodimers or higher oligomers. It demonstrates greater
 CC potency and/or duration of action than the parent peptide itself.
 CC Bradykinin receptors antagonists such as this can be used in the
 CC treatment of burns, perioperative pain, migraine and other forms of
 CC pain, shock CNS injury, asthma, rhinitis, premature labour,
 CC inflammatory arthritis, inflammatory bowel disease etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 11 AA;
SQ

Query Match 36.4%; Score 4; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQNF 5
Db |||||
4 PQNF 7

RESULT 51

AAW76927
ID AAW76927 standard; peptide; 11 AA.

XX AAW76927;

AC AAW76927;

XX 25-JAN-1999 (first entry)

DT

XX Fusion immunoglobulin heavy chain HIV gp120 B cell epitope #67.

DE

XX B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IgH;

KW human immune deficiency virus; HIV; tolerance; treatment; therapy;

XX prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;

KW microbial infection; autoimmune disease; antibody; apoptosis;

XX antiviral T cell immunity.

XX

OS Mus sp.

XX Homo sapiens.

OS

XX WO9836087-A1.

PN

XX 20-AUG-1998.

XX

XX 13-FEB-1998; 98WO-US02766.

PF

XX 13-FEB-1997; 97US-0040581.

PR

XX (AMNA-) AMERICAN NAT RED CROSS.

XX

PA Scott D, Zambidis E;

PI

XX WPI; 1998-506315/43.

XX

XX New fusion immunoglobulin heavy chain including gp120 epitopes and

PT related complete antibodies - DNA, vectors and transformed cells,

PT used to induce tolerance to the epitopes for treatment of human

PT immune deficiency virus infection

PT

XX Disclosure; Page 38; 154pp; English.

PS

XX This sequence is an epitope used in the construction of a novel fusion

XX immunoglobulin heavy chain (IgH) protein with a mammalian, especially

CC human, IgH chain fused in frame at its N-terminus to one or more human

CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or

CC transfected cells are used to tolerate subjects to gp120 epitopes and to

CC maintain this tolerance, particularly for treatment of HIV infection,

CC optionally together with other therapeutic/prophylactic agents such as

CC vaccines, chemotherapeutic agents and immune response modifiers. Such

CC proteins can be used against other diseases where an immune response is

CC deleterious, e.g. microbial infection, tumours or autoimmune disease.

CC Induction of tolerance suppresses production of antibodies against gp120,

CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that

CC are bound to gp120 protein, maximising induction of protective antiviral

CC T cell immunity.

XX

XX Sequence 11 AA;

SQ

Query Match 36.4%; Score 4; DB 19; Length 11;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX Blyse; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

QY 5 FYKL 8
Db |||||
7 FYKL 10

RESULT 52

AAW15279
ID AAW15279 standard; Peptide; 12 AA.

XX AAW15279;

AC AAW15279;

XX 04-AUG-1997 (first entry)

DT

XX Salmonella secreted protein Ssp22 N-terminal sequence.

DE

XX Salmonella secreted protein; Ssp22; bacterial-mediated endocytosis;

KW diagnosis; therapy; vaccine; attenuation; virulence.

XX

OS Salmonella typhimurium.

XX

XX WO9718225-A1.

PN

XX 22-MAY-1997.

PD

XX 14-NOV-1996; 96WO-US18504.

PF

XX 14-NOV-1995; 95US-0006733.

PR

XX (GEHO) GEN HOSPITAL CORP.

PA

XX Miller SI;

PI

XX WPI; 1997-289217/26.

DR

XX New isolated Salmonella secreted proteins and related genes - used

XX to develop products for the detection, treatment or prevention of

PT Salmonella infections

PT

XX Disclosure; Page 57; 95pp; English.

PS

XX N-terminal sequences are provided (AAW15277-79) for Salmonella

CC secreted proteins Ssp54, Ssp42 and Ssp22, respectively. Ssp

CC proteins (see also AAW15268-71) and nucleic acids are useful for

CC the development of products for the detection, treatment or

CC prevention of Salmonella infections.

CC

XX Sequence 12 AA;

SQ

Query Match 36.4%; Score 4; DB 18; Length 12;

Best Local Similarity 100.0%; Pred. No. 4.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

QY 2 PQNF 5

Db |||||

7 PQNF 10

XX

XX AAW15279 standard; peptide; 12 AA.

ID AAW15279;

AC AAW15279;

XX 19-AUG-2002 (first entry)

DT

XX Human Blyse binding scFv VH CDR3 SEQ ID 2884.

DE

XX Blyse; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;

XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX

XX OS Homo sapiens.
 XX FN WO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001WO-US19110.
 XX PR 16-JUN-2000; 2000US-212210P.
 XX PR 17-OCT-2000; 2000US-240816P.
 XX PR 16-MAR-2001; 2001US-276248P.
 XX PR 21-MAR-2001; 2001US-277379P.
 XX PR 25-MAY-2001; 2001US-293499P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX FA (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for
 XX PT the diagnosis and treatment of cancers and immune disorders -
 XX PS Claim 2; Page 3071; 3148pp; English.
 XX CC This invention describes novel antibodies that immunospecifically bind to
 XX CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 XX CC tumour necrosis factor (TNF) super family and induces B cell
 XX CC proliferation and differentiation. The antibodies of the invention have
 XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
 XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 XX CC and so may be used to detect and quantitate the presence of Blys in
 XX CC biological samples and may be used in this way to diagnose disease
 XX CC associated with aberrant expression of Blys. They may also be
 XX CC administered to treat diseases associated with aberrant Blys expression
 XX CC and activity such as cancer, immune, and autoimmune disorders and
 XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX CC the antibodies and fragments of the antibodies described in the method
 XX CC of the invention.
 XX SQ Sequence 12 AA;
 Query Match 36.4%; Score 4; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QNFY 6
 Db |||||
 5 QNFY 8

RESULT 54
 ABP97425
 ID ABP97425 standard; peptide; 12 AA.
 XX
 AC ABP97425;
 XX
 DT 30-MAY-2003 (first entry)
 XX
 DE HAB18G/CD147 protein antagonist peptide, SEQ ID NO:10.
 XX
 XX HAB18G/CD147 protein; peptide antagonist;
 KW leukocyte differentiation antigen CD147 homologue; PCI-neo/ashAb18G;
 KW antitense expression plasmid; gene therapy; antitense therapy;
 KW cancer; stomach; liver; lung; oesophagus; recurrence; metastasis;
 KW rheumatoid arthritis; osteoarthritis; human immunodeficiency virus;
 KW HIV infection; acquired immunodeficiency syndrome; AIDS;
 KW arteriosclerosis; ectatic myocardiopathy; cytostatic; antirheumatic;

KW antiarthritic; anti-HIV; antiarteriosclerotic; cardiant.
 XX Synthetic.
 XX OS WO200294875-A1.
 XX FN 28-NOV-2002.
 XX PD 27-MAY-2002; 2002WO-CN00356.
 XX PR 28-MAY-2001; 2001CN-0115274.
 XX PR 28-SEP-2001; 2001CN-0131735.
 XX XX (CHEN/) CHEN Z.
 XX PA Chen Z, Shang P, Li Y, Qian A, Zhu P, Xing J;
 XX PI WPI; 2003-140362/13.
 XX DR Novel liver cancer tissue-originated protein molecule HAB18G/CD147, its
 XX PT antagonists and expression vector for its antisense RNA, applicable in
 XX PT treating cancer, tumor recurrence or metastasis, and rheumatoid
 XX PT arthritis -
 XX PS Claim 3; Page 14; 24pp; Chinese.
 XX CC The invention relates to a protein originating in liver cancer tissue
 XX CC designated HAB18G/CD147 (ABP97416) which is capable of promoting tumour
 XX CC metastasis. HAB18G/CD147 is encoded by a gene sequence homologous with
 XX CC that of the leukocyte differentiation antigen CD147 and is a member of
 XX CC the CD147 family, and can be isolated by using liver cancer-specific
 XX CC monoclonal antibody HAB18G affinity chromatography. The invention
 XX CC also encompasses an HAB18G/CD147 antisense expression plasmid
 XX CC PCI-neo/ashHAB18G which can inhibit HAB18G/CD147 mRNA translation, and 9
 XX CC HAB18G/CD147 peptide antagonists (ABP97417-ABP97425). The HAB18G/CD147
 XX CC protein, its peptide antagonists and antisense expression vector may be
 XX CC used in the prevention and treatment of cancer (including cancers of the
 XX CC stomach, liver, lung or oesophagus), tumor recurrence or metastasis,
 XX CC rheumatoid arthritis, osteoarthritis, human immunodeficiency virus
 XX CC (HIV) infection and acquired immunodeficiency syndrome (AIDS),
 XX CC arteriosclerosis, and ectatic myocardiopathy. Sequences
 XX CC ABP97417-ABP97425 represent specifically claimed peptide antagonists of
 XX CC the HAB18G/CD147 protein.
 XX SQ Sequence 12 AA;
 Query Match 36.4%; Score 4; DB 24; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 YKLP 9
 Db |||||
 1 YKLP 4

RESULT 55
 AAW88298
 ID AAW88298 standard; Peptide; 14 AA.
 XX
 AC AAW88298;
 XX
 DT 12-APR-1999 (first entry)
 XX
 DE Human guanine nucleotide exchange factor Rac-GEF peptide.
 XX
 XX Rac-GEF; guanine nucleotide exchange factor; human; cancer;
 KW metastasis; cell proliferation; apoptosis; haemostasis;
 KW bone resorption; clot retraction; morphogenesis; inflammation;
 KW therapy; diagnosis; antibody.
 XX
 OS Homo sapiens.
 XX WO9857990-A2.

XX PD 23-DEC-1998.
 XX PF 15-JUN-1998; 98WO-US12391.
 XX PR 17-JUN-1997; 97US-0049879.
 XX (ONYX-) ONYX PHARM INC.
 XX PI Bollag G, Crompton A, North A, Roscoe W, Sharma S;
 XX WPI; 1999-0953328/08.
 XX New isolated Rac-guanine nucleotide exchange factor - used to
 PT develop products for treating conditions involving e.g. cell
 PT proliferation (e.g. cancer), programmed cell death, haemostasis or
 PT bone resorption
 XX Claim 55; Page 50; 62pp; English.
 XX This peptide corresponds to amino acid residues 372-378 and 403-409
 CC of human guanine nucleotide exchange factor Rac-GEF (see AAM80995).
 CC A claimed antibody that is specific for Rac-GEF binds to an amino
 CC acid sequence selected from a group comprising this peptide and 2
 CC other Rac-GEF peptides (see AAM88297 and AAM88299). Such antibodies
 CC may be used to detect the presence of an epitope in a sample, e.g.
 CC in a sample of tissue containing Rac-GEF gene product. Rac-GEF
 CC polypeptides, nucleic acids, ligands and modulators are used in
 CC methods of treating pathological conditions associated or related
 CC to a Ras superfamily GTPase such as Rac, e.g. to treat cell
 CC proliferation (cancer), apoptosis, haemostasis, bone resorption,
 CC etc.
 XX SQ Sequence 14 AA;
 Query Match 36.4%; Score 4; DB 20; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 YKLP 9
 Db 6 YKLP 9
 RESULT 56
 AAM97223
 ID AAM97223 standard; Peptide; 14 AA.
 XX AC AAM97223;
 XX DT 24-JAN-2002 (first entry)
 XX DE Human peptide #498 encoded by a SNP oligonucleotide.
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX OS Homo sapiens.
 XX PN WO200147944-A2.
 XX PD 05-JUL-2001.
 XX PF 28-DEC-2000; 2000WO-US35498.
 XX PR 28-DEC-1999; 99US-0173419.
 XX PR 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.
 XX PI Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX Disclosure; Page 3777; 4143pp; English.
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 XX SQ Sequence 14 AA;
 Query Match 36.4%; Score 4; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KUPQ 10
 Db 1 KUPQ 4
 RESULT 57
 AAU69635
 ID AAU69635 standard; Protein; 14 AA.
 XX AC AAU69635;
 XX DT 30-JAN-2002 (first entry)
 XX DE Cell death protective sequence CNI-00726, protein #14.
 XX Human; protective sequence; cell death; cerebral oedema; infection;
 KW meningitis; degenerative disease; Alzheimer's disease; heart disease;
 KW motor neuron disease; demyelinating disease; multiple sclerosis; asthma;
 KW nutritional condition; peripheral nervous system disorder; ischaemia;
 KW diabetic neuropathy; autoimmune haemolytic anaemia; respiratory system;
 KW oral cavity; gastrointestinal tract; liver; cirrhosis; pancreatitis;
 KW polycystic renal disease; urinary tract; genitalia; endometriosis;
 KW breast; chronic mastitis; thyroid gland; Hashimoto's thyroiditis;
 KW adrenal gland; skin; psoriasis; muscular atrophy; bone marrow;
 KW osteoporosis; cancer; autoimmune disease.
 XX OS Homo sapiens.
 XX PN WO200176532-A2.
 XX PD 18-OCT-2001.
 XX PF 09-APR-2001; 2001WO-US11655.
 XX PR 11-APR-2000; 2000US-0547596.
 XX (COGE-) COGENT NEUROSCIENCE INC.
 XX PA

XX PI Barney S, Thomas MB, Portbury SD, Puranam K, Katz LC, Lo DC;
 XX WPI; 2002-017408/02.
 DR N-PSDB; AAS63035.
 XX
 XX Novel nucleic acids referred as protective sequences and their encoded
 PT products for diagnosing, treating diseases involving cell death,
 PT including neurological disorders e.g. stroke and for identifying
 PT modulators -
 XX
 XX Claim 17; Figure 7N; 256pp; English.
 XX
 CC The invention relates to isolated protective sequence polypeptides (I)
 CC and polynucleotides (II). (I) is useful for transferring a protective
 CC sequence into a cell, which delays and/or prevents the cell from
 CC undergoing cell death. Protective sequences, their products or
 CC antibodies are useful diagnostically, prophylactically, therapeutically
 CC or as targets for treatment and diagnosis of conditions, disorders or
 CC diseases involving cell death. The protective sequences and their
 CC products are useful for preventing or treating disorders of the central
 CC nervous system including neurological and psychiatric conditions,
 CC cerebral oedema, infections such as meningitis, degenerative diseases
 CC such as Alzheimer's and motor neuron disease, demyelinating diseases such
 CC as multiple sclerosis, nutritional conditions, disorders of the
 CC peripheral nervous system including diabetic neuropathy, disorders
 CC which cause cell death in organ systems including blood vessels, heart
 CC (ischaemia), blood cells (autoimmune haemolytic anaemia), respiratory
 CC system (asthma), oral cavity, gastrointestinal tract, liver (cirrhosis),
 CC pancreatitis, polycystic renal disease, urinary tract, genitalia
 CC (congenital anomalies), endometriosis, breast (chronic mastitis), thyroid
 CC gland (Hashimoto's thyroiditis), adrenal gland, skin (psoriasis),
 CC musculoskeletal system (muscular atrophy), bone marrow or bone
 CC (osteoporosis). The compositions promote cell death and are useful for
 CC treating and/or ameliorating cancer and autoimmune diseases. The
 CC compounds are further useful for treating physiological impacts on
 CC organs caused by infection which induce cell death. (I) is useful to
 CC raise an immune response, as a reagent in assays designed to
 CC quantitatively determine levels of the protein in biological fluids, as
 CC markers for tissues in which the corresponding protein is expressed and
 CC to isolate receptors or ligands. AAU69571-AAU69736 represent the
 CC protective polypeptide sequences as described in the invention.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 36.4%; Score 4; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 KLPQ 10
 Db ||||
 2 KLPQ 5
 RESULT 58
 AAP81956
 ID AAP81956 standard; protein; 15 AA.
 AC AAP81956;
 XX
 XX 25-MAR-2003 (updated)
 DT 16-OCT-1990 (first entry)
 XX
 XX Peptide immunogen for HPV.
 DE
 XX Human papilloma virus; immunogen; antibody; antigen; cervical carcinoma;
 KW HPV-16; early reading frame; E6.
 KW
 XX Synthetic.
 OS
 XX EP257754-A.
 FN
 XX 02-MAR-1988.
 PD

XX 09-JUL-1987; 87EP-0306061.
 XX 10-JUL-1986; 86US-0884184.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 XX Schoolnik GK, Palefsky JM;
 PI
 XX WPI; 1988-057971/09.
 DR
 XX Synthetic peptide(s) of human papilloma virus - corresp. to amino
 PT acid sequence region having at least one reverse turn and predicted
 PT hydrophilicity.
 PT
 XX Claim 8; Page 13; 27pp; English.
 FS
 XX The peptide corresponds to amino acids 9-23 of the E6 early open
 CC reading frame of HPV-16. It can be used to raise antibodies for
 CC vaccines or to heighten the immune response to an HPV infection
 CC already present.
 CC See also AAP81955-71.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 CC
 XX Sequence 15 AA;
 SQ
 Query Match 36.4%; Score 4; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 KLPQ 10
 Db ||||
 10 KLPQ 13
 RESULT 59
 AAP43901
 ID AAP43901 standard; peptide; 15 AA.
 XX
 XX AAP43901;
 AC
 XX
 XX 06-JUN-1994 (first entry)
 DT
 XX HIV-1 IIB gp120 monoclonal antibody antigenic peptide VI5P.
 DE
 XX Human immunodeficiency virus; therapy; HIV-1 infection; diagnosis;
 KW post-exposure prophylaxis; infection; cytotoxic agent targeting;
 KW neutralisation domain; BAT085; G3-136.
 KW
 XX Synthetic.
 OS
 XX US5266478-A.
 FN
 XX 30-NOV-1993.
 PD
 XX 25-NOV-1991; 91US-0797692.
 PF
 XX 29-MAY-1987; 87US-0057445.
 PR 24-DEC-1987; 87US-0137861.
 PR 26-APR-1991; 91US-0692299.
 PR 26-SEP-1991; 91US-0767533.
 PR 25-NOV-1991; 91US-0797692.
 PR
 XX (TANO-) TANOX BIOSYSTEMS INC.
 PA
 XX Chang TW, Fung MSC, Sun BNC, Sun CRY;
 PI WPI; 1993-395339/49.
 XX
 XX Monoclonal antibody to HIV-1 gp120 - used for therapy of HIV-1
 PT infection or AIDS, post-exposure prophylaxis and diagnosis of HIV-1

PT HIV-1 infection

PS Example; Page 8; 9pp; Japanese.

XX The sequence is that of a synthetic peptide V1SP corresponding to a
 CC unique neutralisation domain in the V2 region of HIV-1 gp 120, it
 CC can be used in the prodn. of monoclonal antibodies (MAbs) BAT085
 CC and G3-136. The MAbs may be used for therapy of HIV-1 infection or
 CC AIDS, post-exposure prophylaxis and diagnosis of HIV-1 infection and
 CC to reduce or eliminate virus infected T-cells by antibody-dependent
 CC cellular cytotoxicity, complement-mediated cytotoxicity or other
 CC cytolytic or regulatory immune mechanisms. The Mab can also be
 CC used for targeting cytotoxic agents to HIV-1 infected cells.

XX Sequence 15 AA;

Query Match 36.4%; Score 4; DB 14; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1e+02; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8

DB 8 FYKL 11

RESULT 60

AAR43907

ID AAR43907 standard; peptide; 15 AA.

AC AAR43907;

XX

DT 06-JUN-1994 (first entry)

XX

DE HIV-1 RF gp120 monoclonal antibody antigenic peptide T15P.

XX

KW Human immunodeficiency virus; therapy; HIV-1 infection; diagnosis;

KW Post-exposure prophylaxis; infection; cytotoxic agent targeting;

KW Neutralisation domain; G3-136; BAT085.

XX

OS Synthetic.

XX

FN US266478-A.

XX

PD 30-NOV-1993.

XX

PF 25-NOV-1991; 91US-0797692.

XX

PR 29-MAY-1987; 87US-0057445.

XX

PR 24-DEC-1987; 87US-0137861.

XX

PR 26-APR-1991; 91US-0692299.

XX

PR 26-SEP-1991; 91US-0767533.

XX

PR 25-NOV-1991; 91US-0797692.

XX

PA (TANO-) TANOX BIOSYSTEMS INC.

XX

PI Chang TW, Fung MSC, Sun BNC, Sun CRY;

XX

DR WPI; 1993-395339/49.

XX

XX Monoclonal antibody to HIV-1 gp120 - used for therapy of HIV-1

PT infection or AIDS, post-exposure prophylaxis and diagnosis of HIV-1

PT HIV-1 infection

XX

PS Example; Page 9; 9pp; Japanese.

XX

XX The sequence is that of a synthetic peptide corresponding to a

CC unique neutralisation domain in the V2 region of HIV-1 gp 120. It

CC showed no reaction with monoclonal antibody (Mab) BAT085 but

CC reacted with Mab G3-136.

XX

SQ Sequence 15 AA;

Query Match 36.4%; Score 4; DB 14; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8

DB 8 FYKL 11

RESULT 61

AAR72007

ID AAR72007 standard; peptide; 15 AA.

AC AAR72007;

XX

DT 25-MAR-2003 (updated)

DT 20-NOV-1995 (first entry)

XX

DE Biologically active lipopolysaccharide binding protein deriv.

XX

KW Lipopolysaccharide; binding; protein; LBP; inhibitor; toxic; shock;

KW Gram; negative.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 15

FT /note= "amidated"

XX

PN MO9508560-A1.

XX

PD 30-MAR-1995.

XX

PF 22-SEP-1994; 94WO-US10760.

XX

PR 24-SEP-1993; 93US-0126326.

XX

PA (CENZ) CENTOCOR INC.

XX

PI Heavner GA, Sherriis D, Taylor AH;

XX

DR WPI; 1995-139546/18.

XX

XX Novel peptide inhibitors of lipo:polysaccharide binding protein

PT (LBP) - prevent binding of lipo:polysaccharide to LBP, useful for

PT treatment and prevention of Gram-negative toxic shock

XX

PS Claim 4; Page 56; 74pp; English.

XX

CC AAR71993-R72053 are novel peptides which are specifically claimed

CC examples of a highly generic sequence derived from portions of the

CC 95-104 amino acid sequence region of LBP. Peptides corresp. to the

CC generic formula are inhibitors of lipopolysaccharide binding to LBP.

CC Such peptides may be useful in the prevention and treatment

CC of Gram-negative septic shock.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 15 AA;

XX

Query Match 36.4%; Score 4; DB 16; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8

DB 4 FYKL 7

RESULT 62

AAW99862

ID AAW99862 standard; peptide; 15 AA.

XX

AC AAW99862;

XX

DT XX 09-JUN-1999 (first entry)
 DE XX HIV-1 gp120 V1/V2 domain peptide p8.
 XX XX HIV-1; gp120; V1/V2 domain; human immunodeficiency virus; epitope;
 KW KW infection; antibody; immunoassay.
 XX OS Human immunodeficiency virus type 1.
 XX XX WO9912556-A1.
 XX XX 18-MAR-1999.
 XX XX 08-SEP-1998; 98WO-US18679.
 XX XX 08-SEP-1997; 97US-0058155.
 XX XX (PINTV) PINTER A.
 XX XX (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
 XX XX Pinter A;
 XX XX WPI; 1999-229137/19.
 XX XX New gp120 V1/V2 fusion proteins
 XX PS Disclosure; Page 18; 64pp; English.
 XX CC The present invention describes a novel protein (A) comprising a gp120
 CC V1/V2 domain of an HIV-1 strain and not comprising the gp120 V3 domain
 CC of an HIV-1 strain, where the protein does not bind CD4 the gp120 V1/V2
 CC domain of the protein displaying an epitope which is recognized by an
 CC antibody which neutralizes at least one HIV-1 primary isolate with a
 CC ND90 of at most 100 ml/9/ml. The present sequence represents an HIV-1
 CC gp120 V1/V2 domain peptide from the present invention. The novel
 CC proteins can be used for stimulating the formation of antibodies capable
 CC of neutralising infection by an HIV viral isolate in mammals. They can
 CC also be used for therapeutic treatment of subjects already infected with
 CC HIV. They can also be used in immunoassays for anti-HIV antibodies and
 CC for the production of anti-HIV antiserum.
 XX SQ Sequence 15 AA;
 Query Match 36.4%; Score 4; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FYKL 8
 DB 5 FYKL 8
 RESULT 63
 AAW87621
 ID AAW87621 standard; peptide; 15 AA.
 XX AC AAW87621;
 XX DT 20-MAR-2003 (updated)
 XX DT 03-MAR-1999 (first entry)
 XX DE Epitope of HIV-1 gp120 protein which binds antibody BAT085.
 XX KW Epitope; gp120 protein; monoclonal antibody; HIV-1; antibody BAT123;
 KW antibody BAT267; antibody BAT085; T cell infection inhibition;
 XX syncytia formation; acquired immune deficiency syndrome; AIDS;
 KW AIDS-related complex; passive immunisation; antiviral; cytotoxic;
 XX viral load measurement; vaccine.
 XX OS Human immunodeficiency virus type 1.
 XX XX US5854400-A.
 XX XX

PD XX 29-DEC-1998.
 XX PF 22-SEP-1992; 92US-0950571.
 XX XX 24-DEC-1987; 87US-0137861.
 PR PR 29-MAY-1987; 87US-0057445.
 PR PR 26-SEP-1991; 91US-0767533.
 XX XX (TANO-) TANOX INC.
 XX XX Chang NT, Chang TW, Fung MSC, Sun BNC, Sun CRE;
 XX WPI; 1999-095002/08.
 XX XX Monoclonal antibodies directed against regions of gp120 of human
 XX immune deficiency virus-1 - are neutralising and able to inhibit
 XX infection of T cells and formation of syncytia, used for treatment,
 XX prevention or diagnosis of acquired immune deficiency syndrome
 XX PS Claim 8; Column 9; 16pp; English.
 XX CC The present sequence represents an epitope of the gp120 protein of
 CC human immune deficiency virus (HIV)-1. The sequence comprises
 CC amino acids 169 to 183 of gp120. The specification describes
 CC monoclonal antibodies which bind to epitopes of the gp120 protein.
 CC Specifically, these antibodies are designated BAT123, 267 and 085.
 CC Monoclonal antibodies neutralise HIV-1 inhibiting both infection
 CC of T cells and formation of syncytia, so are used to treat acquired
 CC immune deficiency syndrome (AIDS) and AIDS-related complex, by
 CC passive immunisation, as carriers of cytotoxic or antiviral agents,
 CC and in extracorporeal systems. They can also be used as immunoassay
 CC reagents (for diagnosis or measurement of viral load) and to screen
 CC for neutralising epitopes, potentially useful in vaccine development.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 XX SQ Sequence 15 AA;
 Query Match 36.4%; Score 4; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FYKL 8
 DB 8 FYKL 11
 RESULT 64
 AAW72822
 ID AAW72822 standard; peptide; 15 AA.
 XX AC AAW72822;
 XX DT 13-JAN-1999 (first entry)
 XX DE HIV-1 gp120 monoclonal antibody BAT085 residue 178 to 192.
 XX KW HIV-1; gp120; epitope; monoclonal antibody; envelope; neutralise;
 KW inhibit; infection; T-cell; inhibit syncytium formation; AIDS.
 XX OS Human immunodeficiency virus type 1.
 XX XX US5834599-A.
 XX XX 10-NOV-1998.
 XX PF 04-MAR-1993; 93US-0026276.
 XX PR 04-MAR-1993; 93US-0026276.
 PR PR 29-MAY-1987; 87US-0057445.
 PR PR 24-DEC-1987; 87US-0137861.
 PR PR 25-APR-1989; 89US-0343540.
 PR PR 05-JUN-1992; 92US-0895197.
 XX XX

PA (TANO-) TANOX BIOSYSTEMS INC.
 XX Chang NT, Chang T, Fung SC, Kim YW, Sun BN, Sun CR;
 XX WPI; 1999-008810/01.
 XX Antibody conjugate comprising monoclonal antibody - which binds to
 PT epitope within amino acid residue of gp120 which neutralises HIV-1
 PT conjugated with, e.g. cytotoxic agent
 XX Example 4; Column 25; 22pp; English.
 CC The present invention describes an antibody conjugate comprising an
 CC antibody (Ab) which binds to an epitope within amino acid residue
 CC 308-322 of gp120 and neutralises HIV-1, conjugated with a cytotoxic
 CC agent, an anti-viral agent or an agent which facilitates passage through
 CC the blood brain barrier. Also described is an antibody conjugate as
 CC above but where the Ab binds to an epitope within amino acid residue
 CC 298-312 of gp120 which neutralises HIV-1. The present sequence represents
 CC an HIV-1 gp120 monoclonal antibody BAT085 residue 178 to 192 from an
 CC example of the present invention. The Ab are monoclonal Ab which bind
 CC to the gp120 protein on the envelope of HIV-1. They inhibit the
 CC infection of T-cells and also inhibit syncytium formation. The
 CC antibodies are group specific and neutralise different strains and
 CC isolates of HIV-1. The antibodies have a variety of uses, including the
 CC treatment and prevention of AIDS and AIDS related complex. They are
 CC especially used to kill infected T-cells.
 XX Sequence 15 AA;
 SQ Query Match 36.4%; Score 4; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred.No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FYKL 8
 DB 8 FYKL 11
 RESULT 65
 ABB98878
 ID ABB98878 standard; Peptide; 15 AA.
 XX AC ABB98878;
 XX DT 25-MAR-2003 (first entry)
 XX DE Proline rich gamma carboxyl glutamic protein 9.13 peptide fragment.
 XX KW Proline rich gamma carboxyl glutamic protein 9.13;
 KW blood coagulation disorder; tumour; developmental disorder;
 KW inflammation; immunological disease.
 XX OS Unidentified.
 XX PN CN1352002-A.
 XX PD 05-JUN-2002.
 XX PF 02-NOV-2000; 2000CN-0127180.
 XX PR 02-NOV-2000; 2000CN-0127180.
 XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX PI Mao Y, Xie Y;
 XX WPI; 2002-699440/76.
 XX New proline containing rich gamma carboxyl glutamic protein 9.13
 PT polypeptide for treating blood coagulation, tumors, a development
 PT disorder, inflammations, and immunological diseases -

PS Example 5; Page 19 (Disclosure); 34pp; Chinese.
 XX The present invention relates to proline rich gamma carboxyl glutamic
 CC protein 9.13 (see ABB98877). The protein can be used for treating
 CC various diseases, such as blood coagulation disorders, tumours,
 CC developmental disorders, inflammations and immunological diseases.
 CC The present sequence is an N-terminal peptide fragment of the protein,
 CC which was used in an example from the invention.
 XX Sequence 15 AA;
 SQ Query Match 36.4%; Score 4; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred.No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KLQK 10
 DB 4 KLQK 7
 RESULT 66
 ABB98946
 ID ABB98946 standard; Peptide; 15 AA.
 XX AC ABB98946;
 XX DT 14-APR-2003 (first entry)
 XX DE Translation initiation factor eIF-2-11.44 peptide fragment.
 XX KW Translation initiation factor eIF-2-11.44; diabetes; tumour; infection;
 KW cytosstatic.
 XX OS Unidentified.
 XX PN CN1355189-A.
 XX PD 26-JUN-2002.
 XX PF 01-DEC-2000; 2000CN-0127631.
 XX PR 01-DEC-2000; 2000CN-0127631.
 XX PA (UYFU-) UNIV FUDAN.
 XX PI Mao Y, Xie Y;
 XX WPI; 2003-000126/01.
 XX PT Polypeptide-translation initiation factor eIF-2-11.44 and
 PT polynucleotide for coding it -
 XX Example 5; Page 18 (Disclosure); 33pp; Chinese.
 XX The present invention relates to translation initiation factor
 CC eIF-2-11.44 (see ABB98945). The protein can be used for treating diseases
 CC such as diabetes, tumours and infections. The present sequence is an
 CC N-terminal peptide fragment of the protein, which was used in an example
 CC from the invention.
 XX Sequence 15 AA;
 SQ Query Match 36.4%; Score 4; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred.No. 5.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPQN 4
 DB 1 MPQN 4
 RESULT 67
 AAY29641

ID XX AAY29841 standard; peptide; 16 AA.
 AC AAY29841;
 DT 16-NOV-1999 (first entry)
 XX
 DE HIV HXB2 V3 fusion peptide #1.
 XX
 KW Fusion glycoprotein; env polyprotein; SU domain; expression vector;
 KW retrovirus; surface protein; murine leukaemia virus; MuLV; immunoassay;
 KW envelope protein; immunogen; vaccines HIV.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus type 1.
 XX
 FN US952474-A.
 XX
 PD 14-SEP-1999.
 XX
 PF 01-JUL-1997; 97US-0886642.
 XX
 PR 20-AUG-1993; 93US-0110300.
 PR 28-AUG-1992; 92US-0938100.
 XX
 PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
 XX
 PI Pinter A, Kayman S;
 XX
 XX WPI; 1999-550490/46.
 DR
 XX Fusion glycoprotein comprising active polypeptide and retroviral
 PT envelope protein useful in immunoassays and as immunogens, especially
 PT for anti-human immune deficiency vaccines -
 XX
 PS Example; Column 17; 48pp; English.
 XX
 CC The present invention describes a fusion glycoprotein (I) containing the
 CC N-terminal globular domain of a retroviral envelope (env) surface protein
 CC linked to a glycopeptide. (I) is expressed by a vector comprising a
 CC biologically active amino acid sequence (II) from a protein lacking a
 CC hydrophobic glycosylation signal (HGS) located about 7 residues
 CC N-terminal to a Cys-Trip-Leu-Cys sequence. (II) is operably linked to
 CC the C-terminus of a polypeptide sequence (III) from a retroviral env
 CC protein. (III) is an N-terminal fragment of env and includes all Cys
 CC residue with the N-terminal globular domain with a N-glycan attachment
 CC site with an HGS located within 7 residues N-terminal to a
 CC Cys-Trip-Leu-Cys sequence. (II) particularly includes an epitope and can
 CC then be used in immunoassays for diagnostic detection of antibodies,
 CC receptors or other binding partners, in affinity chromatography, or as
 CC immunogens, particularly in protective vaccines or for production of
 CC monoclonal antibodies. Most particularly (I) is used to raise
 CC neutralising antibodies against human immune deficiency virus (HIV)-1.
 CC Vectors used to express (I) can be constructed in bacteria to generate
 CC stable cell lines and can be used to infect a wide variety of cells.
 CC (I)-expressing cell cultures can be made quickly (without use of a
 CC selection marker) and the level of expression in mammalian cells is high,
 CC allowing simple and quick analysis during vaccine development. The
 CC present sequence represents a peptide, which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 16 AA;
 Query Match 36.4%; Score 4; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FYKL 8
 DB 12 FYKL 15
 RESULT 68
 AAW47339

ID XX AAW47339 standard; peptide; 17 AA.
 AC AAW47339;
 DT 01-JUN-1998 (first entry)
 XX
 DE Apolipoprotein B tryptic peptide.
 XX
 KW Binding inhibitor; low-density lipoprotein; LDL; vascular wall;
 KW vascular injury; elastin; collagen; prevention; treatment;
 KW vascular disease; atherosclerosis; apolipoprotein B; apoB;
 KW tryptic peptide.
 XX
 OS Homo sapiens.
 OS
 FN US5726153-A.
 XX
 PD 10-MAR-1998.
 XX
 PF 06-JUN-1995; 95US-0468543.
 XX
 PR 06-JUN-1995; 95US-0469692.
 PR 02-MAY-1988; 88US-0189130.
 PR 03-MAY-1990; 90US-0518142.
 PR 03-MAY-1990; 90US-0518215.
 PR 02-MAY-1991; 91US-0694929.
 PR 16-APR-1993; 93US-0048569.
 PR 24-FEB-1994; 94US-0201057.
 PR 28-FEB-1995; 95US-0394046.
 PR 06-JUN-1995; 95US-0468543.
 XX
 PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 PI Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;
 XX
 DR WPI; 1998-192802/17.
 XX
 CC Inhibiting binding of low-density lipoprotein to vascular walls - by
 CC administering peptide with affinity for vascular injury sites
 PS Disclosure; Column 10; 31pp; English.
 XX
 CC A novel method for inhibiting the binding of a low-density
 CC lipoprotein (LDL) to vascular walls in vivo, comprises
 CC administering a synthetic water soluble peptide containing an
 CC amphiphilic domain and having affinity for sites of vascular
 CC injury, e.g. derived from the present peptide.
 CC The peptide inhibits the binding of LDL to vascular wall
 CC components, e.g. elastin and collagen, and so can be used to
 CC prevent or treat vascular diseases, e.g. atherosclerosis.
 XX
 SQ Sequence 17 AA;
 Query Match 36.4%; Score 4; DB 19; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KLPQ 10
 DB 1 KLPQ 4
 RESULT 69
 AAY55881
 ID AAY55881 standard; peptide; 17 AA.
 XX
 AC AAY55881;
 XX
 DT 01-FEB-2000 (first entry)
 XX
 DE Apolipoprotein fragment peptide #31 for vascular disease imaging.
 XX
 KW Diagnosis; water soluble; amphiphilic domain; affinity; vascular injury;

KW detection; imaging; disease; atherosclerosis; apolipoprotein.
 XX Synthetic.
 OS Homo sapiens.
 XX
 XX US5972890-A.
 XX
 XX 26-OCT-1999.
 XX
 XX 28-FEB-1995; 95US-0398046.
 XX
 XX 02-MAY-1991; 91US-0694929.
 PR 16-APR-1993; 93US-0048569.
 PR 24-FEB-1994; 94US-0201057.
 PR 02-MAY-1988; 88US-0189130.
 PR 03-MAY-1990; 90US-0518142.
 PR 03-MAY-1990; 90US-0518215.
 XX
 XX (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 XX Lees AM, Fischman A, Shih I, Findeis MA, Lees RS;
 XX WPI; 1999-632641/54.
 XX
 XX New diagnostic synthetic peptides which have affinity for and
 PT accumulate at a site of vascular injury useful for detection and
 PT imaging of vascular disease such as atherosclerosis -
 XX
 XX Disclosure; Column 10; 30pp; English.
 XX
 XX The peptides AAY55851-Y55889 represent examples of diagnostic, synthetic
 CC peptides which carry a detectable label, contain 10 or fewer amino
 CC acids, are water soluble, contain an amphiphilic domain and have affinity
 CC for, and propensity to accumulate at, a site of vascular injury. They
 CC are preferably derived from the amino acid sequence of apolipoprotein.
 CC The peptides can be used for the detection or imaging of a vascular
 CC injury or disease, e.g. atherosclerosis.
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 36.4%; Score 4; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KLPQ 10
 Db 1 KLPQ 4
 RESULT 70
 AAY33106
 ID AAX33106 standard; peptide; 17 AA.
 XX
 XX AAY33106;
 AC
 XX 15-NOV-1999 (first entry)
 DT
 XX Alipoprotein B tryptic peptide 2.
 DE
 KW Alipoprotein B; alipoprotein A1; elastin; vascular imaging; detection;
 KW injury; vascular system; atherosclerosis; re-endothelializing; noninvasive;
 KW aortic lesion; trauma; lipoprotein accumulation.
 XX
 XX Synthetic.
 OS
 XX US5955055-A.
 XX
 XX 21-SEP-1999.
 PD
 XX 06-JUN-1995; 95US-0469692.
 XX
 XX 02-MAY-1991; 91US-0694929.
 PR 02-MAY-1988; 88US-0189130.
 PR

PR 03-MAY-1990; 90US-0518142.
 PR 03-MAY-1990; 90US-0518215.
 PR 16-APR-1993; 93US-0048569.
 PR 24-FEB-1994; 94US-0201057.
 PR 28-FEB-1995; 95US-0398046.
 PR 06-JUN-1995; 95US-0469692.
 XX
 XX (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 XX Findeis MA, Fischman A, Lees AM, Lees RS, Shih I;
 PI WPI; 1999-539543/45.
 DR
 XX
 XX Detecting vascular injuries using a labeled peptide useful for the
 PT diagnosis and monitoring of atherosclerosis
 PT
 XX Disclosure; Column 29-30; 31pp; English.
 PS
 XX
 XX This invention describes a novel method (I) for detecting injuries in a
 CC vascular system using a labeled synthetic peptide with an affinity for,
 CC and propensity to accumulate at, a site of vascular injury. The method
 CC is particularly suitable for detecting and monitoring atherosclerosis.
 CC It has been found that the synthetic peptide accumulates at the healing
 CC (re-endothelializing) edge of aortic lesions produced by trauma. These
 CC lesions resemble human atherosclerosis in many important respects
 CC (including accumulation of lipoproteins and other pathological changes).
 CC The ability of the synthetic peptides to localize at the trauma site, and
 CC and to permit imaging, may be used to visualize vascular disease. The
 CC method is noninvasive and the peptides used to target vascular lesions
 CC may be produced inexpensively, quickly and in large quantities.
 CC AAY33088-Y33114 represent synthetic peptides derived from alipoprotein B,
 CC alipoprotein A1 and elastin which are used in the method of the
 CC invention.
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 36.4%; Score 4; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KLPQ 10
 Db 1 KLPQ 4
 RESULT 71
 AAW29567
 ID AAW29567 standard; peptide; 18 AA.
 XX
 XX AAW29567;
 AC
 XX 26-OCT-1998 (first entry)
 DT
 XX Peptide GF52.
 DE
 XX
 XX Immune response; human papillomavirus; HPV; MHC class II; chimeric;
 KW automated peptide synthesis; solution synthesis; solid phase synthesis;
 KW B-cell; Cytotoxic T lymphocyte; CTL; HPV16; antigen;
 KW 9-fluorenylmethoxycarbonyl chemistry; Fmoc; peptide-resin conjugate;
 KW thioanisole; ethanedithiol; purification; precipitation; ether.
 XX
 XX Synthetic.
 OS
 XX WO9823635-A1.
 XX
 XX 04-JUN-1998.
 PD
 XX 01-DEC-1997; 97WO-AU00820.
 XX
 XX 29-NOV-1996; 96AU-0003903.
 PR
 XX (CSLC-) CSL LTD.
 PA (UYQU) UNIV QUEENSLAND.

XX PI Azouy-ziaadeh R, Frazer IH, Tindie R;
 XX DR WPI; 1998-322657/28.
 XX PT New peptide(s) comprising promiscuous T helper cell epitopes from
 XX PT papilloma virus proteins - used for, e.g. generation of immune
 XX PT response, and particularly for treating or preventing papilloma
 XX PT virus infection
 XX PS Disclosure; Figure 1; 70pp; English.
 XX CC Synthetic peptides AAW29566-W29581 cover the entire HPV16 E6 open
 XX CC reading frame, and were constructed to be used as antigens. The
 XX CC synthesis of these peptides was performed by using
 XX CC 9-fluorenylmethoxycarbonyl (Fmoc) chemistry on an applied biosystems 431A
 XX CC peptide synthesizer. This enables peptide-resin conjugates to be
 XX CC obtained which can be cleaved by the addition of thioanisole and
 XX CC ethanedithiol, thus releasing the peptide. To purify these peptides they
 XX CC were precipitated with cold ether. Peptides AAW29572 and AAW29576 both
 XX CC contain the t-helper cell epitopes given in AAW60838 and AAW60839
 XX CC respectively. These T helper cell epitopes generate an immune response
 XX CC against human papillomavirus (HPV), and thus can be used to treat HPV
 XX CC infections. These peptides have been found to provide immunity to HPV
 XX CC infection across a broad spectrum of MHC backgrounds, therefore they
 XX CC would enable a diverse genetically outbred group to be vaccinated.
 XX SQ Sequence 18 AA;
 Query Match 36.4%; Score 4; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KLPQ 10
 Db 4 KLPQ 7
 RESULT 72
 ABJ00634
 ID ABJ00634 standard; Peptide; 18 AA.
 AC ABJ00634;
 XX 05-SEP-2002 (first entry)
 XX B lymphocyte stimulator protein binding peptide #78.
 XX B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KW allergy; proliferative disease; infectious disease; arteriosclerosis;
 KW inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KW ischaemia; graft-versus-host disease; neurodegenerative disease;
 KW immunosuppressive; nephrotropic; antirheumatic; antiarthritic;
 KW neuroprotective; cytostatic; immunostimulant; antitumour; anti-HIV;
 KW antiasthmatic; anti-allergic; thyromimetic; antianaemic; haemostatic;
 KW dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 KW antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX OS Unidentified.
 XX WC200216411-A2.
 XX 28-FEB-2002.
 XX 17-AUG-2001; 2001WO-US25850.
 XX 18-AUG-2000; 2000US-226700P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Beltzer JP, Potter DM, Fleming TL, Rosen CA;
 XX WPI; 2002-499775/53.

XX The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B Lymphocyte stimulator binding polypeptide -
 XX Claim 70; Page 194; 387pp; English.
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with; aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of haematopoietic origin; or proliferative disease; and reducing
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX SQ Sequence 18 AA;
 Query Match 36.4%; Score 4; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QNPF 6
 Db 11 QNPF 14
 RESULT 73
 ABG33495
 ID ABG33495 standard; Peptide; 18 AA.
 AC ABG33495;
 XX 15-JUL-2002 (first entry)
 XX B Lymphocyte Stimulator (Blys) binding peptide #83.
 XX B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide;
 KW Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KW synovial fluid; saliva; mucus.
 XX Synthetic.
 XX WO200216412-A2.
 XX 28-FEB-2002.
 XX 17-AUG-2001; 2001WO-US25891.
 XX 18-AUG-2000; 2000US-226489P.
 XX (DYAX-) DYAX CORP.
 XX Beltzer JP, Potter MD, Fleming TJ, Ladner RC;
 XX WPI; 2002-351647/38.
 XX New B-lymphocyte stimulator binding polypeptide useful in detecting or
 PT isolating Blys or Blys-like polypeptide comprises a specified amino
 PT acid sequence -
 XX Claim 13; Page 74; 269pp; English.
 XX The invention relates to a B Lymphocyte Stimulator (Blys) binding
 CC polypeptide. Blys binding peptides bind Blys or Blys-like proteins
 CC reversibly or irreversibly. The binding peptides are used in detection,
 CC isolation and/or purification of Blys in a solution such as water or a
 CC buffer solution, as well as any fluid and/or cell obtained from an
 CC individual biological fluid, body tissue, body cell, cell line, tissue

CC culture or other source containing Blys or Blys-like polypeptides. The
 CC biological fluids include sera, plasma, lymph, blood, blood fraction,
 CC urine, synovial fluid, spinal fluid, saliva and mucous. Sequences
 CC ABG33406-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and
 CC ABG33852-33862 represent Blys binding peptides of the invention.
 XX
 SQ Sequence 18 AA;

Query Match 36.4%; Score 4; DB 23; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNFY 6
 DB 11 QNFY 14
 |||||

RESULT 74
 ID AAW79176
 XX AAW79176 standard; peptide; 19 AA.
 AC AAW79176;
 XX
 DT 25-JAN-1999 (first entry)
 XX
 DE Fusion immunoglobulin heavy chain HIV gp120 T cell epitope #54.
 DE
 KW B cell; T cell; epitope; immunoglobulin; heavy chain; gp120; IGH;
 KW human immune deficiency virus; HIV; tolerance; treatment; therapy;
 KW prophylaxis; vaccine; chemotherapy; immune response; modifier; tumour;
 KW microbial infection; autoimmune disease; antibody; apoptosis;
 KW antiviral T cell immunity.
 XX
 OS Mus sp.
 OS Homo sapiens.
 XX
 PN WO9836087-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 13-FEB-1998; 98WO-US02766.
 XX
 PR 13-FEB-1997; 97US-0040581.
 XX
 PA (AMNA-) AMERICAN NAT RED CROSS.
 XX
 PI Scott D, Zambidis E;
 XX
 DR WPI; 1998-506315/43.
 XX
 XX New fusion immunoglobulin heavy chain including gp120 epitopes and
 PT related complete antibodies - DNA, vectors and transformed cells,
 PT used to induce tolerance to the epitopes for treatment of human
 PT immune deficiency virus infection
 XX
 PS Disclosure; Page 49; 154pp; English.
 XX
 CC This sequence is an epitope used in the construction of a novel fusion
 CC immunoglobulin heavy chain (IGH) protein with a mammalian, especially
 CC human, IGH chain fused in frame at its N-terminus to one or more human
 CC immune deficiency virus (HIV) gp120 epitopes. Fusion Ig proteins and/or
 CC transfected cells are used to tolerate subjects to gp120 epitopes and to
 CC maintain this tolerance, particularly for treatment of HIV infection,
 CC optionally together with other therapeutic/prophylactic agents such as
 CC vaccines, chemotherapeutic agents and immune response modifiers. Such
 CC proteins can be used against other diseases where an immune response is
 CC deleterious, e.g. microbial infection, tumours or autoimmune disease.
 CC Induction of tolerance suppresses production of antibodies against gp120,
 CC so prevents or inhibits 'bystander' apoptosis of uninfected T cells that
 CC are bound to gp120 protein, maximising induction of protective antiviral
 CC T cell immunity.
 XX
 SQ Sequence 19 AA;

Query Match 36.4%; Score 4; DB 19; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 DB 9 FYKL 12
 |||||

RESULT 75
 ID AAY85068
 XX AAY85068 standard; peptide; 19 AA.
 AC AAY85068;
 XX
 DT 20-JUN-2000 (first entry)
 XX
 DE Immunogenic peptide #6 derived from FMDV non-structural protein 3B.
 XX
 KW Foot and mouth disease; FMDV; epitope; anti-FMDV antibody; diagnose;
 KW vaccine; immunoreagent; non-structural protein.
 XX
 OS Foot and mouth disease virus.
 XX
 PN US6048538-A.
 XX
 PD 11-APR-2000.
 XX
 PF 03-OCT-1997; 97US-0943173.
 XX
 PR -03-OCT-1997; 97US-0943173.
 XX
 PA (UNBI-) UNITED BIOMEDICAL INC.
 XX
 PI Yi Wang C, De Chen P, Shen F;
 XX
 DR WPI; 2000-328034/28.
 XX
 PT Peptide from non-structural proteins useful for detecting
 PT foot-and-mouth disease virus infection in animal comprises an
 PT immunogenic epitope specific to antibodies -
 XX
 PS Claim 1; Column 25-26; 23pp; English.
 XX
 CC This sequence represents a peptide derived from the non-structural
 CC protein 3B of the foot and mouth disease virus (FMDV). The amino acid
 CC sequence of the peptide corresponds to an immunodominant region of the
 CC FMDV non-structural protein and is an immunogenic epitope specific for
 CC anti-FMDV antibodies. The invention relates to peptides derived from
 CC three non-structural FMDV proteins. The peptides are useful as
 CC immunoreagents i.e. reagent in an immunoassay in detecting antibodies to
 CC FMDV or diagnosis of FMDV infection. The immunoassays are used to screen
 CC body fluids and tissues for the presence of FMDV-reactive antibodies and
 CC aid in the diagnosis of FMDV infection and differentiate infected from
 CC the vaccinated animals.
 XX
 SQ Sequence 19 AA;

Query Match 36.4%; Score 4; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
 DB 5 KLPQ 8
 |||||

Search completed: November 25, 2003, 18:15:47
 Job time : 37.633 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 21.883 Seconds
(without alignments)
92.715 Million cell updates/sec

Title: US-09-641-801-6
Perfect score: 11
Sequence: 1 MPQNFYKLPQM 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	15	US-10-281-652-6
2	4	36.4	4	11	US-09-852-910-9
3	4	36.4	7	11	US-09-310-346C-7
4	4	36.4	7	12	US-09-261-894-69
5	4	36.4	7	12	US-09-261-894-102
6	4	36.4	9	10	US-09-835-948-73
7	4	36.4	9	10	US-09-835-948-101
8	4	36.4	9	10	US-09-909-460-101
9	4	36.4	9	12	US-10-172-597-73
10	4	36.4	9	12	US-10-172-597-101
11	4	36.4	9	15	US-10-133-210-278
12	4	36.4	10	10	US-09-867-853-99
13	4	36.4	10	15	US-10-062-710-83
14	4	36.4	12	11	US-09-880-748-2884
15	4	36.4	12	11	US-09-845-612B-10
					Sequence 6, Appli
					Sequence 9, Appli
					Sequence 7, Appli
					Sequence 69, Appl
					Sequence 102, App
					Sequence 73, Appl
					Sequence 101, App
					Sequence 101, App
					Sequence 101, App
					Sequence 101, App
					Sequence 101, App
					Sequence 99, Appl
					Sequence 83, Appl
					Sequence 2884, Ap
					Sequence 10, Appli

16	4	36.4	13	12	US-09-927-734C-10	Sequence 10, Appl
17	4	36.4	15	15	US-10-038-407-16	Sequence 16, Appl
18	4	36.4	18	11	US-09-933-613-92	Sequence 92, Appl
19	4	36.4	18	12	US-09-932-322-92	Sequence 92, Appl
20	4	36.4	19	9	US-09-864-761-43517	Sequence 43517, A
21	4	36.4	20	11	US-09-974-879-610	Sequence 610, App
22	4	36.4	20	11	US-09-305-736-611	Sequence 611, App
23	4	36.4	20	12	US-09-818-683-611	Sequence 611, App
24	3	27.3	4	9	US-09-736-969A-4	Sequence 4, Appli
25	3	27.3	4	11	US-09-071-838-143	Sequence 143, App
26	3	27.3	4	11	US-09-784-641-8	Sequence 8, Appli
27	3	27.3	4	11	US-09-784-642-8	Sequence 8, Appli
28	3	27.3	4	15	US-10-213-512-143	Sequence 143, App
29	3	27.3	4	15	US-10-028-075B-85	Sequence 85, Appl
30	3	27.3	4	15	US-10-029-206A-85	Sequence 85, Appl
31	3	27.3	5	11	US-09-788-006-57	Sequence 57, Appl
32	3	27.3	5	11	US-09-788-006-58	Sequence 58, Appl
33	3	27.3	5	11	US-09-788-006-59	Sequence 59, Appl
34	3	27.3	5	12	US-10-027-038-18	Sequence 18, Appl
35	3	27.3	5	15	US-10-235-483-31	Sequence 31, Appl
36	3	27.3	6	8	US-08-424-550B-208	Sequence 208, App
37	3	27.3	6	8	US-08-424-550B-335	Sequence 335, App
38	3	27.3	6	10	US-09-486-734A-26	Sequence 26, Appl
39	3	27.3	6	10	US-09-529-759-27	Sequence 27, Appl
40	3	27.3	6	10	US-09-842-930A-46	Sequence 46, Appl
41	3	27.3	6	11	US-09-992-331-26	Sequence 26, Appl
42	3	27.3	6	11	US-09-997-961-38	Sequence 38, Appl
43	3	27.3	6	12	US-09-261-894-24	Sequence 24, Appl
44	3	27.3	6	12	US-10-137-867-150	Sequence 150, App
45	3	27.3	6	14	US-10-036-418-13	Sequence 13, Appl
46	3	27.3	6	14	US-10-036-418-14	Sequence 14, Appl
47	3	27.3	6	14	US-10-036-418-15	Sequence 15, Appl
48	3	27.3	6	14	US-10-036-418-16	Sequence 16, Appl
49	3	27.3	6	14	US-10-156-820-36	Sequence 36, Appl
50	3	27.3	6	15	US-10-121-857-16	Sequence 16, Appl
51	3	27.3	6	15	US-10-208-018-16	Sequence 16, Appl
52	3	27.3	6	16	US-10-262-313-26	Sequence 26, Appl
53	3	27.3	6	16	US-10-305-346-1	Sequence 1, Appli
54	3	27.3	7	9	US-09-821-380-9	Sequence 9, Appli
55	3	27.3	7	9	US-09-822-270-5	Sequence 5, Appli
56	3	27.3	7	9	US-09-749-234A-18	Sequence 18, Appl
57	3	27.3	7	9	US-09-832-723-17	Sequence 17, Appl
58	3	27.3	7	9	US-09-832-723-68	Sequence 68, Appl
59	3	27.3	7	10	US-09-347-117-9	Sequence 9, Appli
60	3	27.3	7	10	US-09-771-415-13	Sequence 13, Appl
61	3	27.3	7	10	US-09-771-035A-5	Sequence 5, Appli
62	3	27.3	7	10	US-09-771-035A-8	Sequence 8, Appli
63	3	27.3	7	10	US-09-996-288-102	Sequence 102, App
64	3	27.3	7	10	US-09-996-288-118	Sequence 118, App
65	3	27.3	7	10	US-09-884-767A-23	Sequence 23, Appl
66	3	27.3	7	11	US-09-229-751A-28	Sequence 28, Appl
67	3	27.3	7	11	US-09-845-612B-18	Sequence 18, Appl
68	3	27.3	7	11	US-09-996-265-102	Sequence 102, App
69	3	27.3	7	11	US-09-996-265-118	Sequence 118, App
70	3	27.3	7	11	US-09-954-385-81	Sequence 81, Appl
71	3	27.3	7	12	US-10-052-578-246	Sequence 246, App
72	3	27.3	7	12	US-10-303-331-17	Sequence 17, Appl
73	3	27.3	7	12	US-10-303-331-68	Sequence 68, Appli
74	3	27.3	7	12	US-10-293-371-4	Sequence 4, Appli
75	3	27.3	7	12	US-10-293-371-7	Sequence 7, Appli
76	3	27.3	7	12	US-10-022-066-538	Sequence 538, App
77	3	27.3	7	12	US-10-053-580-46	Sequence 46, App
78	3	27.3	7	12	US-10-262-435-72	Sequence 72, Appl
79	3	27.3	7	12	US-10-262-435-76	Sequence 76, Appl
80	3	27.3	7	12	US-10-262-435-78	Sequence 78, Appl
81	3	27.3	7	12	US-10-262-435-81	Sequence 81, Appl
82	3	27.3	7	12	US-10-262-522A-9	Sequence 9, Appli
83	3	27.3	7	12	US-10-262-522A-19	Sequence 19, Appl
84	3	27.3	7	12	US-10-262-522A-27	Sequence 27, Appl
85	3	27.3	7	12	US-10-262-522A-28	Sequence 28, Appl
86	3	27.3	7	12	US-10-286-457-6	Sequence 6, Appli
87	3	27.3	7	12	US-10-342-371-5	Sequence 5, Appli
88	3	27.3	7	12	US-10-436-826-4	Sequence 4, Appli

89 3 27.3 7 12 US-10-053-498B-246 Sequence 246, Appl
90 3 27.3 7 12 US-10-086-208-72 Sequence 72, Appl
91 3 27.3 7 12 US-10-086-208-76 Sequence 76, Appl
92 3 27.3 7 12 US-10-086-208-78 Sequence 78, Appl
93 3 27.3 7 12 US-10-086-208-81 Sequence 81, Appl
94 3 27.3 7 12 US-10-122-675-11 Sequence 11, Appl
95 3 27.3 7 12 US-09-361-894-4 Sequence 4, Appl
96 3 27.3 7 12 US-09-361-894-22 Sequence 22, Appl
97 3 27.3 7 12 US-09-361-894-23 Sequence 23, Appl
98 3 27.3 7 12 US-09-361-894-34 Sequence 34, Appl
99 3 27.3 7 12 US-09-361-894-35 Sequence 35, Appl
100 3 27.3 7 12 US-09-361-894-36 Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-6
; Sequence 6, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLCISTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-6

Query Match 100.0%; Score 11; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e-06; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0

QY 1 MPQNFYKLPQM 11
Db 1 MPQNFYKLPQM 11

RESULT 2
US-09-852-910-9
; Sequence 9, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: GLOHRIST, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor S
; FILE REFERENCE: 2861-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: mammal

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4)
; OTHER INFORMATION: PAR-34
US-09-852-910-9
Query Match 36.4%; Score 4; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0
QY 8 LPQM 11
Db 1 LPQM 4
RESULT 3
US-09-910-346C-7
; Sequence 7, Application US/09910346C
; Publication No. US20030027752A1
; GENERAL INFORMATION:
; APPLICANT: STEWARD, LANCE E
; APPLICANT: FERNANDEZ-SALAS, ESTER
; APPLICANT: HERRINGTON, TODD M
; APPLICANT: AOKI, KEI R
; TITLE OF INVENTION: Leucine-based motif and clostridial neurotoxins
; FILE REFERENCE: D-2885CIP
; CURRENT APPLICATION NUMBER: US/09/910,346C
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 09/620,840
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: This fragment may have come from
; OTHER INFORMATION: a rat source.
US-09-910-346C-7

Query Match 36.4%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0

QY 5 FYKL 8
Db 3 FYKL 6

RESULT 4
US-09-261-894-69
; Sequence 69, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/261,894
; FILING DATE: March 3, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-69

Query Match 36.4%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKLP 9
Db 3 YKLP 6

RESULT 5
US-09-261-894-102
; Sequence 102, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzheng
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,894
; FILING DATE: March 3, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-102

Query Match 36.4%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
Db 4 KLPQ 7

RESULT 6
US-09-835-948-73
; Sequence 73, Application US/09835948
; Patent No. US20020160365A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-B/D
; CURRENT APPLICATION NUMBER: US/09/835,948
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 09/492,543
; PRIOR FILING DATE: 01-27-2000
; NUMBER OF SEQ ID NOS: 189
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-09-835-948-73

Query Match 36.4%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5
Db 4 PQNF 7

RESULT 7
US-09-835-948-101
; Sequence 101, Application US/09835948
; Patent No. US20020160365A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-B/D
; CURRENT APPLICATION NUMBER: US/09/835,948
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 09/492,543
; PRIOR FILING DATE: 01-27-2000
; NUMBER OF SEQ ID NOS: 189
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-09-835-948-101

Query Match 36.4%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5
Db 4 PQNF 7

RESULT 8
US-09-909-460-101
; Sequence 101, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:

```

; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
; US-09-909-460-101

Query Match      36.4%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLPQ 10
DB      1 KLPQ 4

RESULT 9
US-10-172-597-73
; Sequence 73, Application US/10172597
; Publication No. US20030180736A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Methods for the Early Diagnosis of Ovarian Cancer
; FILE REFERENCE: D6223CIPB/D/CIP
; CURRENT APPLICATION NUMBER: US/10/172,597
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 09/835,948
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 189
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-10-172-597-73

Query Match      36.4%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PQNF 5
DB      4 PQNF 7

RESULT 10
US-10-172-597-101
; Sequence 101, Application US/10172597
; Publication No. US20030180736A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Methods for the Early Diagnosis of Ovarian Cancer
; FILE REFERENCE: D6223CIPB/D/CIP
; CURRENT APPLICATION NUMBER: US/10/172,597
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 09/835,948
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 189
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
US-10-172-597-101

Query Match      36.4%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PQNF 5
DB      4 PQNF 7

RESULT 11
US-10-133-210-278
; Sequence 278, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-095AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 278
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-278

Query Match      36.4%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLPQ 10
DB      1 KLPQ 4

RESULT 12
US-09-867-852-99
; Sequence 99, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RES2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13

```

```

; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-99

Query Match      36.4%; Score 4; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLPQ 10
DB      6 KLPQ 9

RESULT 13
US-10-062-710-83
; Sequence 83, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV CTL-Epitopes
US-10-062-710-83

Query Match      36.4%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 FYKL 8
DB      4 FYKL 7

RESULT 14
US-09-880-748-2884
; Sequence 2884, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2884
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2884

Query Match      36.4%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 QNFY 6
DB      5 QNFY 8

RESULT 15
US-09-845-612B-10
; Sequence 10, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANYUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOCH.
; TITLE OF INVENTION: POINT PROTEIN MAD2
; FILE REFERENCE: UMSD:795
; CURRENT APPLICATION NUMBER: US/09/845,612B
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(12)
; OTHER INFORMATION: synthetic peptide
US-09-845-612B-10

Query Match      36.4%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 YKLP 9
DB      3 YKLP 6

RESULT 16
US-09-927-734C-10
; Sequence 10, Application US/09927734C
; Publication No. US20030194758A1
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Nakata, Mitsunori
; TITLE OF INVENTION: Method for the Identification of Fungal Glucose Utilization
; TITLE OF INVENTION: Inhibitors and Antifungal Agents
; FILE REFERENCE: MYCOLOGX-06279
; CURRENT APPLICATION NUMBER: US/09/927,734C
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-927-734C-10

Query Match      36.4%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFYK 7
|
|
|
|
Db 6 NFYK 9

RESULT 17
US-10-038-407-16
; Sequence 16, Application US/10038407
; Publication No. US20030105282A1
; GENERAL INFORMATION:
; APPLICANT: Biotex
; TITLE OF INVENTION: HIV-1 gp120 V1/V2 DOMAIN EPITOPES
; TITLE OF INVENTION: CAPABLE OF GENERATING NEUTRALIZING ANTIBODIES
; FILE REFERENCE: 07763-048001
; CURRENT APPLICATION NUMBER: US/10/038,407
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: 09/508,208
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US98/18679
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: 60/058,155
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus (HIV)
US-10-038-407-16

Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8
|
|
|
|
Db 5 FYKL 8

RESULT 18
US-09-932-613-92
; Sequence 92, Application US/09932613
; Publication No. US2003091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BlyS binding polypeptide
US-09-932-613-92

Query Match 36.4%; Score 4; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6
|
|
|
|
Db 11 QNFY 14

RESULT 19

US-09-932-322-92
; Sequence 92, Application US/09932322
; Publication No. US20030194743A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Lachner, Robert Charles
; TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)
; FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
; CURRENT APPLICATION NUMBER: US/09/932,322
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BlyS binding polypeptide
US-09-932-322-92

Query Match 36.4%; Score 4; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6
|
|
|
|
Db 11 QNFY 14

RESULT 20
US-09-864-761-43517
; Sequence 43517, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662

```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43517
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002088.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
; OTHER INFORMATION: EST_HUMAN HIT: H56539.1, EVALUATE 6.00e-03
US-09-864-761-43517

```

```

Query Match          36.4%; Score 4; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 KLPQ 10
DB 4 KLPQ 7

```

```

RESULT 21
US-09-974-879-610
; Sequence 610, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020F2
; CURRENT APPLICATION NUMBER: US 09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066,090
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07

```

```

; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 610
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-610

```

```

Query Match          36.4%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 5 FYKL 8
DB 9 FYKL 12

```

```

RESULT 22
US-09-305-736-611
; Sequence 611, Application US/09305736
; Publication No. US2003008078A1
; GENERAL INFORMATION:
; APPLICANT: Peng et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020F1
; CURRENT APPLICATION NUMBER: US/09/305,736
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: PCT/US98/23435
; EARLIER FILING DATE: 1998-11-04
; EARLIER APPLICATION NUMBER: 60/064,911
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,912
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,983
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,900
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,988
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,987
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,908
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,984
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/064,985
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: 60/066,094
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,100
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,089
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,095
; EARLIER FILING DATE: 1997-11-17
; EARLIER APPLICATION NUMBER: 60/066,090
; NUMBER OF SEQ ID NOS: 612
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 611
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens

```


; MOLECULE TYPE: peptide
US-09-071-838-143

Query Match 27.3%; Score 3; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFY 6
|||
Db 1 NFY 3

RESULT 26

US-09-784-641-8
; Sequence 8, Application US/09784641
; Publication No. US20030050260A1
; GENERAL INFORMATION:
; APPLICANT: NewMillennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: METHOD FOR TREATING DIABETES BY REDUCING IN VIVO CATHPSIN L ACTI
; FILE REFERENCE: 26748-702
; CURRENT APPLICATION NUMBER: US/09/784,641
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-641-8

Query Match 27.3%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
|||
Db 1 FYK 3

RESULT 27

US-09-784-642-8
; Sequence 8, Application US/09784642
; Publication No. US20030054984A1
; GENERAL INFORMATION:
; APPLICANT: NewMillennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: METHOD FOR REDUCING BLOOD INSULIN LEVELS BY REDUCING IN VIVO CAT
; FILE REFERENCE: 26748-703
; CURRENT APPLICATION NUMBER: US/09/784,642
; CURRENT FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-784-642-8

Query Match 27.3%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
|||
Db 1 FYK 3

RESULT 28

US-10-213-512-143
; Sequence 143, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.

; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; FILE REFERENCE: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-143

Query Match 27.3%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFY 6
|||
Db 1 NFY 3

RESULT 29

US-10-028-075B-85
; Sequence 85, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pcd/IGBR/IGBR-B
US-10-028-075B-85

Query Match 27.3%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 2 KLP 4

RESULT 30

US-10-029-206A-85
; Sequence 85, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert


```

; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pdb/1GBR/1GBR-B
US-10-029-206A-85

Query Match      27.3%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 KLP 9
      |||
Db      2 KLP 4

RESULT 31
US-09-788-006-57
; Sequence 57, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; TITLE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-57

Query Match      27.3%; Score 3; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 YKL 8
      |||
Db      1 YKL 3

RESULT 34
US-10-027-038-18
; Sequence 18, Application US/10027038
; Publication No. US20030159380A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, S.
; TITLE OF INVENTION: Modular peptide-based reagent
; FILE REFERENCE: 1443.026US1
; CURRENT APPLICATION NUMBER: US/10/027,038
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide interactive domain.
US-10-027-038-18

Query Match      27.3%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 YKL 8
      |||
Db      1 YKL 3

RESULT 35
US-10-235-483-31
; Sequence 31, Application US/10235483
; Publication No. US20030087407A1

```

```
/
/
/ GENERAL INFORMATION:
/ APPLICANT: SOTO-JARA, Claudio
/ BAUMANN, Marc
/ FRANGIONE, Blas
/
/ TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
/ COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
/ ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
/ DEPOSITS
/
/ NUMBER OF SEQUENCES: 69
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEWMARK
/ STREET: 419 Seventh Street, N.W., Suite 400
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/235,483
/ FILING DATE: 06-Sep-2002
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/766,596
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US/08/630,645
/ FILING DATE: 10-APR-1996
/ APPLICATION NUMBER: US/08/478,326
/ FILING DATE: 06-JUN-1995
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: YUN, Allen C.
/ REGISTRATION NUMBER: 37,971
/ REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 31:
/
/ US-10-235-483-31
/
/
/ Query Match 27.3%; Score 3; DB 15; Length 5;
/ Best Local Similarity 100.0%; Pred. No. 6e+05;
/ Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 7 KLP 9
/ DB 1 KLP 3
/
/ RESULT 36
/ US-08-424-550B-208
/ Sequence 208, Application US/08424550B
/ Publication No. US20020119447A1
/
/ GENERAL INFORMATION:
/ APPLICANT: JOHN N. SIMONS
/ APPLICANT: TAMI J. PILOT-MATIAS
/ APPLICANT: GEORGE J. DAWSON
/ APPLICANT: GEORGE G. SCHLAUDER
/ APPLICANT: SURESH M. DESAI
/ APPLICANT: THOMAS P. LEARY
/ APPLICANT: ANTHONY SCOTT MUEHROFF
/ APPLICANT: JAMES C. ERKER
/ APPLICANT: SHERI L. BUIJK
/ APPLICANT: ISA K. MUSHAWAR
/
/ TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
/ NUMBER OF SEQUENCES: 716
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ABBOTT LABORATORIES
/ STREET: 100 ABBOTT PARK ROAD
/ CITY: ABBOTT PARK
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60064-3500
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/
/ US-08-424-550B-208
```

```
/
/
/ TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
/ TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
/ NUMBER OF SEQUENCES: 716
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ABBOTT LABORATORIES
/ STREET: 100 ABBOTT PARK ROAD
/ CITY: ABBOTT PARK
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60064-3500
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/424,550B
/ FILING DATE:
/ CLASSIFICATION: 435435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: FOREMSKI, PRISCILLA E.
/ REGISTRATION NUMBER: 33,207
/ REFERENCE/DOCKET NUMBER: 5527.PC.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 708-937-6365
/ TELEFAX: 708-938-2623
/
/ INFORMATION FOR SEQ ID NO: 208:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: protein
/
/ US-08-424-550B-208
/
/
/ Query Match 27.3%; Score 3; DB 8; Length 6;
/ Best Local Similarity 100.0%; Pred. No. 6e+05;
/ Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 8 LPQ 10
/ DB 4 LPQ 6
/
/ RESULT 37
/ US-08-424-550B-335
/ Sequence 335, Application US/08424550B
/ Publication No. US20020119447A1
/
/ GENERAL INFORMATION:
/ APPLICANT: JOHN N. SIMONS
/ APPLICANT: TAMI J. PILOT-MATIAS
/ APPLICANT: GEORGE J. DAWSON
/ APPLICANT: GEORGE G. SCHLAUDER
/ APPLICANT: SURESH M. DESAI
/ APPLICANT: THOMAS P. LEARY
/ APPLICANT: ANTHONY SCOTT MUEHROFF
/ APPLICANT: JAMES C. ERKER
/ APPLICANT: SHERI L. BUIJK
/ APPLICANT: ISA K. MUSHAWAR
/
/ TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
/ NUMBER OF SEQUENCES: 716
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ABBOTT LABORATORIES
/ STREET: 100 ABBOTT PARK ROAD
/ CITY: ABBOTT PARK
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60064-3500
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/
/ US-08-424-550B-335
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 335:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-424-550B-335

```

```

Query Match      27.3%; Score 3; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      8 LPQ 10
      |||
Db      3 LPQ 5

```

```

RESULT 39
US-09-486-734A-26
; Sequence 26, Application US/09486734A
; Patent No. US2002016473A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dusko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; APPLICANT: Institut National de la Recherche Agronomique
; TITLE OF INVENTION: Resistance Mechanisms to IC Type R/M
; FILE REFERENCE: Bacteriophages of Lactic Acid Bacteria
; CURRENT APPLICATION NUMBER: US/09/486,734A
; CURRENT FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: PCT/FR98/01873
; PRIOR FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: FR 97/10885
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HsdM subunit
; US-09-486-734A-26

```

```

Query Match      27.3%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 FYK 7
      |||
Db      1 FYK 3

```

```

RESULT 39
US-09-523-759-27
; Sequence 27, Application US/09529759
; Publication No. US2002019264A1
; GENERAL INFORMATION:
; APPLICANT: Vivier, Eric

```

```

; APPLICANT: Vely, Frederic
; TITLE OF INVENTION: DOCUMENTATION MEANS FOR REPERTOIRES OF
; TITLE OF INVENTION: NKR IMMUNORECEPTORS AND/OR ACTIVATORY OR NON-INHIBITORY
; TITLE OF INVENTION: IMMUNORECEPTOR COUNTERPARTS OF NKR IMMUNORECEPTORS
; FILE REFERENCE: A33131 PCT USA 067858.0101
; CURRENT APPLICATION NUMBER: US/09/529,759
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: FR 97/13115
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Human
; US-09-529-759-27

```

```

Query Match      27.3%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 KLP 9
      |||
Db      1 KLP 3

```

```

RESULT 40
US-09-842-930A-46
; Sequence 46, Application US/09842930A
; Publication No. US20020197681A1
; GENERAL INFORMATION:
; APPLICANT: Weigel, Paul
; TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis
; FILE REFERENCE: 5820.603
; CURRENT APPLICATION NUMBER: US/09/842,930A
; CURRENT FILING DATE: 2001-04-22
; PRIOR APPLICATION NUMBER: 60/245,320
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 60/199,538
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-842-930A-46

```

```

Query Match      27.3%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MPQ 3
      |||
Db      1 MPQ 3

```

```

RESULT 41
US-09-992-331-26
; Sequence 26, Application US/09992331
; Publication No. US20030022186A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, JOHN N.
; APPLICANT: MINTIER, GABE
; APPLICANT: RAMANATHAN, CHANDRA S.
; APPLICANT: RAMANATHAN, DONALD R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV18.
; TITLE OF INVENTION: EXPRESSED HIGHLY IN PITUITARY GLAND AND COLON CARCINOMA
; FILE REFERENCE: D0048NP
; CURRENT APPLICATION NUMBER: US/09/992,331
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/308,540

```

;
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/261,782
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/248,483
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
; OTHER INFORMATION: Peptide
US-09-992-331-26

Query Match 27.3%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5
Db 1 QNF 3

RESULT 42
US-09-997-961-38
; Sequence 38, Application US/0997961
; Publication No. US20030060613A1
; GENERAL INFORMATION:
; APPLICANT: DEDHAR, Shoukat
; TITLE OF INVENTION: NOVEL USE OF CALRETICULIN IN MODULATING
; HORMONE RESPONSIVENESS AND NEW PHARMACEUTICALS FOR
; TREATING CANCER, OSTEOPOROSIS AND CHRONIC INFLAMMATORY
; DISEASE
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 29-Jan-1995
; APPLICATION NUMBER: US/09/997,961
; FILING DATE: 24-JAN-1995
; CLASSIFICATION: Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,935
; FILING DATE: Unknown>
; APPLICATION NUMBER: US/08/377,432
; FILING DATE: 24-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mooi, Leslie A
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 007315-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-997-961-38

Query Match 27.3%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
Db 3 FYK 5

RESULT 43
US-09-261-894-24
; Sequence 24, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: March 3, 1999
; APPLICATION NUMBER: US/09/261,894
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-24

Query Match 27.3%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
Db 4 KLP 6

RESULT 44
US-10-137-967-150
; Sequence 150, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.

```

; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3390RIC146
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 150
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-150

Query Match 27.3%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPO 10
Db 3 LPQ 5

RESULT 45
US-10-036-418-13
; Sequence 13, Application US/10036418
; Publication No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-13

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
Db 4 KLP 6

RESULT 46
US-10-036-418-14
; Sequence 14, Application US/10036418
; Publication No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07

```

```

; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-14

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
Db 3 KLP 5

RESULT 47
US-10-036-418-15
; Sequence 15, Application US/10036418
; Publication No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-15

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
Db 2 KLP 4

RESULT 48
US-10-036-418-16
; Sequence 16, Application US/10036418
; Publication No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Cricetulus
US-10-036-418-16

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 7 KLP 9
|||
Db 1 KLP 3

RESULT 49

US-10-156-820-36
; Sequence 36, Application US/10156820
; Publication No. US2002015058A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karavan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCI/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope
US-10-156-820-36

Query Match 27.3%; Score 3; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 4 KLP 6

RESULT 50

US-10-121-857-16
; Sequence 16, Application US/10121857
; Publication No. US20030028923A1
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.143
; CURRENT APPLICATION NUMBER: US/10/121,857
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mortierella ramanniana
US-10-121-857-16

Query Match 27.3%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 1 KLP 3

RESULT 51

US-10-208-018-16
; Sequence 16, Application US/10208018
; Publication No. US20030115632A1
; GENERAL INFORMATION:
; APPLICANT: Lardizabal, Kathryn D
; APPLICANT: Hawkins, Deborah J
; APPLICANT: Thompson, Gregory A
; TITLE OF INVENTION: Diacylglycerol Acyltransferase Proteins
; FILE REFERENCE: 16515.155
; CURRENT APPLICATION NUMBER: US/10/208,018
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 10/121,857
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 09/345,461
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/091,631
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/130,829
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mortierella ramanniana
US-10-208-018-16

Query Match 27.3%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
|||
Db 1 KLP 3

RESULT 52

US-10-262-313-26
; Sequence 26, Application US/10262313
; Publication No. US20030129653A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP8MW18, EXPRESSED HIGH
; FILE REFERENCE: D0048 CIP
; CURRENT APPLICATION NUMBER: US/10/262,313
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: U.S. 09/992,331
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-313-26

Query Match 27.3%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QNF 5
|||
Db 1 QNF 3

RESULT 53

```
US-10-305-346-1
; Sequence 1, Application US/10305346
; Publication No. US20030130195A1
; GENERAL INFORMATION:
; APPLICANT: AMIOT, Jean
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57"US"-1
; CURRENT APPLICATION NUMBER: US/10/305,346
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins
US-10-305-346-1

Query Match      27.3%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LPQ 10
      |||
Db      2 LPQ 4

RESULT 54
US-09-821-380-9
; Sequence 9, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Amed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/????.???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-9

Query Match      27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 LPQ 10
      |||
Db      5 LPQ 7

RESULT 55
US-09-822-270-5
; Sequence 5, Application US/09822270
; Patent No. US20020068697A1
; GENERAL INFORMATION:
; APPLICANT: TOURNAIRE, ROSELYNE
; APPLICANT: DEMANGEL, CAROLINE
; APPLICANT: DERBIN, CLAUDE
; APPLICANT: PERRET, GERARD
; APPLICANT: MAZIE, JEAN-CLAUDE
; APPLICANT: PLOUET, JEAN
; APPLICANT: VASSAY, ROGER
; TITLE OF INVENTION: PEPTIDES BLOCKING VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-MEDIA
; FILE REFERENCE: 205060USO
; CURRENT APPLICATION NUMBER: US/09/822,270
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/193,396
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-09-822-270-5

Query Match      27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 YKL 8
      |||
Db      5 YKL 7

RESULT 56
US-09-749-234A-18
; Sequence 18, Application US/09749234A
; Patent No. US20020068817A1
; GENERAL INFORMATION:
; APPLICANT: HOFMANN, Joachim
; APPLICANT: SCHMID, Karlheirich
; APPLICANT: PAULI, Adriette
; TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR THE
; DIAGNOSIS OF LONGWORM INFESTATION AND FOR VACCINATION
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/749,234A
; FILING DATE: 27-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/403,092
; FILING DATE: 199-10-15
; APPLICATION NUMBER: DE 197 15 586.3
; FILING DATE: 15-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 038311/0103
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
```

```
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 7 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-749-234A-18

Query Match          27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PON 4
Db 4 PON 6

RESULT 57
US-09-832-723-17
; Sequence 17, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides screened from a phage display random
; OTHER INFORMATION: Peptide library
US-09-832-723-17

Query Match          27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
Db 5 KLP 7

RESULT 58
US-09-832-723-68
; Sequence 68, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides screened from a phage display random
; OTHER INFORMATION: Peptide library
US-09-832-723-68

Query Match          27.3%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
Db 5 KLP 7

RESULT 59
US-09-947-137-3
; Sequence 3, Application US/09947137
; Patent No. US20020137023A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Bruce F.
; APPLICANT: Samoilova, Tatiana
; TITLE OF INVENTION: Methods and Compositions for Targeting
; FILE REFERENCE: 5721-8
; CURRENT APPLICATION NUMBER: US/09/947,137
; CURRENT FILING DATE: 2001-09-05
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phage display library peptides
US-09-947-137-3

Query Match          27.3%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLP 9
Db 5 KLP 7

RESULT 60
US-09-771-415-13
; Sequence 13, Application US/09771415
; Patent No. US20020164326A1
; GENERAL INFORMATION:
; APPLICANT: Young, James F.
; APPLICANT: Koenig, Scott
; APPLICANT: Johnson, Leslie S.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; APPLICANT: Watkins, Jeffrey D.
; TITLE OF INVENTION: Ultra High Affinity Neutralizing Antibodies
; FILE REFERENCE: 469201-520
; CURRENT APPLICATION NUMBER: US/09/771,415
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```


; GENERAL INFORMATION:
 ; APPLICANT: DYAX Corp.
 ; APPLICANT: Ley, Arthur C.
 ; APPLICANT: Luneau, Christopher J.
 ; APPLICANT: Ladner, Robert C.
 ; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
 ; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
 ; CURRENT APPLICATION NUMBER: US/09/884,767A
 ; CURRENT FILING DATE: 2001-06-19
 ; PRIOR APPLICATION NUMBER: US 09/597,321
 ; PRIOR FILING DATE: 2000-06-19
 ; NUMBER OF SEQ ID NOS: 217
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic enterokinase cleavage sequence
 US-09-884-767A-23

Query Match 27.3%; Score 3; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MPQ 3
 DB 2 MPQ 4

RESULT 66
 US-09-229-751A-28
 ; Sequence 28, Application US/09229751A
 ; Publication No. US20030044838A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Turbough, Charles K
 ; TITLE OF INVENTION: PEPTIDE LIGANDS THAT BIND TO SURFACES
 ; NUMBER OF SEQUENCES: 80
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Glenna Hendricks
 ; STREET: P.O. Box 2509
 ; CITY: Fairfax
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22031
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/09/229,751A
 ; APPLICATION NUMBER: US/09/229,751A
 ; FILING DATE: 14-Jan-1999
 ; CLASSIFICATION: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hendricks, Glenna M
 ; REGISTRATION NUMBER: 32,535
 ; REFERENCE/DOCKET NUMBER: turn
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 425-8405
 ; TELEFAX: (703) 425-8406
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: amino acid
 ; LENGTH: 7 amino acids
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
 US-09-229-751A-28

Query Match 27.3%; Score 3; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 2 PQN 4
 DB 5 PQN 7

RESULT 67
 US-09-845-612B-18
 ; Sequence 18, Application US/09845612B
 ; Publication No. US200300303261A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YU, HONGTAO
 ; APPLICANT: TANG, ZHANYUN
 ; APPLICANT: LUO, XUELIAN
 ; APPLICANT: RIZO-REY, JOSE
 ; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOTIC
 ; FILE REFERENCE: UTSID:795
 ; CURRENT APPLICATION NUMBER: US/09/845,612B
 ; CURRENT FILING DATE: 2001-04-27
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 18
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (4)..(5)
 ; OTHER INFORMATION: X is any
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (1)..(7)
 ; OTHER INFORMATION: Synthetic Peptide
 US-09-845-612B-18

Query Match 27.3%; Score 3; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 6 YKL 8
 DB 2 YKL 4

RESULT 68
 US-09-996-265-102
 ; Sequence 102, Application US/09996265
 ; Publication No. US20030091584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, James
 ; APPLICANT: Scott, Koenig
 ; APPLICANT: Leslie, Johnson
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
 ; FILE REFERENCE: 10271-048-999
 ; CURRENT APPLICATION NUMBER: US/09/996,265
 ; CURRENT FILING DATE: 2001-11-28
 ; NUMBER OF SEQ ID NOS: 259
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 102
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-996-265-102

Query Match 27.3%; Score 3; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 7 KLP 9
 DB 4 KLP 6

RESULT 69

US-09-996-265-118
 ; Sequence 118, Application US/09996265
 ; Publication No. US20030091584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, James
 ; APPLICANT: Scott, Koenig
 ; APPLICANT: Leslie, Johnson
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
 ; FILE REFERENCE: 10271-048-999
 ; CURRENT APPLICATION NUMBER: US/09/996,265
 ; CURRENT FILING DATE: 2001-11-28
 ; NUMBER OF SEQ ID NOS: 259
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 118
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-996-265-118

Query Match 27.3%; Score 3; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
 DB 4 KLP 6

RESULT 70

US-09-954-385-81
 ; Sequence 81, Application US/09954385
 ; Publication No. US20030100467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aehle, Wolfgang
 ; APPLICANT: Baldwin, Toby L.
 ; APPLICANT: Van Gastel, Franciscus J.C.
 ; APPLICANT: Janssen, Giselle G.
 ; APPLICANT: Murray, Christopher J.
 ; APPLICANT: Wang, Huang
 ; APPLICANT: Winetzk, Deborah S.
 ; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
 ; FILE REFERENCE: GC690
 ; CURRENT APPLICATION NUMBER: US/09/954,385
 ; CURRENT FILING DATE: 2001-09-12
 ; NUMBER OF SEQ ID NOS: 433
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 81
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: binding peptide
 US-09-954-385-81

Query Match 27.3%; Score 3; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 DB 1 LPQ 3

RESULT 71

US-10-052-578-246
 ; Sequence 246, Application US/10052578
 ; Publication No. US20030134787A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sloan-Kettering Institute for Cancer Research
 ; APPLICANT: Rothman, James E.
 ; APPLICANT: Mayhew, Mark
 ; APPLICANT: Hoe, Mee H.
 ; APPLICANT: Houghton, Alan
 ; APPLICANT: Hartl, Ulrich
 ; APPLICANT: Ouerfelli, Ouathek
 ; APPLICANT: Moroi, Yoichi
 ; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
 ; FILE REFERENCE: 11746/46003
 ; CURRENT APPLICATION NUMBER: US/10/052,578
 ; CURRENT FILING DATE: 2002-01-17
 ; PRIOR APPLICATION NUMBER: 08/961,707
 ; PRIOR FILING DATE: 1997-10-31
 ; NUMBER OF SEQ ID NOS: 321
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 246
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide in m13 coliphage
 US-10-052-578-246

Query Match 27.3%; Score 3; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
 DB 1 KLP 3

RESULT 72

US-10-303-331-17
 ; Sequence 17, Application US/10303331
 ; Publication No. US20030152976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Janssen, Giselle G.
 ; APPLICANT: Murray, Christopher J.
 ; APPLICANT: Winetzk, Deborah S.
 ; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
 ; FILE REFERENCE: GC617-3
 ; CURRENT APPLICATION NUMBER: US/10/303,331
 ; CURRENT FILING DATE: 2002-11-25
 ; PRIOR APPLICATION NUMBER: US 09/832,723
 ; PRIOR FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: US 60/197,259
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptides screened from a phage display random
 ; OTHER INFORMATION: peptide library
 US-10-303-331-17

Query Match 27.3%; Score 3; DB 12; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
 DB 5 KLP 7

RESULT 73

US-10-303-331-68
; Sequence 68, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Muiray, Christopher J.
; APPLICANT: Winetzky, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-10-303-331-68

Query Match 27.3%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQ 3
|||
DB 1 MPQ 3

RESULT 74

US-10-293-371-4
; Sequence 4, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELOUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-4

Query Match 27.3%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQ 3
|||
DB 5 MPQ 7

RESULT 75

US-10-293-371-7
; Sequence 7, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELOUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-7

Query Match 27.3%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQ 3
|||
DB 5 MPQ 7

Search completed: November 25, 2003, 20:25:32
Job time : 22.883 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 11.9947 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-6
Perfect score: 11
Sequence: 1 MPQNFYKLQW 11

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCFUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	4	US-09-641-803-6
2	4	36.4	7	2	US-08-968-676-69
3	4	36.4	7	2	US-08-968-676-102
4	4	36.4	9	1	US-08-787-547-101
5	4	36.4	9	4	US-08-492-543-73
6	4	36.4	9	4	US-09-492-543-101
7	4	36.4	10	1	US-07-797-692-5
8	4	36.4	10	2	US-08-310-912A-99
9	4	36.4	10	3	US-08-841-089-99
10	4	36.4	10	3	US-08-301-085-99
11	4	36.4	10	5	PCT-US95-04570-99
12	4	36.4	10	5	PCT-US95-04589-99
13	4	36.4	15	1	US-07-797-692-1
14	4	36.4	15	1	US-07-797-692-7
15	4	36.4	15	1	US-07-909-122-2
16	4	36.4	15	1	US-08-709-047-11
17	4	36.4	15	1	US-08-410-360-11
18	4	36.4	15	1	US-08-707-804A-11
19	4	36.4	15	1	US-08-709-006-11
20	4	36.4	15	1	US-08-711-175-11
21	4	36.4	15	2	US-07-950-571A-4
22	4	36.4	15	3	US-08-075-541D-52
23	4	36.4	16	1	US-08-110-300A-22
24	4	36.4	16	2	US-08-886-642-22
25	4	36.4	17	1	US-08-468-543-19
26	4	36.4	17	1	US-08-469-692-19
27	4	36.4	17	2	US-08-398-046-19
28	4	36.4	4	3	Sequence 6, Appl
29	4	36.4	4	3	Sequence 69, Appl
30	4	36.4	4	3	Sequence 102, Appl
31	4	36.4	4	3	Sequence 101, Appl
32	3	27.3	3	2	Sequence 73, Appl
33	3	27.3	3	2	Sequence 101, Appl
34	3	27.3	3	2	Sequence 5, Appl
35	3	27.3	3	2	Sequence 99, Appl
36	3	27.3	3	2	Sequence 99, Appl
37	3	27.3	3	2	Sequence 99, Appl
38	3	27.3	3	2	Sequence 99, Appl
39	3	27.3	3	2	Sequence 7, Appl
40	3	27.3	3	2	Sequence 2, Appl
41	3	27.3	3	2	Sequence 11, Appl
42	3	27.3	3	2	Sequence 11, Appl
43	3	27.3	3	2	Sequence 11, Appl
44	3	27.3	3	2	Sequence 4, Appl
45	3	27.3	3	2	Sequence 52, Appl
46	3	27.3	3	2	Sequence 22, Appl
47	3	27.3	3	2	Sequence 19, Appl
48	3	27.3	3	2	Sequence 19, Appl
49	3	27.3	3	2	Sequence 19, Appl
50	3	27.3	3	2	Sequence 19, Appl
51	3	27.3	3	2	Sequence 19, Appl
52	3	27.3	3	2	Sequence 19, Appl
53	3	27.3	3	2	Sequence 19, Appl
54	3	27.3	3	2	Sequence 19, Appl
55	3	27.3	3	2	Sequence 19, Appl
56	3	27.3	3	2	Sequence 19, Appl
57	3	27.3	3	2	Sequence 19, Appl
58	3	27.3	3	2	Sequence 19, Appl
59	3	27.3	3	2	Sequence 19, Appl
60	3	27.3	3	2	Sequence 19, Appl
61	3	27.3	3	2	Sequence 19, Appl
62	3	27.3	3	2	Sequence 19, Appl
63	3	27.3	3	2	Sequence 19, Appl
64	3	27.3	3	2	Sequence 19, Appl
65	3	27.3	3	2	Sequence 19, Appl
66	3	27.3	3	2	Sequence 19, Appl
67	3	27.3	3	2	Sequence 19, Appl
68	3	27.3	3	2	Sequence 19, Appl
69	3	27.3	3	2	Sequence 19, Appl
70	3	27.3	3	2	Sequence 19, Appl
71	3	27.3	3	2	Sequence 19, Appl
72	3	27.3	3	2	Sequence 19, Appl
73	3	27.3	3	2	Sequence 19, Appl
74	3	27.3	3	2	Sequence 19, Appl
75	3	27.3	3	2	Sequence 19, Appl
76	3	27.3	3	2	Sequence 19, Appl
77	3	27.3	3	2	Sequence 19, Appl
78	3	27.3	3	2	Sequence 19, Appl
79	3	27.3	3	2	Sequence 19, Appl
80	3	27.3	3	2	Sequence 19, Appl
81	3	27.3	3	2	Sequence 19, Appl
82	3	27.3	3	2	Sequence 19, Appl
83	3	27.3	3	2	Sequence 19, Appl
84	3	27.3	3	2	Sequence 19, Appl
85	3	27.3	3	2	Sequence 19, Appl
86	3	27.3	3	2	Sequence 19, Appl
87	3	27.3	3	2	Sequence 19, Appl
88	3	27.3	3	2	Sequence 19, Appl
89	3	27.3	3	2	Sequence 19, Appl
90	3	27.3	3	2	Sequence 19, Appl
91	3	27.3	3	2	Sequence 19, Appl
92	3	27.3	3	2	Sequence 19, Appl
93	3	27.3	3	2	Sequence 19, Appl
94	3	27.3	3	2	Sequence 19, Appl
95	3	27.3	3	2	Sequence 19, Appl
96	3	27.3	3	2	Sequence 19, Appl
97	3	27.3	3	2	Sequence 19, Appl
98	3	27.3	3	2	Sequence 19, Appl
99	3	27.3	3	2	Sequence 19, Appl
100	3	27.3	3	2	Sequence 19, Appl

Sequence 9, Appl
Sequence 158, App
Sequence 159, App
Sequence 6, Appl
Sequence 182, App
Sequence 143, App
Patent No. 5258287
Sequence 41, Appl
Sequence 42, Appl
Sequence 22, Appl
Sequence 11, Appl
Sequence 4, Appl
Sequence 81, Appl
Sequence 17, Appl
Sequence 31, Appl
Sequence 21, Appl
Sequence 3, Appl
Sequence 27, Appl
Sequence 5, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 57, Appl
Sequence 38, Appl
Sequence 24, Appl
Sequence 3, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 76, Appl
Sequence 36, Appl
Sequence 30, Appl
Sequence 2, Appl
Sequence 208, App
Sequence 335, App
Sequence 335, App
Sequence 26, Appl
Sequence 10, Appl
Sequence 14, Appl
Sequence 5, Appl
Sequence 72, Appl
Sequence 76, Appl
Sequence 78, Appl
Sequence 81, Appl
Sequence 4, Appl
Sequence 28, Appl
Sequence 22, Appl
Sequence 34, Appl
Sequence 35, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 43, Appl
Sequence 44, Appl
Sequence 59, Appl
Sequence 60, Appl
Sequence 61, Appl
Sequence 62, Appl
Sequence 63, Appl
Sequence 64, Appl
Sequence 65, Appl

US-08-943-173-9
US-08-934-915-158
US-08-934-915-159
US-08-667-001-6
US-08-974-549A-182
US-09-177-249-143
5258287-45
US-08-014-979-41
US-08-014-979-42
US-08-447-010-22
US-08-667-001-11
US-08-581-122-4
US-08-652-877-81
US-08-476-515A-81
US-09-381-244B-17
US-08-766-596A-31
US-09-043-877-21
US-08-106-493A-3
US-08-429-264-3
US-08-260-199A-27
US-08-532-065B-5
US-07-923-724-62
US-08-609-426A-62
US-08-374-652C-57
US-08-377-432-38
US-08-968-676-24
US-08-819-444-3
US-08-819-444-5
US-09-186-934-6
US-08-803-346-76
US-09-155-613A-36
US-09-581-944A-30
US-08-000-286A-2
US-08-469-260A-208
US-08-469-260A-335
US-09-492-766-1
US-08-900-241-38
US-09-209-676-40
US-09-555-352-26
US-08-488-446-208
US-08-488-446-335
US-08-467-344A-208
US-08-467-344A-335
PCT-US93-01669-26
US-08-127-499A-10
US-08-537-069-14
US-08-177-109A-5
US-08-893-853-72
US-08-893-853-76
US-08-893-853-78
US-08-893-853-81
US-08-968-676-4
US-08-968-676-22
US-08-968-676-23
US-08-968-676-34
US-08-968-676-35
US-08-968-676-36
US-08-968-676-37
US-08-968-676-38
US-08-968-676-39
US-08-968-676-40
US-08-968-676-41
US-08-968-676-42
US-08-968-676-43
US-08-968-676-44
US-08-968-676-59
US-08-968-676-60
US-08-968-676-61
US-08-968-676-62
US-08-968-676-63
US-08-968-676-64
US-08-968-676-65

ALIGNMENTS

RESULT 1
 US-09-641-803-6
 ; Sequence 6, Application US/09641803
 ; Patent No. 6500798
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan
 ; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
 ; FILE REFERENCE: 265.00220101
 ; CURRENT APPLICATION NUMBER: US/09/641,803
 ; PRIOR FILING DATE: 2000-08-17
 ; PRIOR APPLICATION NUMBER: 60/149,310
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: peptide
 US-09-641-803-6

Query Match 100.0%; Score 11; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQM 11
 |||||
 Db 1 MPQNFYKLPQM 11

RESULT 2
 US-08-968-676-69
 ; Sequence 69, Application US/08968676
 ; Patent No. 5913639
 ; GENERAL INFORMATION:
 ; APPLICANT: Humphreys, Robert E
 ; APPLICANT: Adams, Shariene
 ; APPLICANT: Xu, Minzhen
 ; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
 ; NUMBER OF SEQUENCES: 165
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kevin M. Farrell, P.C.
 ; STREET: P.O. Box 999
 ; CITY: York Harbor
 ; STATE: ME
 ; COUNTRY: USA
 ; ZIP: 03911
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Farrell, Kevin M
 ; REGISTRATION NUMBER: 35,505
 ; REFERENCE/DOCKET NUMBER: REH-9601
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (207) 363-0558
 ; INFORMATION FOR SEQ ID NO: 125
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-968-676-69

Query Match 36.4%; Score 4; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
 ||||
 Db 4 KLPQ 7

RESULT 4
 US-08-787-547-101
 ; Sequence 101, Application US/08787547
 ; Patent No. 5783567

; INFORMATION FOR SEQ ID NO: 69;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-968-676-69

Query Match 36.4%; Score 4; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKLP 9
 ||||
 Db 3 YKLP 6

RESULT 3
 US-08-968-676-102
 ; Sequence 102, Application US/08968676
 ; Patent No. 5913639
 ; GENERAL INFORMATION:
 ; APPLICANT: Humphreys, Robert E
 ; APPLICANT: Adams, Shariene
 ; APPLICANT: Xu, Minzhen
 ; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
 ; NUMBER OF SEQUENCES: 165
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kevin M. Farrell, P.C.
 ; STREET: P.O. Box 999
 ; CITY: York Harbor
 ; STATE: ME
 ; COUNTRY: USA
 ; ZIP: 03911
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Farrell, Kevin M
 ; REGISTRATION NUMBER: 35,505
 ; REFERENCE/DOCKET NUMBER: REH-9601
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (207) 363-0558
 ; INFORMATION FOR SEQ ID NO: 102;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-968-676-102

Query Match 36.4%; Score 4; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
 ||||
 Db 4 KLPQ 7

RESULT 4
 US-08-787-547-101
 ; Sequence 101, Application US/08787547
 ; Patent No. 5783567

```

;
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-787-547-101

```

```

Query Match 36.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 7 KLPQ 10
Db 1 KLPQ 4

```

```

RESULT 5
US-09-492-543-73
; Sequence 73, Application US/09492543A
; Patent No. 6316213
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-B
; CURRENT APPLICATION NUMBER: US/09/492,543A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: WORD 6.0.1 for Macintosh
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
;
US-09-492-543-73

```

```

Query Match 36.4%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PQNF 5
Db 4 PQNF 7

RESULT 6
US-09-492-543-101
; Sequence 101, Application US/09492543A
; Patent No. 6316213
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; FILE REFERENCE: D6223CIP-B
; CURRENT APPLICATION NUMBER: US/09/492,543A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: WORD 6.0.1 for Macintosh
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 238-246 of the PUMP-1 protein
;
US-09-492-543-101

```

```

Query Match 36.4%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PQNF 5
Db 4 PQNF 7

```

```

RESULT 7
US-07-797-692-5
; Sequence 5, Application US/07797692
; Patent No. 5266478
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C.; Sun, Cecily R.Y.; Sun, Bill N.C.
; TITLE OF INVENTION: Products which target a Neutralization Site Within the Second
; TITLE OF INVENTION: Region of Human Immunodeficiency Virus Type 1 gp120
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/797,692
; FILING DATE: 19911125
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/767,533; 07/692,299
; FILING DATE: 9/26/1991; 4/25/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
;
US-07-797-692-5

```

;; REFERENCE/DOCKET NUMBER: TXN91-6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (713) 664-2288
;; TELEFAX: (713) 664-8914
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
US-07-797-692-5

Query Match 36.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8
Db 3 FYKL 6

RESULT 8
US-08-310-912A-99
; Sequence 99, Application US/08310912A
; Patent No. 5981730
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE: September 22, 1994
; CLASSIFICATION: S36
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/227,360
; FILING DATE: April 13, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/254001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-310-912A-99

Query Match 36.4%; Score 4; DB 2; Length 10;

Best Local Similarity 100.0%; Pred.No.76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
Db 6 KLPQ 9

RESULT 9
US-08-841-089-99
; Sequence 99, Application US/08841089
; Patent No. 6127607
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-841-089-99

Query Match 36.4%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No.76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
Db 6 KLPQ 9

RESULT 10
US-09-301-085-99
; Sequence 99, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:


```

; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301.085
; EARLIER FILING DATE: 1999-04-28
; EARLIER FILING DATE: 1994-09-22
; EARLIER FILING DATE: 1994-09-22
; EARLIER FILING DATE: 1994-09-22
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-301-085-99

```

```

Query Match          36.4%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 KLPQ 10
        ||||
DB      6 KLPQ 9

```

```

RESULT 11
PCT-US95-04570-99
; Sequence 99, Application PC/TUS9504570
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: PCT/US95/04570
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-5070
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04570-99

```

```

Query Match          36.4%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04570-99

```

```

Query Match          36.4%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 KLPQ 10
        ||||
DB      6 KLPQ 9

```

```

RESULT 12
PCT-US95-04589-99
; Sequence 99, Application PC/TUS9504589
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 201
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: PCT/US95/04589
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04589-99

```

```

Query Match          36.4%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 7 KLPQ 10
 Db 6 KLPQ 9

RESULT 13

US-07-797-692-1
 ; Sequence 1, Application US/07797692
 ; Patent No. 5266478
 ; GENERAL INFORMATION:
 ; APPLICANT: Fung, Michael S.C.; Sun, Cecily R.Y.; Sun, Bill N.C.
 ; TITLE OF INVENTION: Products which target a Neutralization Site within the Second
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Tanox Biosystems, Inc.
 ; STREET: 10301 Stella Link Rd.
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: DOS 3.30
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/797,692
 ; FILING DATE: 19911125
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/767,533; 07/692,299
 ; FILING DATE: 9/26/1991; 4/25/91
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mirabel, Eric P.
 ; REGISTRATION NUMBER: 31,211
 ; REFERENCE/DOCKET NUMBER: TNX91-6
 ; TELEPHONE: (713) 664-2288
 ; TELEFAX: (713) 664-8914
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; US-07-797-692-1

Query Match 36.4%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 Db 8 FYKL 11

RESULT 14

US-07-797-692-7
 ; Sequence 7, Application US/07797692
 ; Patent No. 5266478
 ; GENERAL INFORMATION:
 ; APPLICANT: Fung, Michael S.C.; Sun, Cecily R.Y.; Sun, Bill N.C.
 ; TITLE OF INVENTION: Products which target a Neutralization Site within the Second
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Tanox Biosystems, Inc.
 ; STREET: 10301 Stella Link Rd.
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77025

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: DOS 3.30
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/797,692
 ; FILING DATE: 19911125
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/767,533; 07/692,299
 ; FILING DATE: 9/26/1991; 4/25/91
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mirabel, Eric P.
 ; REGISTRATION NUMBER: 31,211
 ; REFERENCE/DOCKET NUMBER: TNX91-6
 ; TELEPHONE: (713) 664-2288
 ; TELEFAX: (713) 664-8914
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; US-07-797-692-7

Query Match 36.4%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 Db 8 FYKL 11

RESULT 15

US-07-909-122-2
 ; Sequence 2, Application US/07909122
 ; Patent No. 5415995
 ; GENERAL INFORMATION:
 ; APPLICANT: SCHOOLNIK, GARY K.
 ; APPLICANT: PALEFSKY, JOEL M.
 ; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
 ; TITLE OF INVENTION: VIRUS
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/909,122
 ; FILING DATE: 19920706
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENZ, WILLIAM H.
 ; REGISTRATION NUMBER: 25,952
 ; REFERENCE/DOCKET NUMBER: 28600-20105.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: AMINO ACID

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-909-122-2

Query Match          36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
DB 10 KLPQ 13

RESULT 16
US-08-709-047-11
; Sequence 11, Application US/08709047
; Patent No. 5692333
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
; APPLICANT: Limiting
; TITLE OF INVENTION: THE GC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,047
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,360
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TXN95-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 664-2288
; TELEFAX: (713) 664-8914
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-709-047-11

Query Match          36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
DB 8 FYKL 11

RESULT 17
US-08-410-360-11
; Sequence 11, Application US/08410360
; Patent No. 5691447
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
; APPLICANT: Limiting
; TITLE OF INVENTION: THE GC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/707,801A
; FILING DATE: 09/04/1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,360
; FILING DATE: 03/24/1995

```

```

; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,360
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TXN95-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 664-2288
; TELEFAX: (713) 664-8914
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-410-360-11

Query Match          36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
DB 8 FYKL 11

RESULT 18
US-08-707-801A-11
; Sequence 11, Application US/08707801A
; Patent No. 5728814
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
; APPLICANT: Limiting
; TITLE OF INVENTION: THE GC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/707,801A
; FILING DATE: 09/04/1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,360
; FILING DATE: 03/24/1995

```

ATTORNEY/AGENT INFORMATION:
 NAME: Mirabel, Eric P.
 REGISTRATION NUMBER: 31,211
 REFERENCE/DOCKET NUMBER: TNX95-1A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (713) 664-2288
 TELEFAX: (713) 664-8914
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-707-801A-11

Query Match 36.4%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 ||||
 Db 8 FYKL 11

RESULT 19
 US-08-709-006-11
 Sequence 11, Application US/08709006
 Patent No. 5731428
 GENERAL INFORMATION:

APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y.,
 TITLE OF INVENTION: THE 9C1q RECEPTOR, HIV-1 gp120 REGION BINDING
 TITLE OF INVENTION: THERETO, AND RELATED PEPTIDES AND TARGETING
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Tanox Biosystems, Inc.
 STREET: 10301 Stella Link Rd.
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: DOS 3.30
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,006
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/410,360
 FILING DATE: 24-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mirabel, Eric P.
 REGISTRATION NUMBER: 31,211
 REFERENCE/DOCKET NUMBER: TNX95-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (713) 664-2288
 TELEFAX: (713) 664-8914
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

Query Match 36.4%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 ||||

Db 8 FYKL 11

RESULT 20
 US-08-711-175-11
 Sequence 11, Application US/08711175
 Patent No. 5739306
 GENERAL INFORMATION:

APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y.,
 TITLE OF INVENTION: THE 9C1q RECEPTOR, HIV-1 gp120 REGION BINDING
 TITLE OF INVENTION: THERETO, AND RELATED PEPTIDES AND TARGETING
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Tanox Biosystems, Inc.
 STREET: 10301 Stella Link Rd.
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77025

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: DOS 3.30
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/711,175
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/410,360
 FILING DATE: 24-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mirabel, Eric P.
 REGISTRATION NUMBER: 31,211
 REFERENCE/DOCKET NUMBER: TNX95-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (713) 664-2288
 TELEFAX: (713) 664-8914
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

Query Match 36.4%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred.No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 ||||
 Db 8 FYKL 11

RESULT 21
 US-07-950-571A-4
 Sequence 4, Application US/07950571A
 Patent No. 5854400
 GENERAL INFORMATION:

APPLICANT: Chang, Tse Wen, Fung, Michael S.C., Sun, Bill N.C., Sun, Cecily R.Y.
 TITLE OF INVENTION: Monoclonal Antibodies which Neutralize HIV-1 Infection
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Tanox Biosystems, Inc.
 STREET: 10301 Stella Link Rd.
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77025

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: 3.5" Hi Density Diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS, Version 3.30
; SOFTWARE: Workorder-fact 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/950.571A
; FILING DATE: 19920922
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5854400 07/767.533
; FILING DATE: 09/26/1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX87-11BBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-664-2288
; TELEFAX: 713-664-8914
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; US-07-950-571A-4
Query Match 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
QY 5 FYKL 8
Db 8 FYKL 11

```

```

RESULT 22
US-08-075-541D-52
; Sequence 52, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAITICH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075.541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

```

```

; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-075-541D-52
Query Match 36.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
QY 7 KLPQ 10
Db 10 KLPQ 13

```

```

RESULT 23
US-08-110-300A-22
; Sequence 22, Application US/08110300A
; Patent No. 5643756
; GENERAL INFORMATION:
; APPLICANT: Pitter, Abraham
; APPLICANT: Kauter, Samuel
; TITLE OF INVENTION: FUSION GLYCOPROTEINS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davis Hoxie Faithfull and Hapgood
; STREET: 45 Rockefeller Pl.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,300A
; FILING DATE: 20-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H.
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER: 11698A50
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-757-2200
; TELEFAX: 212-586-1461
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-16
; OTHER INFORMATION: /note= "An analogous peptide
; OTHER INFORMATION: matching the consensus sequence for HXB2d V2
; OTHER INFORMATION: domain and homologs with an additional C-terminal
; OTHER INFORMATION:
; OTHER INFORMATION: and AIDS database (ADP 794.1)."
; US-08-110-300A-22

```

```

Query Match 36.4%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

```

QY 5 FYKL 8
 Db 12 FYKL 15

RESULT 24
 US-08-886-642-22
 ; Sequence 22, Application US/08886642
 ; Patent No. 5952474
 ; GENERAL INFORMATION:
 ; APPLICANT: Pinter, Abraham
 ; APPLICANT: Kayman, Samuel
 ; TITLE OF INVENTION: FUSION GLYCOPROTEINS
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 45 Rockefeller Plaza, Suite 2800
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/886,642
 FILING DATE: 01-JUL-1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/110,300
 FILING DATE: 20-AUG-1993
 APPLICATION NUMBER: 07/938,100
 FILING DATE: 28-AUG-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Hone, William J.
 REGISTRATION NUMBER: 26,739
 REFERENCE/DOCKET NUMBER: 07763/010002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212/765-5070
 TELEFAX: 212/258-2291

INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:

LOCATION: 1...16 /note= "An analogous peptide matching the
 OTHER INFORMATION: consensus sequence for HB2d V2 domain and homologs with an
 OTHER INFORMATION: additional C-terminal (Cys) as defined in the Los Alamos Human
 OTHER INFORMATION: Retrovirus and AIDS database (ADP 794.11)."
 US-08-886-642-22

Query Match 36.4%; Score 4; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYKL 8
 Db 12 FYKL 15

RESULT 25
 US-08-468-543-19
 ; Sequence 19, Application US/08468543
 ; Patent No. 5726153
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Robert S. et al.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING
 ; NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,543
 FILING DATE: 06-JUN-1995

CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/398,046
 FILING DATE: 02-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/201,057
 FILING DATE: 24-FEB-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/048,569
 FILING DATE: 16-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/694,929
 FILING DATE: 02-MAY-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,215
 FILING DATE: 03-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/189,130
 FILING DATE: 02-MAY-1988

ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 04547/002003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/542-5070
 TELEFAX: 617/542-8906
 TELEX: 200154

INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-468-543-19

Query Match 36.4%; Score 4; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
 Db 1 KLPQ 4

RESULT 26
 US-08-469-692-19
 ; Sequence 19, Application US/08469692
 ; Patent No. 5955055
 ; GENERAL INFORMATION:
 ; APPLICANT: Lees, Robert S. et al.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR ARTERIAL IMAGING
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street

```

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,692
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,046
FILING DATE: 02-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/201,057
FILING DATE: 24-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/048,569
FILING DATE: 16-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,929
FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,215
FILING DATE: 03-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,142
FILING DATE: 03-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/189,130
FILING DATE: 02-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04547/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-469-692-19

Query Match 36.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
Db 1 KLPQ 4

RESULT 27
US-08-398-046-19
Sequence 19, Application US/08398046
Patent No. 5972890
GENERAL INFORMATION:
APPLICANT: Lees, Robert S. et al.
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR
TITLE OF INVENTION: ARTERIAL IMAGING
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts

```

```

COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,046
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/201,057
FILING DATE:
APPLICATION NUMBER: US/08/048,569
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/694,929
APPLICATION NUMBER: 07/517,215
FILING DATE: May 3, 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/518,142
FILING DATE: May 3, 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/189,130
FILING DATE: May 2, 1988
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04547/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-398-046-19

Query Match 36.4%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLPQ 10
Db 1 KLPQ 4

RESULT 28
US-08-943-173-9
Sequence 9, Application US/08943173
Patent No. 6048538
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
APPLICANT: Shen, Fan
APPLICANT: Chen, Pei De
TITLE OF INVENTION: PEPTIDES DERIVED
TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF
TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS
TITLE OF INVENTION: DIAGNOSTIC REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,173
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4152
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-943-173-9

Query Match 36.4%; Score 4; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
|||
Db 5 KLPQ 8

RESULT 29
US-08-934-915-158
; Sequence 158, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 158:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-159

LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-158
Query Match 36.4%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 KLPQ 10
|||
Db 17 KLPQ 20
RESULT 30
US-08-934-915-159
; Sequence 159, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. FOUTCH
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-159
Query Match 36.4%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 KLPQ 10
|||
Db 2 KLPQ 5
RESULT 31

US-08-667-001-6
; Sequence 6, Application US/08667001
; Patent No. 5827827
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D.
; APPLICANT: Wirsching, Peter
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,001
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,039
; FILING DATE: 16-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewis, Donald G.
; REGISTRATION NUMBER: 28,636
; REFERENCE/DOCKET NUMBER: TSRI 282.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "sequence = Y1 in formula
; OTHER INFORMATION: (III A) and (III B)"
US-08-667-001-6
Query Match 27.3%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QNF 5
DB 2 QNF 4
RESULT 32
US-08-974-549A-182
; Sequence 182, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-182
Query Match 27.3%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 NPY 6
DB 2 NPY 4
RESULT 33
US-09-177-249-143
; Sequence 143, Application US/09177249
; Patent No. 6229064

```

; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramon
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; EARLIER FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-143

```

```

Query Match      27.3%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 NFY 6
Db      1 NFY 3

```

```

RESULT 34
5258287-45
; Patent No. 5258287
; APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.
; TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
; OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
; NUMBER OF SEQUENCES: 58
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/171,623
; FILING DATE: 22-MAR-1988
; SEQ ID NO:45:
; LENGTH: 4
5258287-45

```

```

Query Match      27.3%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 FYK 7
Db      2 FYK 4

```

```

RESULT 35
US-08-014-979-41
; Sequence 41, Application US/08014979
; Patent No. 5510240
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S. et al.
; TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
; Synthesis Thereof, and a Method of Use Thereof
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,979
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-014-979-41

```

```

Query Match      27.3%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 PQN 4
Db      3 PQN 5

```

```

RESULT 36
US-08-014-979-42
; Sequence 42, Application US/08014979
; Patent No. 5510240
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S. et al.
; TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
; Synthesis Thereof, and a Method of Use Thereof
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,979
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown

```

```

; MOLECULE TYPE: peptide
; US-08-014-979-42

Query Match      27.3%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PQN 4
      |||
Db      3 PQN 5

RESULT 37
US-08-447-010-22
; Sequence 22, Application US/08447010
; Patent No. 5770718
; GENERAL INFORMATION:
; APPLICANT: MOFFATT, BARBARA
; TITLE OF INVENTION: GENE FOR APRT FROM PLANT TISSUE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: sim & McBurney
; STREET: 330 University Avenue, Suite 701
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,010
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 08/230,695
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 07/888,132
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1811-183 MIS:vg
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-447-010-22

Query Match      27.3%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 KLP 9
      |||
Db      1 KLP 3

RESULT 38
US-08-667-001-11
; Sequence 11, Application US/08667001

```

```

; Patent No. 5827827
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D.
; APPLICANT: Wirsching, Peter
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,001
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER: US 08/335,039
; FILING DATE: 16-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewis, Donald G.
; REGISTRATION NUMBER: 28,636
; REFERENCE/DOCKET NUMBER: TSRI 282.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "sequence = Y1 in formula
; OTHER INFORMATION: (III A) and (III B)"
; US-08-667-001-11

Query Match      27.3%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 QNF 5
      |||
Db      3 QNF 5

RESULT 39
US-08-981-122-4
; Sequence 4, Application US/08981122B
; Patent No. 6127339
; GENERAL INFORMATION:
; APPLICANT: Hatanaka, Yoshihiro
; APPLICANT: Arizumi, Masaharu
; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/08/981,122B
; CURRENT FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: JP 7-176904
; PRIOR FILING DATE: 1995-06-21
; PRIOR APPLICATION NUMBER: PCT/Jp96/01734
; PRIOR FILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4

```

LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence of a peptide synthesized in Example 1 from L-form
Patent No. 6127319
OTHER INFORMATION: F-moc amino acids by solid phase method using a multi-peptide
OTHER INFORMATION: synthesizing system (RAMPS)
US-08-981-122-4

Query Match 27.3%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
|||
Db 2 FYK 4

RESULT 40
US-08-652-877-81
; Sequence 81, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: Thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

HYPOTHEICAL: NO
FRAGMENT TYPE: internal
US-08-652-877-81
Query Match 27.3%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 KLP 9
|||
Db 3 KLP 5

RESULT 41
US-08-476-515A-81
; Sequence 81, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; TITLE OF INVENTION: thereof and DNA Encoding Same
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Compaq PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: internal
; US-08-476-515A-81

Query Match 27.3%; Score 3; DB 3; Length 5;

```

Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 3 KLP 5

RESULT 42
US-09-381-244B-17
; Sequence 17, Application US/09381244B
; Patent No. 6462170
; GENERAL INFORMATION:
; APPLICANT: BLASI, Francesca
; APPLICANT: FAZIOI, Francesca
; APPLICANT: RESNATI, Massimo
; APPLICANT: NICOLAI, Sidenius
; TITLE OF INVENTION: UPAR Mimicking Peptide
; FILE REFERENCE: 0471-0143P
; CURRENT APPLICATION NUMBER: US/09/381,244B
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: PCT/EP98/01547
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide analogue of the human uPAR
US-09-381-244B-17

Query Match 27.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
DB 1 PQN 3

RESULT 43
US-08-766-596A-31
; Sequence 31, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3538
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-766-596A-31

Query Match 27.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KLP 9
DB 1 KLP 3

RESULT 44
US-09-043-877-21
; Sequence 21, Application US/09043877
; Patent No. 6495314
; GENERAL INFORMATION:
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Muir, Tom W.
; APPLICANT: Dawson, Philip E.
; APPLICANT: Fitzgerald, Michael C.
; TITLE OF INVENTION: PROTEIN SIGNATURE ANALYSIS
; FILE REFERENCE: GRY0039S
; CURRENT APPLICATION NUMBER: US/09/043,877
; CURRENT FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PCT/US96/15516
; PRIOR FILING DATE: 1996-09-27
; PRIOR APPLICATION NUMBER: 60/004,563
; PRIOR FILING DATE: 1995-09-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
US-09-043-877-21

Query Match 27.3%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YKL 8
DB 1 YKL 3

RESULT 45
US-08-106-493A-3
; Sequence 3, Application US/08106493A
; Patent No. 5457049
; GENERAL INFORMATION:
; APPLICANT: Antonio Giordano
; TITLE OF INVENTION: TUMOR SUPPRESSOR PROTEIN PRE2,

```

```

; TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODING
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University Of The Commonwealth
; ADDRESS: System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/106,493A
; FILING DATE: August 12, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mullins, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 6056-188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5457049e
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-106-493A-3

Query Match 27.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYK 7
Db 1 FYK 3

RESULT 46
US-08-429-264-3
; Sequence 3, Application US/08429264
; Patent No. 5532340
; GENERAL INFORMATION:
; APPLICANT: Antonio Giordano
; TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN"
; TITLE OF INVENTION: PRE2"
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,264
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: 08/106,493
; FILING DATE: August 12, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, D.A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-188 D11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5532340e
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-429-264-3

Query Match 27.3%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYK 7
Db 1 FYK 3

RESULT 47
US-08-260-199A-27
; Sequence 27, Application US/08260199A
; Patent No. 5738996
; GENERAL INFORMATION:
; APPLICANT: Hodges, Robert S.
; APPLICANT: Irvin, Randall T.
; APPLICANT: Holm, A
; APPLICANT: Wong, W.Y.
; APPLICANT: Sheth, H.B.
; APPLICANT: Husband, Devon L.
; TITLE OF INVENTION: Combinatorial Library Composition and
; TITLE OF INVENTION: Method
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/260,199A
; FILING DATE: 15-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dehlinger, Peter J.
; REGISTRATION NUMBER: 28,006
; REFERENCE/DOCKET NUMBER: 8900-0008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

```

Query Match	27.3%; Score 3; DB 1; Length 6;	Best Local Similarity 100.0%; Pred.No. 2.5e+05;	Mismatches 0; Indels 0;
QY	3 QNF 5 		
DB	1 QNF 3		
<p>ORIGINAL SOURCE: QNFIPK peptide, . 15 INDIVIDUAL ISOLATE: QNFIPK peptide, . 15 US-08-260-199A-27</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 0; Indels 0; Gaps 0;</p>			
QY	3 QNF 5 		
DB	1 QNF 3		
<p>RESULT 48 US-08-532-065B-5 Sequence 5, Application US/08532065B Patent No. 5753507 GENERAL INFORMATION: APPLICANT: Ohta, Daikaku APPLICANT: Mizutani, Masaharu TITLE OF INVENTION: Plant Geraniol/Nerol 10-Hydroxylase and TITLE OF INVENTION: DNA Coding Therefor NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 5753507artis Corporation STREET: 59 Route 10 CITY: East Hanover STATE: NJ COUNTRY: USA ZIP: 07916 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/532,065B FILING DATE: 22-SEP-1995 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: Melgs, J. Timothy REGISTRATION NUMBER: 38,241 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587 TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 6 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: not relevant MOLECULE TYPE: peptide US-08-532-065B-5</p>			
QY	7 KLP 9 		
DB	1 KLP 3		
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 0; Indels 0; Gaps 0;</p>			
QY	7 KLP 9 		
DB	1 KLP 3		
<p>RESULT 49 US-07-923-724-62 Sequence 62, Application US/07923724 Patent No. 5780292 GENERAL INFORMATION: APPLICANT: Nevalainen, Helena K.M. APPLICANT: Paloheimo, Marja T. APPLICANT: Miettinen-Oinonen, Arja S.K. APPLICANT: Torkkeli, Tuula K. APPLICANT: Cantrell, Michael APPLICANT: Piddington, Christopher S. APPLICANT: Rambossek, John A. APPLICANT: Turunen, Marja K. APPLICANT: Fagerstr m, Richard B. APPLICANT: Houston, Christine S. TITLE OF INVENTION: Production of Phytase Degrading Enzymes TITLE OF INVENTION: in Trichoderma NUMBER OF SEQUENCES: 69</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			
<p>Query Match 27.3%; Score 3; DB 1; Length 6; Best Local Similarity 100.0%; Pred.No. 2.5e+05; Mismatches 3; Conservative 0; Mismatches 0; Indels 0;</p>			
QY	8 LPQ 10 		
DB	2 LPQ 4		
<p>US-07-923-724-62</p>			

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/609,426A
 ; FILING DATE: 01-MAR-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION NUMBER: US 07/923,724
 ; FILING DATE: 31-JUL-1992
 ; PRIOR APPLICATION NUMBER: US 07/496,155
 ; FILING DATE: 19-MAR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/044,077
 ; FILING DATE: 29-APR-1987
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: UK 8610600
 ; FILING DATE: 30-APR-1986
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reed, Grant E.
 ; REGISTRATION NUMBER: P-41,264
 ; REFERENCE/DOCKET NUMBER: 1050.0080001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; INFORMATION FOR SEQ ID NO: 62:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: both
 ;
 ; US-08-609-426A-62

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPQ 10
 Db 2 LPQ 4

RESULT 51
 ; US-08-374-652C-57
 ; Sequence 57, Application US/08374652C
 ; Patent No. 584286
 ; GENERAL INFORMATION:
 ; APPLICANT: NEVALAINEN, HELENA K.M.
 ; APPLICANT: PALOHEIMO, MARJA T.
 ; APPLICANT: FAGERSTROM, RICHARD B.
 ; APPLICANT: MIETTINEN-ONINEN, ARJA S.
 ; APPLICANT: TURUNEN, MARJA K.
 ; APPLICANT: RAMBOSEK, JOHN A.
 ; APPLICANT: PIDDINGTON, CHRISTOPHER S.
 ; APPLICANT: HOUSTON, CHRISTINE S.
 ; APPLICANT: CANTRELL, MICHAEL A.
 ; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
 ; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
 ; TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
 ; NUMBER OF SEQUENCES: 94
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, SUITE 600
 ; CITY: WASHINGTON

; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/374,652C
 ; FILING DATE: 24-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/07058
 ; FILING DATE: 27-JUL-1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/925,401
 ; FILING DATE: 31-JUL-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: REED, GRANT E.
 ; REGISTRATION NUMBER: 41,264
 ; REFERENCE/DOCKET NUMBER: 1050.071001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 57:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ;
 ; US-08-374-652C-57

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPQ 10
 Db 2 LPQ 4

RESULT 52
 ; US-08-377-432-38
 ; Sequence 38, Application US/08377432
 ; Patent No. 5854202
 ; GENERAL INFORMATION:
 ; APPLICANT: DEDHAR, Shoukat
 ; TITLE OF INVENTION: NOVEL USE OF CALRETICULIN IN MODULATING
 ; TITLE OF INVENTION: HORMONE RESPONSIVENESS AND NEW PHARMACEUTICALS FOR
 ; TITLE OF INVENTION: TREATING CANCER, OSTEOPOROSIS AND CHRONIC INFLAMMATORY
 ; TITLE OF INVENTION: DISEASE
 ; NUMBER OF SEQUENCES: 49
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/377,432
 ; FILING DATE: 24-JAN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:

NAME: Mool, Leslie A
 REGISTRATION NUMBER: 37,047
 REFERENCE/DOCKET NUMBER: 007315-005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-377-432-38

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 5 FYK 7
 |||
 Db 3 FYK 5

RESULT 53
 US-08-968-676-24
 ; Sequence 24, Application US/08968676
 ; Patent No. 5918639
 ; GENERAL INFORMATION:
 ; APPLICANT: Humphreys, Robert E
 ; APPLICANT: Adams, Sharlene
 ; APPLICANT: Xu, Minzhen
 ; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
 ; NUMBER OF SEQUENCES: 165
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Kevin M. Farrell, P.C.
 ; STREET: P.O. Box 999
 ; CITY: York Harbor
 ; STATE: ME
 ; COUNTRY: USA
 ; ZIP: 03911
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: US/08/968,676
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Farrell, Kevin M
 ; REGISTRATION NUMBER: 35,505
 ; REFERENCE/DOCKET NUMBER: REH-9601
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (207) 363-0558
 ; TELEFAX: (207) 363-0528
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-968-676-24

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 7 KLP 9
 |||
 Db 4 KLP 6

RESULT 54
 US-08-819-444-3
 ; Sequence 3, Application US/08819444A
 ; Patent No. 5968763
 ; GENERAL INFORMATION:
 ; APPLICANT: FISCHETTI, Vincent A.
 ; APPLICANT: PANCHOLI, Vijaykumar
 ; TITLE OF INVENTION: ENZYME FOR CLEAVAGE OF THE ANCHOR REGION OF SURFACE
 ; TITLE OF INVENTION: PROTEINS FROM GRAM POSITIVE BACTERIA
 ; FILE REFERENCE: 016921-105
 ; CURRENT APPLICATION NUMBER: US/08/819,444A
 ; CURRENT FILING DATE: 1997-03-17
 ; EARLIER APPLICATION NUMBER: US 08/319,540
 ; EARLIER FILING DATE: 1994-10-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 ; US-08-819-444-3

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 LPQ 10
 |||
 Db 1 LPQ 3

RESULT 55
 US-08-819-444-5
 ; Sequence 5, Application US/08819444A
 ; Patent No. 5968763
 ; GENERAL INFORMATION:
 ; APPLICANT: FISCHETTI, Vincent A.
 ; APPLICANT: PANCHOLI, Vijaykumar
 ; TITLE OF INVENTION: ENZYME FOR CLEAVAGE OF THE ANCHOR REGION OF SURFACE
 ; TITLE OF INVENTION: PROTEINS FROM GRAM POSITIVE BACTERIA
 ; FILE REFERENCE: 016921-105
 ; CURRENT APPLICATION NUMBER: US/08/819,444A
 ; CURRENT FILING DATE: 1997-03-17
 ; EARLIER APPLICATION NUMBER: US 08/319,540
 ; EARLIER FILING DATE: 1994-10-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Enterococcus faecalis
 ; US-08-819-444-5

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 LPQ 10
 |||
 Db 1 LPQ 3

RESULT 56
 US-09-196-934-6
 ; Sequence 6, Application US/09196934
 ; Patent No. 6131256
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Li Ang
 ; APPLICANT: Beutner, Joseph A.
 ; APPLICANT: Carbonell, Ruben G.
 ; TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 LPQ 10
 |||
 Db 1 LPQ 3

RESULT 57
 US-09-196-934-6
 ; Sequence 6, Application US/09196934
 ; Patent No. 6131256
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Li Ang
 ; APPLICANT: Beutner, Joseph A.
 ; APPLICANT: Carbonell, Ruben G.
 ; TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 LPQ 10
 |||
 Db 1 LPQ 3

RESULT 58
 US-09-196-934-6
 ; Sequence 6, Application US/09196934
 ; Patent No. 6131256
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Li Ang
 ; APPLICANT: Beutner, Joseph A.
 ; APPLICANT: Carbonell, Ruben G.
 ; TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 LPQ 10
 |||
 Db 1 LPQ 3

RESULT 59
 US-09-196-934-6
 ; Sequence 6, Application US/09196934
 ; Patent No. 6131256
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Li Ang
 ; APPLICANT: Beutner, Joseph A.
 ; APPLICANT: Carbonell, Ruben G.
 ; TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides

Query Match 27.3%; Score 3; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 LPQ 10
 |||
 Db 1 LPQ 3

Wed Nov 26 09:08:38 2003

```
FILE REFERENCE: MSB-7251
CURRENT APPLICATION NUMBER: US/09/196,934
CURRENT FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-196-934-6

Query Match      27.3%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 FYK 7
Db      4 FYK 6

RESULT 57
US-08-803-346-76
; Sequence 76, Application US/0803346
; Patent No. 6281346
; GENERAL INFORMATION:
; APPLICANT: HESS, JOHN W.
; APPLICANT: CASKEY, C. THOMAS
; APPLICANT: LIU, QINGYUN
; APPLICANT: PHILLIPS, MICHAEL SEAN
; TITLE OF INVENTION: RAT OB RECEPTORS AND NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOANNE M. GIESSEY - MERCK & CO., INC.
; STREET: 126 EAST LINCOLN AVENUE - P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,346
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: GIESSEY, JOANNE M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 19642Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-3046
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-803-346-76

Query Match      27.3%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MPQ 3
Db      1 MPQ 3
```

```
RESULT 58
US-09-155-613A-36
; Sequence 36, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use Of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotome
US-09-155-613A-36
```

```
Query Match      27.3%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      7 KLP 9
Db      4 KLP 6
```

```
RESULT 59
US-09-581-944A-30
; Sequence 30, Application US/09581944A
; Patent No. 644131
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: PEPTIDES, METHOD FOR ASSAYING HUMAN PEPSINOGEN II OR HUMAN PEPSIN
; FILE REFERENCE: ASSAY KIT
; FILE REFERENCE: Q59565
; CURRENT APPLICATION NUMBER: US/09/581,944A
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: P. Hei. 9-364796
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: P. Hei. 10-213513
; PRIOR FILING DATE: 1998-07-13
; PRIOR APPLICATION NUMBER: PCT/JP98/05780
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: substrate for human pepsin II or pepsinogen II
; NAME/KEY: MISC FEATURE
; LOCATION: (5)..(5)
; OTHER INFORMATION: 2-naphthyl Ala
; FEATURE:
```

NAME/KEY: MISC FEATURE
 LOCATION: (6) (6)
 OTHER INFORMATION: Ala which binds to p-nitroaniline
 US-09-561-944A-30

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
 Db 1 PQN 3

RESULT 60

US-09-000-286A-2
 Sequence 2, Application US/09000286A
 Patent No. 6449562
 GENERAL INFORMATION:
 APPLICANT: Lumindex Corporation
 APPLICANT: Chandler, Van S.
 APPLICANT: Fulton, Jerrold R.
 APPLICANT: Chandler, Mark B.
 TITLE OF INVENTION: Multiplexed Analysis of Clinical Specimens Apparatus and Method
 FILE REFERENCE: 112602 560
 CURRENT APPLICATION NUMBER: US/09/000,286A
 CURRENT FILING DATE: 1996-08-18
 PRIOR APPLICATION NUMBER: PCT/US96/16198
 PRIOR FILING DATE: 1996-10-10
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 2
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-000-286A-2

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 Db 4 LPQ 6

RESULT 61

US-08-469-260A-208
 Sequence 208, Application US/08469260A
 Patent No. 6451578
 GENERAL INFORMATION:
 APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER
 APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT MUEHROFF
 APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BUIJK
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,260A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: FOREMSKI, PRISCILLA E.

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,260A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: FOREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 208:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-260A-208

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 Db 4 LPQ 6

RESULT 62

US-08-469-260A-335
 Sequence 335, Application US/08469260A
 Patent No. 6451578
 GENERAL INFORMATION:
 APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER
 APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT MUEHROFF
 APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BUIJK
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,260A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: FOREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 335:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-260A-335

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 DB 3 LPQ 5

RESULT 63
 US-09-492-766-1
 ; Sequence 1, Application US/09492766
 ; Patent No. 6506732
 ; GENERAL INFORMATION:
 ; APPLICANT: AMIOT, Jean
 ; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS
 ; FILE REFERENCE: 6013-57"US"
 ; CURRENT APPLICATION NUMBER: US/09/492,766
 ; CURRENT FILING DATE: 2000-01-27
 ; EARLIER APPLICATION NUMBER: 60/117,661
 ; EARLIER FILING DATE: 1999-01-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk
 ; OTHER INFORMATION: proteins
 US-09-492-766-1

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 DB 2 LPQ 4

RESULT 64
 US-08-900-241-38
 ; Sequence 38, Application US/08900241A
 ; Patent No. 6518397
 ; GENERAL INFORMATION:
 ; APPLICANT: DEDHAR, Shoukat
 ; TITLE OF INVENTION: PHARMACEUTICALS FOR MODULATING HORMONE
 ; RESPONSIVENESS
 ; NUMBER OF SEQUENCES: 70
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/900,241A
 FILING DATE: 24-Jul-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/377,432
 FILING DATE: 24-JAN-1995
 APPLICATION NUMBER: PCT/CA95/00664
 FILING DATE: 23-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Mooi, Leslie A.
 REGISTRATION NUMBER: 37,047
 REFERENCE/DOCKET NUMBER: 007315-015
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650)622-2300
 TELEFAX: (650)622-2499
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 38:
 US-08-900-241-38

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FYK 7
 DB 3 FYK 5

RESULT 65
 US-09-209-676-40
 ; Sequence 40, Application US/09209676
 ; Patent No. 6524856
 ; GENERAL INFORMATION:
 ; APPLICANT: Pangene Corporation
 ; TITLE OF INVENTION: The Use of Consensus Sequences for Targeted Homologous
 ; RECOMBINATION
 ; FILE REFERENCE: A-65678-1/rf7/Nsc
 ; CURRENT APPLICATION NUMBER: US/09/209,676
 ; CURRENT FILING DATE: 2002-06-18
 ; PRIOR APPLICATION NUMBER: US 60/070,734
 ; PRIOR FILING DATE: 1997-12-11
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 40
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: consensus
 ; OTHER INFORMATION: sequence
 US-09-209-676-40

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PQN 4
 DB 2 PQN 4

RESULT 66
 US-09-555-352-26
 ; Sequence 26, Application US/09555352

Patent No. 6544779
 GENERAL INFORMATION:
 APPLICANT: Cichutek, Klaus
 TITLE OF INVENTION: PSEUDO-TYPE RETROVIRAL VECTORS WITH
 MODIFIABLE SURFACE CAPSID PROTEINS
 FILE REFERENCE: 11692-005001
 CURRENT APPLICATION NUMBER: US/09/555,352
 FILING DATE: 2000-08-24
 PRIOR APPLICATION NUMBER: PCT/DE98/03542
 PRIOR FILING DATE: 1998-11-27
 PRIOR APPLICATION NUMBER: DE 197 52 855.4
 PRIOR FILING DATE: 1997-11-28
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: Fast-Seq for Windows Version 4.0
 SEQ ID NO 26
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Murine leukemia virus
 US-09-555-352-26

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPQ 3
 |||
 Db 1 MPQ 3

RESULT 67
 US-08-488-446-208
 Sequence 208, Application US/08488446
 Patent No. 6558898
 GENERAL INFORMATION:
 APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER
 APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT MUEHRHOFF
 APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BULJK
 TITLE OF INVENTION: NON-B, NON-C, NON-D, NON-E HEPATITIS
 REAGENTS AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,446
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: FOREMBSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-937-6365
 INFORMATION FOR SEQ ID NO: 34
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-488-446-208

Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 208:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-488-446-208
 Query Match 27.3%; Score 3; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;
 QY 8 LPQ 10
 |||
 Db 4 LPQ 6
 RESULT 68
 US-08-488-446-335
 Sequence 335, Application US/08488446
 Patent No. 6558898
 GENERAL INFORMATION:
 APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER
 APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT MUEHRHOFF
 APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BULJK
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 REAGENTS AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/488,446
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: FOREMBSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 335:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-488-446-335

Qy 8 LPQ 10
Db 3 LPQ 5

RESULT 69
US-08-467-344A-208
; Sequence 208, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUEHROFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-937-6365
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
; US-08-467-344A-208
; Query Match 27.3%; Score 3; DB 4; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 8 LPQ 10
; Db 4 LPQ 6

RESULT 70
US-08-467-344A-335
; Sequence 335, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUEHROFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-937-6365
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
; US-08-467-344A-208
; Query Match 27.3%; Score 3; DB 4; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; Qy 8 LPQ 10
; Db 4 LPQ 6

RESULT 71
PCT-US93-01669-26
; Sequence 26, Application PC/TUS9301669
; GENERAL INFORMATION:
; APPLICANT: Trowbridge, Ian S.
; APPLICANT: Collant, Jr., James P.
; APPLICANT: Tainer, John A.
; APPLICANT: Kuhn, Leslie A.
; TITLE OF INVENTION: RECEPTOR INTERNALIZATION SIGNALS
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA

; ZIP: 90067
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 01-MAR-1993
 ; FILING DATE: 01-MAR-1993
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/844.852
 ; FILING DATE: 03-MAR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wetherell, Jr. Ph.D., John R.
 ; REGISTRATION NUMBER: 31,678
 ; REFERENCE/DOCKET NUMBER: PD-1636
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 455-5100
 ; TELEFAX: (619) 455-5110
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; PCT-US93-01669-26

Query Match 27.3%; Score 3; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NFY 6
 ||||
 Db 1 NFY 3

RESULT 72
 US-08-127-499A-10
 ; Sequence 10, Application US/08127499A
 ; Patent No. 5510264
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN ALSTYNE, Diane
 ; APPLICANT: SHARMA, Lawrence Rajendra
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
 ; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 28-SEP-1993
 ; APPLICATION NUMBER: US/08/127,499A
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 51916/102/INBI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEFAX: 904136
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown

; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-08-127-499A-10
 Query Match 27.3%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 ||||
 Db 1 LPQ 3

RESULT 73
 US-08-482-847-10
 ; Sequence 10, Application US/08482847
 ; Patent No. 5556757
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN ALSTYNE, Diane
 ; APPLICANT: SHARMA, Lawrence Rajendra
 ; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
 ; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/482,847
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/127,499
 ; FILING DATE: 28-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 51916/104/INBI
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELEFAX: 904136
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-08-482-847-10

Query Match 27.3%; Score 3; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LPQ 10
 ||||
 Db 1 LPQ 3

RESULT 74
 US-08-537-069-14
 ; Sequence 14, Application US/08537069
 ; Patent No. 5688912

```

; GENERAL INFORMATION:
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Peptide Ligands Which Bind to
; TITLE OF INVENTION: von Willebrand Factor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,069
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gidlin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
US-08-537-069-14

```

```

Query Match      27.3%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 FYK 7
Db      5 FYK 7

```

```

RESULT 75
US-08-177-109A-5
; Sequence 5, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-177-109A-5

```

```

Query Match      27.3%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 PQN 4
Db      1 PQN 3

```

```

Search completed: November 25, 2003, 20:16:02
Job time : 12.9947 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 13.8032 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKFPPTQETVT 15

Scoring table: OLIGO

Gapex 60.0 , Gapex 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	26.7	7	S71299	IC12 protein - Par
2	4	26.7	9	S66607	quinoxaline 2-oxid
3	4	26.7	10	A36454	trypsin-modulating
4	4	26.7	13	D39690	neural cell adhesi
5	4	26.7	14	C33098	223K exoantigen -
6	4	26.7	15	PT0037	light harvesting c
7	4	26.7	17	S57991	hydroxyproline-ric
8	4	26.7	17	S59481	hydroxyproline-ric
9	3	20.0	9	PT0272	Ig heavy chain CRD
10	3	20.0	9	A60427	macrophage cytotox
11	3	20.0	9	B30572	T-cell receptor be
12	3	20.0	10	S63478	dihydrofolamide d
13	3	20.0	10	S70721	heat shock protein
14	3	20.0	10	B59272	peptide-N4-(N-acet
15	3	20.0	10	A61354	carnitine medium/1
16	3	20.0	10	C30572	T-cell receptor be
17	3	20.0	10	PH0923	T-cell receptor be
18	3	20.0	11	PC4267	ribosomal protein
19	3	20.0	11	B60769	Ig H2 chain - Paci
20	3	20.0	11	D45900	complement C3b rec
21	3	20.0	11	PH0804	T-cell receptor be
22	3	20.0	12	C39109	hypothetical 1.2K
23	3	20.0	12	FN0663	cytrophin-associ
24	3	20.0	12	B39690	neural cell adhesi
25	3	20.0	12	S69095	ubiquinol-cytochro
26	3	20.0	13	S21152	tryptophyllin-rela
27	3	20.0	13	A05174	tryptophyllin-13
28	3	20.0	13	S09716	2S albumin large c
29	3	20.0	13	PN0048	unidentified QM002

Ha-transporting tw
16K protein S404 -
protein kinase IIC
Ig heavy chain J r
alpha-2-macroglobu
phosphoprotein, bo
unspecific monooxy
integration host f
glycine cleavage s
seed storage prote
Ig heavy chain J r
Ig heavy chain J r
7.5k surfactant-as
T-cell receptor be
T-cell receptor be
T-cell receptor be
voltage-dependent
epoxypropan isomer
Ig heavy chain J r
Ig heavy chain J r
insulin-like growt
T-cell receptor be
T-cell receptor be
Ig heavy chain J r
Ig heavy chain J r
Ig heavy chain J r
osteonectin - rat
gingipain, 44K - P
protein P4 - curle
T-cell receptor be
hypothetical prote
proteasome endopep
Ig heavy chain J1
prolylendopeptidas
alkanal monooxygen
hypothetical prote
protein gp45.1 - p
Na+/K+-exchanging
superoxide dismuta
nitrogenase (EC 1
ermG leader peptid
beta-1,3-glucanase
promoter P8 hypoth
PS 1 complex subun
wd-repeat protein
Ig heavy chain DJ
octamer-binding pr
hypothetical prote
aminopeptidase, 30
malate dehydrogena
myosin light chain
T-cell receptor be
water-soluble 35K
apolipoprotein A-I
hypothetical prote
dTPDglucose 4,6-de
retinoid-X-recepto
zona pellucida gly
alpha-1-antitrypsi
J-Kappa recombinat
lectin, galactose/
temperature-labile
thyrotropin-releas
histidinol dehydro
cell surface adhes
phospholipase C (E
endoglycanase F -
hypothetical prote

ALIGNMENTS

RESULT 1

ICL2 protein - Paramacium tetraurelia (fragment)
 C:Species: Paramacium tetraurelia
 C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C:Accession: S71299
 R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A>Title: Characterization of centrin genes in Paramacium.
 A:Reference number: S71298; PMID:96248429; PMID:8665928
 A:Accession: S71299
 A:Molecule type: protein
 A:Residues: 1-7 <MAD>
 A:Experimental source: strain d4-2
 C:Genetics:
 A:Genetic code: SGCS

Query Match 26.7%; Score 4; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQ 11
 |||||
 Db 3 PPPQ 6

RESULT 2

quinoline 2-oxidoreductase beta chain - Comamonas testosteroni (fragment)
 C:Species: Comamonas testosteroni
 C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S6607
 R:Schach, S.; Tshitsuaka, B.; Fetzner, S.; Lingens, F.
 Eur. J. Biochem. 232, 536-544, 1995
 A>Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from
 A:Reference number: S66606; PMID:96035889; PMID:7556204
 A:Accession: S66607
 A:Molecule type: protein
 A:Residues: 1-9 <SCH>
 A:Experimental source: strain 63

Query Match 26.7%; Score 4; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKFP 7
 |||||
 Db 1 MKFP 4

RESULT 3

trypsin-modulating oostatic factor - yellow fever mosquito
 C:Species: Aedes aegypti (yellow fever mosquito)
 C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-May-1996
 C:Accession: A36454; A61630
 R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
 FASEB J. 4, 3015-3020, 1990
 A>Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi
 A:Reference number: A36454; PMID:90367888; PMID:2394318
 A:Accession: A36454
 A:Molecule type: protein
 A:Residues: 1-10 <BOR>
 R:Borovsky, D.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
 Insect Biochem. Mol. Biol. 23, 703-712, 1993
 A>Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
 A:Reference number: A61630; PMID:93357794; PMID:8353526
 A:Accession: A61630
 A:Molecule type: protein
 A:Residues: 1-10 <BO2>

A>Note: none of the amino acids is modified

C:Function:
 A:Description: Inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ep
 C:Keywords: hormone

Query Match 26.7%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
 |||||
 Db 5 PPPP 8

RESULT 4

neural cell adhesion molecule, cardiac splice form +,-,+ - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 C:Accession: D39690
 R:Reyes, A.A.; Small, S.J.; Akeson, R.
 Mol. Cell. Biol. 11, 1654-1661, 1991
 A>Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mR
 A:Reference number: A39690; PMID:9141516; PMID:1996115
 A:Accession: D39690
 A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: mRNA
 A:Residues: 1-13 <REY>
 A:Cross-references: GB:M63970
 C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
 C:Keywords: cardiac muscle; cell adhesion; heart

Query Match 26.7%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQ 11
 |||||
 Db 6 PPPQ 9

RESULT 5

223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C>Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
 C:Accession: C33098
 R:Nichols, J.H.; Hager, L.P.
 Submitted to the Protein Sequence Database, May 1990
 A:Reference number: A33098
 A:Accession: C33098
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <NIC>

Query Match 26.7%; Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQE 12
 |||||
 Db 3 PPQE 6

RESULT 6

light harvesting complex chain III/b, photosystem I - rice (fragment)
 C:Species: Oryza sativa (rice)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
 C:Accession: P70037; P80205
 R:Uchiyama, Y.; Tsugita, A.
 submitted to JIPID, June 1991
 A:Reference number: P80169

A;Accession: PT0037
A;Molecule type: protein
A;Residues: 1-15 <UCH>

Query Match 26.7%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
|||
Db 8 PPPP 11

RESULT 7

S57991 hydroxyproline-rich protein - Sesbania rostrata (fragment)

C;Species: Sesbania rostrata
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 11-Jan-2000
C;Accession: S57991

R;Goornachtig, S.; Valerio-Lepiniec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.
submitted to the EMBL Data Library, March 1995
A;Description: Use of differential display to identify novel Sesbania rostrata genes and

A;Reference number: S57991
A;Accession: S57991
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-17 <GOO>
A;Cross-references: EMBL:Z48673; NID:G899484; PID:G899485
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
|||
Db 10 PPPP 13

RESULT 8

S59481 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)

C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C;Accession: S59481

R;Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A;Title: Specificity in the immobilisation of cell wall proteins in response to different

A;Reference number: S59481; MUID:96011753; PMID:7548825

A;Accession: S59481

A;Molecule type: protein

A;Residues: 1-17 <WOJ>

C;Keywords: glycoprotein; hydroxyproline

F;6,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
|||
Db 8 PPPP 11

RESULT 9

PT0272 Ig heavy chain CRD3 region (clone 3-103B) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0272

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0272

A;Molecule type: DNA

A;Residues: 1-9 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5
|||
Db 6 EMK 8

RESULT 10

A60427

macrophage cytotoxicity-inducing factor, 29K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993

C;Accession: A60427

R;Jones, C.M.; Prince, C.A.; Williams, J.S.

Exp. Hematol. 19, 704-709, 1991

A;Title: Purification and amino acid analysis of a human macrophage cytotoxicity-inducin

A;Reference number: A60427; MUID:91372335; PMID:1909970

A;Accession: A60427

A;Molecule type: protein

A;Residues: 1-9 <JON>

A;Note: the sequence from the text on page 706 is inconsistent with that from page 708 in

C;Keywords: cytokine

Query Match 20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
|||
Db 4 VLE 6

RESULT 11

B30572

T-cell receptor beta chain C region (CRTB29) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997

C;Accession: B30572

R;Williams, C.B.; Gutman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz

A;Reference number: A30563; MUID:89110036; PMID:2563271

A;Accession: B30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-9 <WIL>

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TWT 15
|||
Db 5 TWT 7

RESULT 12

S63478

dihydrolipoamide dehydrogenase (EC 1.8.1.4) beta chain E1 - Pseudomonas aeruginosa (frag

N;Alternate names: branched-chain-oxoacid dehydrogenase chain E1

C;Species: Pseudomonas aeruginosa

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S63478

R;Hester, K.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.

Eur J. Biochem. 233: 828-836, 1995

A;Title: Purification of active EL-alpha(2)-beta(2) of Pseudomonas putida branched-chain

A;Reference number: S63475; MUID:96065147; PMID:8521848

A;Accession: S63478

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <HES>

C;Keywords: FAD; flavoprotein; lipoamide; NAD; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTV 15

Db 6 TTV 8

RESULT 13

heat shock protein C62.5 homolog - Salmonella typhimurium (fragment)

N;Alternate names: high temperature protein G

C;Species: Salmonella typhimurium

C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C;Accession: S70721

R;Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.

Mol. Microbiol. 17: 523-531, 1995

A;Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophils

A;Reference number: S70719; MUID:96100451; PMID:8559071

A;Accession: S70721

A;Molecule type: protein

A;Residues: 1-10 <QIS>

A;Experimental source: strain SH1344

C;Keywords: ATP binding; heat shock; molecular chaperone

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13

Db 4 QET 6

RESULT 14

peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain

N;Alternate names: peptidase N-glycosidase

C;Species: Prunus dulcis var. sativa (sweet almond)

C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000

C;Accession: B59272

R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

Eur J. Biochem. 252: 118-123, 1998

A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A

A;Reference number: A59272; MUID:96181894; PMID:9523720

A;Accession: B59272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <ALT>

C;Keywords: hydrolase

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPP 8

Db 8 FPP 10

RESULT 15

A61354

carnitine medium/long chain acyltransferase (EC 2.3.1.1-) - rat (fragment)

N;Alternate names: endoplasmic reticulum protein ERP61; glucose regulated protein GRP58;

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999

C;Accession: A61354

R;Murthy, M.S.R.; Pande, S.V.

Mol. Cell. Biochem. 122, 133-138, 1993

A;Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previa

A;Reference number: A61354; MUID:94049728; PMID:8232244

A;Accession: A61354

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <MUR>

C;Keywords: acyltransferase

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3

Db 3 VLE 5

RESULT 16

T-cell receptor beta chain C region (CRTB49) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997

C;Accession: C30572

R;Williams, C.B.; Gutman, G.A.

J. Immunol. 142, 1027-1035, 1989

A;Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz

A;Reference number: A30563; MUID:89110038; PMID:2563271

A;Accession: C30572

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-10 <WIL>

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTV 15

Db 5 TTV 7

RESULT 17

PH0923

T-cell receptor beta chain V-D-J region (isolate 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0923

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0923

A;Molecule type: mRNA

A;Residues: 1-10 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13

Db 8 QET 10

RESULT 18

PC4267
ribosomal protein L12.1 - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C:Accession: PC4267
R:Kawakami, T.; Kano, M.; Chen, M.C.; Tsugita, A.
Submitted to JPIB, April 1997
A:Reference number: PC4267
A:Accession: PC4267
A:Molecule type: protein
A:Residues: 1-11 <KAW>
A:Experimental source: strain Japonica Nihonbare

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
|||
DB 9 VLE 11

RESULT 19

BE0769
Ig H2 chain - Pacific hagfish (fragment)
C:Species: Eptatretus stouti (Pacific hagfish)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C:Accession: BE0769
R:Hanley, P.J.; Seppelt, I.M.; Gooley, A.A.; Hook, J.W.; Raison, R.L.
J. Immunol. 145, 3823-3828, 1990
A:Title: Distinct Ig H chains in a primitive vertebrate, Eptatretus stouti.
A:Reference number: A60769; PMID:91060965; PMID:2123225
A:Accession: BE0769
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <HAN>

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13
|||
DB 9 QET 11

RESULT 20

D45900
complement C3b receptor type 2 - mouse (clone 12) (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: D45900
R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
J. Immunol. 144, 3581-3591, 1990
A:Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene.
A:Reference number: A45900; PMID:90229754; PMID:2139460
A:Accession: D45900
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-11 <KUR>

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
|||
DB 9 PPP 11

RESULT 21

PH0904

T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0904
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; PMID:92078857; PMID:1836012
A:Accession: PH0904
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: myelin basic protein-immunized T-cell
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13
|||
DB 8 QET 10

RESULT 22

C39109
hypothetical 1.2K protein - hepatitis C virus
N:Alternate names: hypothetical protein 3
C:Species: hepatitis C virus
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999
C:Accession: C39109; J01586
R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-
Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991
A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identification
A:Reference number: A39109; PMID:91156678; PMID:1705704
A:Accession: C39109
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-12 <HAN>

Query Match 20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11
|||
DB 8 PPQ 10

RESULT 23

PN0663
dyatrophin-associated glycoprotein A3a-II - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C:Accession: PN0663
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A:Title: A dyatrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained
A:Reference number: PN0662; PMID:94156881; PMID:8113213
A:Accession: PN0663
A:Molecule type: protein
A:Residues: 1-12 <YOS>
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

```

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      5 PPP 7

RESULT 24
B39690
neural cell adhesion molecule, cardiac splice form +,-,- - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: B39690
R:Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule m
A:Reference number: A39690; MUID:91141516; PMID:1996115
A:Accession: B39690
A>Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-12 <REI>
A:Cross-references: GB:M33970
C:Keywords: cardiac muscle; cell adhesion; heart

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      6 PPP 8

RESULT 25
S69095
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein - Sulfolobus acidocal
N;Alternate names: Rieske iron-sulfur protein
C:Species: Sulfolobus acidocaldarius
C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 03-Jun-2002
C:Accession: S69095
R:Schmidt, C.L.; Anemuller, S.; Teixeira, M.; Schaefer, G.
FEBS Lett. 359, 239-243, 1995
A:Title: Purification and characterization of the Rieske iron-sulfur protein from the th
A:Reference number: S69095; MUID:95172243; PMID:7867807
A:Accession: S69095
A:Molecule type: protein
A:Residues: 1-12 <SCH>
C:Keywords: oxidoreductase

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TVT 15
      |||
Db      8 TVT 10

RESULT 26
S21152
tryptophyllin-related peptide - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S21152
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A:Title: Identification and characterization of two dermorphins from skin extracts of th
A:Reference number: S21152; MUID:92339502; PMID:1633846
A:Accession: S21152
A:Molecule type: protein

A;Residues: 1-13 <MIG>
A;Experimental source: skin
C;Superfamily: unassigned animal peptides

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      7 PPP 9

RESULT 27
A05174
tryptophyllin-13 - Rohde's leaf frog
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 18-Aug-2000
C:Accession: A05174
R:Montecucchi, P.C.; Gozzini, L.; Erspamer, V.
Int. J. Pept. Protein Res. 27, 175-182, 1986
A:Reference number: A05174
A:Accession: A05174
A:Molecule type: protein
A:Residues: 1-13 <MON>
C;Superfamily: unassigned animal peptides
C;Keywords: pyrrolidonic acid; skin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      7 PPP 9

RESULT 28
S09716
2S albumin large chain (1 and 2) nII - rape (fragments)
N;Alternate names: 2S albumin large chain nIII
C:Species: Brassica napus (rape)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
C:Accession: S09716; S09718; S09717
R;Monbalve, R.L.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:9042374; PMID:2185951
A:Accession: S09716
A:Molecule type: protein
A;Residues: 1-9;10-13 <MON>
A;Experimental source: seed
A;Note: 3-Ser was also found
A:Accession: S09718
A:Molecule type: protein
A;Residues: 1-9;10-13 <MO2>
A;Experimental source: seed
A:Accession: S09717
A:Molecule type: protein
A;Residues: 1-9;10-13 <MO3>
A;Experimental source: seed

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPP 9
      |||
Db      8 PPP 10

RESULT 29

```

```

PN0048
unidentified QM0023 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C:Accession: PN0048
R:Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A:Reference number: PN0041
A:Accession: PN0048
A:Molecule type: protein
A:Residues: 1-13 <XAP>
A:Experimental source: neuroblastoma cell
C:Comment: The molecular mass is 30,500 and the pI is 6.19.
C:Keywords: brain

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TVT 15
Db      11 TVT 13

RESULT 30
S01904
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloro
C:Species: chloroplast Arabidopsis thaliana (mouse-ear cress)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 03-Jun-2002
C:Accession: S01904
R:Chen, H.C.; Wintz, H.; Weill, J.H.; Pillay, D.T.N.
Nucleic Acids Res. 16, 10372, 1988
A:Title: Nucleotide sequence of chloroplast CF1-ATPase epsilon-subunit and elongator TRN
A:Reference number: S01903; MUID:89057486; PMID:29041134
A:Accession: S01904
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-13 <CHE>
A:Cross-references: EMBL:X12889; NID:gl1332; PIDN:CAA31380.1; PID:g829297
C:Genetics:
A:Gene: atpB
A:Genome: chloroplast
C:Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LEM 4
Db      5 LEM 7

RESULT 31
PS0252
16k protein 5404 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Apr-1995
C:Accession: PS0252
R:Tsubota, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0252
A:Molecule type: protein
A:Residues: 1-14 <TSU>
A:Experimental source: strain Nihonbare
C:Comment: Molecular weight 16k, pI 4.9.

Query Match      20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PN0048
unidentified QM0023 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C:Accession: PN0048
R:Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
A:Reference number: PN0041
A:Accession: PN0048
A:Molecule type: protein
A:Residues: 1-13 <XAP>
A:Experimental source: neuroblastoma cell
C:Comment: The molecular mass is 30,500 and the pI is 6.19.
C:Keywords: brain

Query Match      20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TVT 15
Db      11 TVT 13

RESULT 32
S12904
protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)
C:Species: Pisaster ochraceus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C:Accession: S12904
R:Sanhara, J.S.; Ahersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A:Title: Identification of the sites in myelin basic protein that are phosphorylated by
A:Reference number: S12904; MUID:91032166; PMID:1699809
A:Accession: S12904
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SAN>
C:Keywords: phosphotransferase

Query Match      20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPP 9
Db      8 PPP 10

RESULT 33
S03530
Ig heavy chain J region (JH-4) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000
C:Accession: S03530
R:Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenop
A:Reference number: S01158; MUID:89052653; PMID:2903824
A:Accession: S03530
A:Molecule type: DNA
A:Residues: 1-14 <SCH>
A:Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33043.1; PID:gl1334657

Query Match      20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TVT 15
Db      11 TVT 13

RESULT 34
B20872
alpha-2-macroglobulin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
C:Accession: B20872
R:Nagase, H.; Harris Jr., E.D.; Woessner Jr., J.F.; Brew, K.
J. Biol. Chem. 258, 7481-7489, 1983
A:Title: Oostatin: a novel proteinase inhibitor from chicken egg white. I. Purification
A:Reference number: A92427; MUID:83238315; PMID:6408074
A:Accession: B20872
A:Molecule type: protein
A:Residues: 1-14 <NAG>

Query Match      20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 TVT 15

```

Db 2 TVT 4
|||

RESULT 35
S11129
phosphoprotein, bone - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 25-Oct-1996
C:Accession: S11129
R:MiKuni-Takagaki, Y.; Glincher, M.J.
Biochem. J. 268, 565-591, 1990
A:Title: Post-translational processing of chicken bone phosphoproteins. Identification of
A:Reference number: S11127; PMID:90303246; PMID:2363696
A:Accession: S11129
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MIK>
C:Keywords: phosphoprotein

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
|||

Db 5 PPP 7
|||

RESULT 36
B26997
unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 2A1, hepatic - rat (fragment)
N:Alternate names: cytochrome P450a
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-Mar-1999
C:Accession: B26997
R:Graves, P.E.; Kaminsky, L.S.; Halpert, J.
Biochemistry 26, 3887-3894, 1987
A:Title: Evidence for functional and structural multiplicity of pregnenolone-16-alpha-ca
A:Reference number: A26997; PMID:88000604; PMID:3651420
A:Accession: B26997
A:Molecule type: protein
A:Residues: 1-15 <GRA>
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homolog
C:Keywords: electron transfer; heme; liver; monooxygenase; oxidoreductase; transmembrane

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
|||

Db 8 VLE 10
|||

RESULT 37
PN0629
integration host factor-like protein beta chain - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: PN0629
R:Toussaint, B.; Delic-Attrée, I.; Vignais, P.M.
Biochem. Biophys. Res. Commun. 196, 416-421, 1993
A:Title: Pseudomonas aeruginosa contains an IHF-like protein that binds to the algD prom
A:Reference number: PN0628; PMID:94030028; PMID:8216322
A:Accession: PN0629
A:Molecule type: protein
A:Residues: 1-15 <TOU>
C:Comment: This protein forms a stable complex with the algD promoter in vitro, indicati

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
|||

Db 10 TVT 12
|||

RESULT 38
PA0036
glycine cleavage system protein H1 and H2 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: PA0036
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
A:Reference number: PA0001
A:Accession: PA0036
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: stem

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
|||

Db 3 VLE 5
|||

RESULT 39
PA0014
seed storage protein 12S 3 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: PA0014
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
A:Reference number: PA0001
A:Accession: PA0014
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Experimental source: seed
C:Keywords: seed; storage protein

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11
|||

Db 7 PPQ 9
|||

RESULT 40
PN0173
seed storage protein 12S4 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 23-Mar-2001
C:Accession: PN0173
R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A:Description: Two dimensional electrophoresis of plant proteins and standardization of
A:Reference number: PN0173
A:Accession: PN0173
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: seeds

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PPQ 11
|||
Db 7 PPQ 9

RESULT 41

S10388
Ig heavy chain J region (clone Rel02) - little skate (fragment)
C:Species: Raja erinacea (little skate)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
C:Accession: S10388
R:Harding, F.A.; Cohen, N.; Litman, G.W.
Nucleic Acids Res. 18, 1015-1020, 1990
A:Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja
A:Reference number: S08462; MUID:90192082; PMID:2107524
A:Accession: S10388
A:Molecule type: DNA
A:Residues: 1-15 <HAR>
A:Cross-references: EMBL:X16146; NID:964284; PIDN:CAA34271.1; PID:gl334773
C:Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15
|||
Db 12 TVT 14

RESULT 42

S10386
Ig heavy chain J region (clone Rel07) - little skate (fragment)
C:Species: Raja erinacea (little skate)
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Aug-1996
C:Accession: S10386
R:Harding, F.A.; Cohen, N.; Litman, G.W.
Nucleic Acids Res. 18, 1015-1020, 1990
A:Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja
A:Reference number: S08462; MUID:90192082; PMID:2107524
A:Accession: S10386
A:Molecule type: DNA
A:Residues: 1-15 <HAR>
A:Cross-references: EMBL:X15124
C:Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15
|||
Db 12 TVT 14

RESULT 43

A61522
7.5k surfactant-associated protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 15-Oct-1994
C:Accession: A61522
R:Singh, G.; Katyal, S.L.; Brown, W.E.; Kennedy, A.L.; Wong-Chong, M.L.; Gottron, S.A.
Exp. Lung Res. 17, 559-567, 1991
A:Title: Identification, isolation, and partial characterization of a 7.5-kDa surfactant
A:Reference number: A61522; MUID:91317170; PMID:1860454
A:Accession: A61522
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <SIN>

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VLE 3
|||
Db 6 VLE 8

RESULT 44

D28587
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C:Accession: D28587
R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A:Title: Organization and sequences of the diversity, joining, and constant region genes
A:Reference number: A94081; MUID:86094276; PMID:3866244
A:Accession: D28587
A:Molecule type: DNA
A:Residues: 1-15 <TOY>
A:Cross-references: GB:M14159; NID:g338852; PIDN:AAA60679.1; PID:g553690
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QET 13
|||
Db 1 QET 3

RESULT 45

D28587
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C:Accession: D28587
R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A:Title: Organization and sequences of the diversity, joining, and constant region genes
A:Reference number: A94081; MUID:86094276; PMID:3866244
A:Accession: D28587
A:Molecule type: DNA
A:Residues: 1-15 <TOY>
A:Cross-references: GB:M14159; NID:g338852; PIDN:AAA60681.1; PID:g553692
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15
|||
Db 13 TVT 15

RESULT 46

I53284
T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: I53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity and j
A:Reference number: A53284; MUID:91342695; PMID:1678859
A:Accession: I53284
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <HAR>
A:Cross-references: GB:S60737; NID:q233916; PIDN:AAB19525.1; PID:q233925
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60747)

C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 13 TVT 15

RESULT 47

I46909
voltage-dependent dihydropyridine-sensitive calcium channel alpha 1 subunit 155 kDa isoform
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C;Accession: I46909
R;Malouf, N.N.; McMahon, D.K.; Hainsworth, C.N.; Kay, B.K.
Neuron 8, 899-906, 1992
A;Title: A two-motif isoform of the major calcium channel subunit in skeletal muscle.
A;Reference number: I46909; PMID:92265303; PMID:1316766
A;Accession: I46909
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-15 <MAL>
A;Cross-references: GB:S36895; NID:9249481; PIDN:AA822180.1; PID:9249482

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
DB 13 LEM 15

RESULT 48

S72432
epoxypropan isomerase component B - Xanthobacter sp. (strain Py2) (fragment)
C;Species: Xanthobacter sp.
A;Variety: strain Py2
C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 07-May-1999
C;Accession: S72432
R;Chan Kwo Chion, C.K.N.; Leak, D.J.
Biochem. J. 319, 499-506, 1996
A;Title: Purification and characterization of two components of epoxypropane isomerase/
A;Reference number: S72431; PMID:97069704; PMID:8912687
A;Accession: S72432
A;Molecule type: protein
A;Residues: 1-15 <CHA>
A;Note: 3-Met and 13-Leu were also found
C;Complex: homodimer
C;Function:
A;Description: NADP-dependent lipamide reductase
A;Pathway: epoxypropane degradation
A;Note: sensitive to N-ethyl-maleimide and p-chloromercuribenzoate
C;Keywords: PAD

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKF 6
DB 1 MKF 3

RESULT 49

S03532
Ig heavy chain J region (JH-7) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
C;Accession: S03532

R;Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988

A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis
A;Reference number: S01158; PMID:89052653; PMID:2903824

A;Accession: S03532
A;Molecule type: DNA
A;Residues: 1-16 <SCH>

A;Cross-references: EMBL:X14918; NID:964805; PIDN:CAA33046.1; PID:gi334660
A;Note: the authors translated the codon AAC for residue 1 as Asp
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 13 TVT 15

RESULT 50

D49021
Ig heavy chain J7 region - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: D49021
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990

A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A;Reference number: A47824; PMID:90237760; PMID:2110243
A;Accession: D49021

A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-16 <HAI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 13 TVT 15

RESULT 51

JH0517
insulin-like growth factor-binding protein 4 - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
C;Accession: JH0517
R;Coleman, M.E.; Pan, Y.C.E.; Ehterton, T.D.
Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth
A;Reference number: JH0515; PMID:92109718; PMID:1722398
A;Accession: JH0517
A;Molecule type: protein
A;Residues: 1-16 <COL>
A;Experimental source: serum

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB 7 PPP 9

RESULT 52

PH0763
T-cell receptor beta chain (F15) - mouse (fragment)

C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C;Accession: PH0763
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-homologous genes: allelic exclusion and antigen-specific repertoire.
 A;Reference number: PH0746; MUID:92078846; PMID:1836010
 A;Accession: PH0763
 A;Molecule type: mRNA
 A;Residues: 1-16 <CAS>
 A;Cross-references: EMBL:X60857; NID:g50933; PIDN:CAA43247.1; PID:g50934
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11
 |||
 Db 5 PPQ 7

RESULT 53
 PH0759
 T-cell receptor beta chain (QB7.3.2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C;Accession: PH0759
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-homologous genes: allelic exclusion and antigen-specific repertoire.
 A;Reference number: PH0746; MUID:92078846; PMID:1836010
 A;Accession: PH0759
 A;Molecule type: mRNA
 A;Residues: 1-16 <CAS>
 A;Cross-references: EMBL:X60854; NID:g53878; PIDN:CAA43244.1; PID:g53879
 A;Experimental source: T lymphocyte
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11
 |||
 Db 5 PPQ 7

RESULT 54
 S03531
 Ig heavy chain J5 region - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
 C;Accession: S03531; C43021
 R;Schwager, J.; Grossberger, D.; du Pasquier, L.
 EMBO J. 7, 2409-2415, 1988
 A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis.
 A;Reference number: S01158; MUID:89052653; PMID:2903824
 A;Accession: S03531
 A;Molecule type: DNA
 A;Residues: 1-17 <SCH>
 A;Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33044.1; PID:g1334658
 R;Haere, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
 J. Exp. Med. 171, 1721-1737, 1990
 A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation in the V-H region of the immunoglobulin heavy chain.
 A;Reference number: A47624; MUID:90237760; PMID:2110243
 A;Accession: C43021
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 3-17 <HA1>

C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
 |||
 Db 14 TVT 16

RESULT 55
 S24570
 Ig heavy chain J region - channel catfish
 C;Species: Ictalurus punctatus (channel catfish)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
 C;Accession: S24570
 R;Wilson, M.R.
 submitted to the EMBL Data Library, March 1992
 A;Reference number: S24570
 A;Accession: S24570
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-17 <WIL>
 A;Cross-references: EMBL:X65182; NID:g64015; PIDN:CAA46293.1; PID:g64016
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
 |||
 Db 14 TVT 16

RESULT 56
 S26744
 Ig heavy chain J region JH1 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 25-Feb-1994 #sequence_revision 24-Oct-1998 #text_change 17-Mar-1999
 C;Accession: S26744
 R;Solari, M.L.; Kaartinen, M.
 Immunogenetics 36, 306-313, 1992
 A;Title: Allelic polymorphism of mouse Igh-J locus, which encodes immunoglobulin heavy chain.
 A;Reference number: S26744; MUID:92355114; PMID:1644448
 A;Accession: S26744
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-17 <SOL>
 A;Cross-references: EMBL:X63164
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
 |||
 Db 12 TVT 14

RESULT 57
 A34572
 osteonectin - rat (fragment)
 N;Alternate names: BM-40; SPARC
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 17-Nov-2000
 C;Accession: A34572
 R;Cheng, C.Y.

Biochem. Biophys. Res. Commun. 167, 1393-1399, 1990
 A>Title: Purification of a calcium binding protein (rat SPARC) from primary Sertoli cell
 A/Reference number: A34572; MUID:90211328; PMID:232281
 A/Accession: A34572

A/Molecule type: Protein
 A/Residues: 1-17 <HE>
 C/Superfamily: osteonectin; calmodulin repeat homology; kazal proteinase inhibitor homol
 C/Keywords: calcium binding; collagen binding; disulfide bond; EF hand; extracellular ma

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
 |||
 Db 14 ETV 16

RESULT 58

E53113

gingipain, 44K - Porphyromonas gingivalis (fragment)

N/Alternate names: arginine-specific cysteine proteinase, 44K

C/Species: Porphyromonas gingivalis

C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 05-Apr-1995

C/Accession: E53113

R/Pike, R.; McGraw, W.; Potempa, J.; Travis, J.

J. Biol. Chem. 269, 406-411, 1994

A>Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolab

A/Reference number: A53113; MUID:94103245; PMID:8276827

A/Accession: E53113

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-17 <PIK>

A/Experimental source: H66

A/Note: sequence extracted from NCBI backbone (NCBIP:141695)

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
 |||
 Db 7 VLE 9

RESULT 59

B28027

protein P4 - curled-leaved tobacco (fragment)

C/Species: Nicotiana glauca (curled-leaved tobacco)

C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993

C/Accession: B28027

R/Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.

Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987

A>Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-

A/Reference number: A94167

A/Accession: B28027

A/Molecule type: protein

A/Residues: 1-17 <BAU>

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
 |||
 Db 4 ETV 6

RESULT 60

I24687

T-cell receptor beta-1 chain J-B1.6 segment - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999

C/Accession: I24687
 R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
 A>Title: Organization and sequences of the diversity, joining, and constant region genes
 A/Reference number: A94081; MUID:86094276; PMID:3866244
 A/Accession: I24687

A/Molecule type: DNA

A/Residues: 1-17 <TOY>

A/Cross-references: GB:M14158; NID:g338844; PIDN:AAA60673.1; PID:g553685

C/Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
 |||
 Db 15 TVT 17

RESULT 61

G85956

hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C/Accession: G85956

R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: G85956

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-17 <STO>

A/Cross-references: GB:AF005174; NID:gl2517539; PIDN:AA959115.1; GSPDB:GN00145; UMGF:Z43

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: Z4331

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
 |||
 Db 2 ETV 4

RESULT 62

PC2319

proteasome endopeptidase complex (EC 3.4.25.1), 2 chain - human (fragment)

N/Alternate names: protein

C/Species: Homo sapiens (man)

C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 17-Feb-2003

C/Accession: PC2319

R/Kristensen, P.; Johnsen, A.H.; Uerkvitz, W.; Tanaka, K.; Hendil, K.B.

Biochem. Biophys. Res. Commun. 205, 1785-1789, 1994

A>Title: Human proteasome subunits from 2-dimensional gels identified by partial sequenc

A/Reference number: PC2315; MUID:95110324; PMID:7811265

A/Accession: PC2319

A/Molecule type: protein

A/Residues: 1-17 <KKI>

A/Experimental source: placenta

C/Comment: The proteasome consists of subunits of 21K-30K arranged in 4 stacked rings.

C/Keywords: hydrolase; proteinase

Query Match 20.0%; Score 3; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
 |||

Db 8 VLE 10

RESULT 63

S03528
Ig heavy chain J1 region - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 20-Jun-2000
C:Accession: S03528; G49021
R:Schwager, J.; Groseberger, D.; du Pasquier, L.
EMBO J. 7, 2403-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis
A:Reference number: S01159; MUID:89052653; PMID:2903824
A:Accession: S03528
A:Molecule type: DNA
A:Residues: 1-18 <SCH>
A:Cross-references: EMBL:X14917; NID:964802; PIDN:CAA33041.1; PID:g1334655
R:Hairst, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A:Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A:Reference number: A47624; MUID:90237760; PMID:2110243
A:Accession: G49021
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 2-18 <HAI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TVT 15

Db 13 TVT 15

RESULT 64

PC2280
Prolylendopeptidase-inhibiting peptide - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-May-1997
C:Accession: PC2280
R:Ohmori, T.; Nakagami, T.; Tanaka, H.; Maruyama, S.
Biochem. Biophys. Res. Commun. 202, 809-815, 1994
A:Title: Isolation of prolylendopeptidase-inhibiting peptides from bovine brain.
A:Reference number: PC2280; MUID:94324971; PMID:8048952
A:Accession: PC2280
A:Molecule type: protein
A:Residues: 1-18 <OHM>
A:Experimental source: brain
C:Superfamily: cytoskeletal keratin

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 EPP 9

Db 2 EPP 4

RESULT 65

B44995
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) beta chain - flashlight fish symbiont
C:Species: flashlight fish symbiont bacterium
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C:Accession: B44995
R:Harwood, M.G.
Arch Microbiol. 154, 496-503, 1990
A:Title: Relationship of the luminous bacterial symbiont of the Caribbean flashlight fish
A:Reference number: A44995; MUID:91076680; PMID:2256783

A:Accession: B44995

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-18 <HAY>

A:Cross-references: GB:M36597; NID:g213345; PIDN:AAA91214.1; PID:g1204253

C:Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match

20.0%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKF 6

Db 1 MKF 3

RESULT 66

S10452
hypothetical protein (bpha 5' region) - Aspergillus niger
C:Species: Aspergillus niger
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Sep-1997
C:Accession: S10452
R:van Gorcom, R.F.M.; Boschloo, J.G.; Kuijvenhoven, A.; Lange, J.; Bos, C.J.; van Balken
submitted to the EMBL Data Library, March 1990
A:Reference number: S10452
A:Accession: S10452
A:Molecule type: DNA
A:Residues: 1-18 <VAN>
A:Cross-references: EMBL:X52521; NID:g23336; PID:g23337

Query Match 20.0%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QET 13

Db 9 QET 11

RESULT 67

T13132
protein GP45.1 - phage N15
C:Species: phage N15
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C:Accession: T13132
R:Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z17603
A:Accession: T13132
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <HEN>
A:Cross-references: EMBL:AF064539; NID:g3192683; PID:g3192731; PIDN:AAC19084.1

A:Note: gene 45.1

Query Match

20.0%; Score 3; DB 2; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QET 13

Db 15 QET 17

RESULT 68

A54195
Na+/K+-exchanging ATPase (EC 3.6.3.9) - spiny dogfish (fragment)
C:Species: Squalus acanthias (spiny dogfish)
C>Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 19-Apr-2002
C:Accession: A54195
R:Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994

A;Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase

A;Reference number: A54195; MUID:94297020; PMID:8025109

A;Accession: A54195

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <ESM>

A;Experimental source: rectal gland

A;Note: sequence extracted from NCBI backbone (NCBIP:149363)

C;Keywords: hydrolase

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred.No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9

DB 8 PPP 10

RESULT 69

PS0186

Superoxide dismutase (EC 1.15.1.1) (Nm) - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 05-Mar-1999

C;Accession: PS0186

R;Kamo, M.; Tsugita, A.

submitted to JIPID, June 1991

A;Reference number: PS0184

A;Accession: PS0186

A;Molecule type: protein

A;Residues: 1-19 <RAM>

A;Experimental source: callus

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Superfamily: superoxide dismutase (Nm)

C;Keywords: manganese; metalloprotein; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14

DB 2 ETV 4

RESULT 70

PN0467

Nitrogenase (EC 1.18.6.1) molybdenum-iron protein alpha chain - Azotobacter chroococcum

C;Species: Azotobacter chroococcum

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001

C;Accession: PN0467

R;Jones, R.; Woodley, P.; Birkmann-Zinoni, A.; Robson, R.L.

Gene 123, 145-146, 1993

A;Title: The nifH gene encoding the Fe protein Component of the molybdenum nitrogenase

A;Reference number: JN0516; MUID:93138425; PMID:8423000

A;Accession: PN0467

A;Molecule type: DNA

A;Residues: 1-19 <JON>

A;Cross-references: GB:M73020; NID:g142326; PIDN:AAA22141.1; PID:g289238

C;Genetics:

A;Gene: nifD

C;Superfamily: dinitrogenase alpha chain; nitrogenase vanadium-iron protein alpha chain

C;Keywords: ATP; nitrogen fixation; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3

DB 16 VLE 18

RESULT 71

B26930

ermG leader peptide 2 - Bacillus sphaericus

C;Species: Bacillus sphaericus

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 26-Aug-1999

C;Accession: B26930

R;Monod, M.; Mohan, S.; Dubnau, D.

J. Bacteriol. 169, 340-350, 1987

A;Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resis

A;Reference number: A51840; MUID:87083389; PMID:3025178

A;Accession: B26930

A;Molecule type: DNA

A;Residues: 1-19 <MON>

A;Cross-references: GB:M15332; NID:g142881; PIDN:AAA22418.1; PID:g142883

C;Superfamily: ermC leader peptide

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14

DB 10 ETV 12

RESULT 72

S31613

Beta-1,3-glucanase homolog (clone A28) - rape (fragment)

C;Species: Brassica napus (rape)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Nov-2000

C;Accession: S31613

R;Hird, D.; Morrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R.

submitted to the EMBL Data Library, December 1992

A;Description: The anther-specific protein encoded by the Brassica napus and Arabidopsis

A;Reference number: S31612

A;Accession: S31613

A;Molecule type: mRNA

A;Residues: 1-19 <HIR>

A;Cross-references: EMBL:X69890; NID:g17735; PID:g17736

A;Experimental source: clone A28

C;Superfamily: beta-1,3-glucanase

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFP 7

DB 13 KFP 15

RESULT 73

A49780

Promoter P8 hypothetical protein - Streptococcus thermophilus (strain A054) (fragment)

C;Species: Streptococcus thermophilus

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999

C;Accession: A49780

R;Glos, P.; Bourquin, J.C.; Lemoine, Y.; Mercenier, A.

Appl. Environ. Microbiol. 57, 1333-1339, 1991

A;Title: Isolation and characterization of chromosomal promoters of Streptococcus saliva

A;Reference number: A49780; MUID:91307302; PMID:1854195

A;Accession: A49780

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-19 <SLO>

A;Cross-references: GB:M69234

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5

```

Db          2 EMK 4
|||
RESULT 74
G56819
PS I complex subunit 6 - cucumber (fragment)
C:Species: Cucumis sativus (cucumber)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C:Accession: G56819
R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-te
A:Reference number: A56819; MUID:91355209; PMID:1883835
A:Accession: G56819
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <IWA>
A>Note: sequence extracted from NCBI backbone (NCBIP:58604)

Query Match      20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPP 9
|||
Db      6 PPP 8

RESULT 75
T50329
wd-repeat protein popl. [imported] - fission yeast (Schizosaccharomyces pombe) (fragment
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50329
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25062
A:Accession: T50329
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-19 <LYN>
A:Cross-references: EMBL:AL157874; PIDN:CA875991.1; GSFDB:GN00067; SPDB:SPBC1718.01
A:Experimental source: strain 972h(-); cosmid ci718
C:Genetics:
A:Gene: SPBC2G2.18; SPDB:SPBC1718.01
A:Map position: 2

Query Match      20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLE 3
|||
Db     10 VLE 12

Search completed: November 25, 2003, 18:28:18
Job time : 14.8032 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 7.26064 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKPPPPQETWT 15

Scoring table: OLIGO

Gapex 60.0 , Gapext 60.0

Searched: 127863 segs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	33.3	15	1 PRP_MYCBO	P80149 mycobacteri
2	4	26.7	10	1 Q20B_COMTE	P80465 comamonas t
3	4	26.7	10	1 TNOF_AEDAE	P19425 aedes aegypt
4	3	20.0	9	1 FLA2_TREHY	P80159 treponema h
5	3	20.0	12	1 FIP1_SARBU	P83349 sarcophaga
6	3	20.0	13	1 IDHA_CANFA	P54836 canis fami
7	3	20.0	13	1 NO40_PEA	P55959 pisum sativ
8	3	20.0	13	1 TY13_PHYRO	P04096 phyllomedus
9	3	20.0	14	1 KLPS_SCARA	P58396 scaptocosa
10	3	20.0	16	1 AF2S_MALPA	P83142 malva parvi
11	3	20.0	16	1 IBP4_FIG	P24854 sus scrofa
12	3	20.0	17	1 APID_BOMPA	P81464 bombus pasc
13	3	20.0	18	1 LUXB_KRYAS	P18300 kryptophana
14	3	20.0	19	1 HI70_RAT	P21794 rattus norv
15	3	20.0	19	1 PSAE_CUCSA	P42047 cucumis sat
16	3	20.0	20	1 APAL_ERYPA	P18647 erythrocebu
17	3	20.0	20	1 CS21_STRTR	P81621 streptococ
18	3	20.0	20	1 DNAK_MYCAV	P80462 mycobacteri
19	3	20.0	20	1 MDH_KIBAR	P19978 kidelespor
20	3	20.0	20	1 MDH_MICGL	P19979 microtetras
21	3	20.0	24	1 RM01_YEAST	P36515 saccharomyc
22	2	13.3	5	1 EI04_LITRU	P82100 litorea rub
23	2	13.3	5	1 PAP2_PARMA	P81864 pardachirus
24	2	13.3	6	1 ACPH_RABIT	P25154 oryctolagus
25	2	13.3	6	1 VP19_HSVIK	P23210 herpes simp
26	2	13.3	7	1 CCF1_ENTFA	P20104 enterococcu
27	2	13.3	7	1 TFYF_PACDA	P83455 pachymedusa
28	2	13.3	7	1 UF04_MOUSE	P38642 mus musculu
29	2	13.3	7	1 WWA1_ACHFU	P35919 achatina fu
30	2	13.3	7	1 WWA3_ACHFU	P35921 achatina fu
31	2	13.3	8	1 ALL5_CALVO	P41841 calliphora
32	2	13.3	8	1 CAD1_ENTFA	P13268 enterococcu
33	2	13.3	8	1 CLP_THICU	P80488 thiobacilli

34	2	13.3	8	1 COW2_CONPU	P58785 conus purpu
35	2	13.3	8	1 NPB_BOVIN	P15507 bos taurus
36	2	13.3	8	1 PFK2_PRRAM	P82692 periplaneta
37	2	13.3	8	1 UH09_RAT	P56575 rattus norv
38	2	13.3	8	1 UPAL1_HUMAN	P30087 homo sapien
39	2	13.3	8	1 AL10_CARMA	P81813 carcinus ma
40	2	13.3	9	1 BS43_SRRPL	P83375 serrattia pl
41	2	13.3	9	1 FAR1_CALVO	P41856 calliphora
42	2	13.3	9	1 FIBB_ERYPA	P18246 erythrocebu
43	2	13.3	9	1 FIBB_PAPAN	P18244 papio anubi
44	2	13.3	9	1 FIBB_PAPHA	P18243 papio hamad
45	2	13.3	9	1 FIBB_THEGE	P18242 theriopthec
46	2	13.3	9	1 KNL5_BOWMA	P83058 bombina var
47	2	13.3	9	1 LPCA_STAAR	P36884 staphylococ
48	2	13.3	9	1 OXYT_RAJUL	P42994 raja clavav
49	2	13.3	9	1 SAMP_MUSCA	P15095 mustelus ca
50	2	13.3	9	1 SAP_STOVA	P24047 stomopneute
51	2	13.3	9	1 UHA2_HUMAN	P40929 homo sapien
52	2	13.3	9	1 ULAE_HUMAN	P31931 homo sapien
53	2	13.3	9	1 ULAH_HUMAN	P31934 homo sapien
54	2	13.3	9	1 UN19_CLOPA	P81355 clostridium
55	2	13.3	9	1 UP43_HUMAN	P30089 homo sapien
56	2	13.3	9	1 YBFR_AZOVI	P25825 azotobacter
57	2	13.3	10	1 AH3_BRUSE	P29261 prunus sero
58	2	13.3	10	1 AKH3_LOOMI	P81626 locusta mig
59	2	13.3	10	1 BPP2_BOTIN	P30422 bothrops in
60	2	13.3	10	1 BPP2_BOTJA	P30422 bothrops ja
61	2	13.3	10	1 BPP8_BOTIN	P30426 bothrops in
62	2	13.3	10	1 BPP_VIPAS	P31351 vipera aspi
63	2	13.3	10	1 BRK_ONCMY	Q9PRZ1 oncorhynch
64	2	13.3	10	1 COXA_ONCMY	P80328 oncorhynch
65	2	13.3	10	1 ESL_LACCA	P81758 lactobacill
66	2	13.3	10	1 FAR6_PANRE	P82660 panagrellus
67	2	13.3	10	1 GONI_PETMA	P04378 petromyzon
68	2	13.3	10	1 LABA_JATMU	P13270 jatropha mu
69	2	13.3	10	1 ODP2_BOVIN	P11180 bos taurus
70	2	13.3	10	1 PVK_LOQMI	P83382 locusta mig
71	2	13.3	10	1 SLAP_BACTG	P49325 bacillus th
72	2	13.3	10	1 TKL3_LOQMI	P30249 locusta mig
73	2	13.3	10	1 TKN1_SCYCA	P08608 scyllorhinu
74	2	13.3	10	1 TKS1_AEDAE	P42634 aedes aegypt
75	2	13.3	10	1 TKS2_AEDAE	P42635 aedes aegypt
76	2	13.3	10	1 UP42_HUMAN	P30088 homo sapien
77	2	13.3	10	1 UP45_HUMAN	P30091 homo sapien
78	2	13.3	10	1 URE3_MORMO	P17339 morganella
79	2	13.3	11	1 BPP3_BOTIN	P30423 bothrops in
80	2	13.3	11	1 BPP4_BOTIN	P30424 bothrops in
81	2	13.3	11	1 BPPB_AKSHA	P01021 agkistrodon
82	2	13.3	11	1 BPP_AKHP	P04562 agkistrodon
83	2	13.3	11	1 BRK_MEGFL	P12797 megascolia
84	2	13.3	11	1 CEPI_ACHFU	P22790 achatina fu
85	2	13.3	11	1 COXA_CANFA	P99501 canis fami
86	2	13.3	11	1 EFG_CLOPA	P81350 clostridium
87	2	13.3	11	1 ESI1_RAT	P56571 rattus norv
88	2	13.3	11	1 LADD_ONCMY	P85018 oncorhynch
89	2	13.3	11	1 MBI_KLEPN	P80580 klebsiella
90	2	13.3	11	1 MLG_THETS	P41989 thermozym
91	2	13.3	11	1 MORN_HUMAN	P01163 homo sapien
92	2	13.3	11	1 NXSNN_PSETE	P59072 pseudonaja
93	2	13.3	11	1 RANC_RANPI	P08951 rana pipien
94	2	13.3	11	1 RR2_CONAM	P42341 conopholis
95	2	13.3	11	1 TKN1_CHICK	P19850 gallus gall
96	2	13.3	11	1 TKN1_GADMO	P28498 gadus morhu
97	2	13.3	11	1 TKN1_HORSE	P01290 equus cabal
98	2	13.3	11	1 TKN1_PHYFU	P08615 physalaema
99	2	13.3	11	1 TKN1_PENMO	P83322 peneaus mon
100	2	13.3	12	1 HCYE_MEGCR	Q10584 megathura c

ALIGNMENTS

RESULT 1


```

PRP_MYCBO
ID PRP MYCBO STANDARD; PRT; 15 AA.
AC P80149;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Prolin-rich protein (Fragment).
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1785;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;
RX MEDLINE=93281750; PubMed=8506381;
RA Romain F., Augier J., Pescher P., Marchal G.A.;
RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-
RT type hypersensitivity reactions only in guinea pigs immunized with
RT living mycobacteria."
RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY
CC REACTIONS IN GUINEA PIGS.
FT NON TER 15
SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPQ 11
Db 7 PPPQ 11

RESULT 2
Q2OB COMTE STANDARD; PRT; 10 AA.
AC P80465;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
RT Quinolone 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation."
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
CC 1,2-DIHYDROQUINOLINE.
CC -!- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first
CC step.
CC -!- SUBUNIT: HETEROHXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
CC TWO GAMMA CHAINS (PROBABLE).
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON TER 10
SQ SEQUENCE 10 AA; 1241 MW; C2B2C25DD9DC769 CRC64;

Query Match 26.7%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 MKFP 7
Db 1 MKFP 4

RESULT 3
ID TMOF AEDAE STANDARD; PRT; 10 AA.
AC P19435;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Trypsin-modulating costatic factor (TMOF) (COOH).
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito costatic factor: a novel decapeptide modulating
RT trypsin-like enzyme biosynthesis in the midgut."
RL FASEB J. 4:3015-3020(1990).
RN [2]
RP SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=9357794; PubMed=835326;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
RT modulating costatic factor (TMOF) and its analogs."
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
CC DEVELOPMENT.
CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
CC 36 HRS AND STOPS AT 56 HRS.
CC PIR; A36454; A36454.
KW Hormone.
DM DOMAIN 3 10 POLY-PRO.
FT VARIANT 1 2 YD -> DY [IN TMOF(B)].
SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 26.7%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 5 PPPP 8

RESULT 4
ID FLA2 TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
RN FLA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC STRAIN=C5;
RX MEDLINE=93139764; PubMed=1487733;
RA Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,

```

RA van der Zeijst B.A.M., Kusters J.G.;
 RT "The periplasmic flagella of *Serpulina* (Treponema) hyodysenteriae are
 RL composed of two sheath proteins and three core proteins.";
 CC J. Gen. Microbiol. 138:2697-2706(1992).
 CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLUM.
 CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
 CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE
 CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND
 CC FLAB3 (32 kDa).
 CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
 KW Flagella; Periplasmic.
 KW UNSURE 2;
 KW UNSURE 2;
 KW UNSURE 3;
 KW NON-TER 9;
 KW SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;
 SQ
 Query Match 20.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 12 ETV 14
 Db 1 ETV 3
 RESULT 5
 FIF_SARBU STANDARD; PRT; 12 AA.
 AC P83349;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FIRamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Sarcophagidae; Sarcophaga.
 CC NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AMIDATION, AND FUNCTION.
 RC TISSUE=CNS;
 RX MEDLINE=22342733; PubMed=12438685;
 RA Weusens I., Mercens I., Clynen E., Baggerman G., Nichols R.,
 RA Nachman R.J., Huybrechts R., De loof A., Schoofs L.;
 RT "Identification in *Drosophila melanogaster* of the invertebrate G
 RT protein-coupled FMRFamide receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
 CC junctions.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 KW MOD RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 PPO 11
 Db 2 PPO 4
 RESULT 6
 IDHA CANFA STANDARD; PRT; 13 AA.
 AC P54836;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial

DE (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD+-specific ICDH)
 DE (fragment).
 GN IDH3A.
 OS Canis familiaris (Dog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 CC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RC MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler, C.H.;
 RT HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- CATALYTIC ACTIVITY: Isocitrate + NAD(+) = 2-oxoglutarate + CO(2) +
 CC NADH.
 CC -!- SUBUNIT: HETEROOLIGOMER OF SUBUNITS ALPHA, BETA, AND GAMMA IN THE
 CC APPARENT RATIO OF 2:1:1 (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
 CC DEHYDROGENASES FAMILY.
 DR HSC-2DPAGE; P54836; DOG.
 DR InterPro; IPR001804; Isodh.
 DR PROSITE; PS00470; IDH IMDH; PARTIAL.
 KW Oxidoreductase; NAD; Tricarboxylic acid cycle; Mitochondrion.
 KW NON-TER 13 13
 KW SEQUENCE 13 AA; 1356 MW; 9ABFBC2B2A34B2D1 CRC64;
 SQ
 Query Match 20.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 TVT 15
 Db 6 TVT 8
 RESULT 7
 NC40_PEA STANDARD; PRT; 13 AA.
 AC P55959;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-DEC-1998 (Rel. 37, Last annotation update)
 DE Early nodulin 40.
 GN ENOD40.
 OS Pisum sativum (Garden pea).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
 CC NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Sparkle; TISSUE=Root nodules;
 RX MEDLINE=95036021; PubMed=7948896;
 RA Matvienko M., van de Sande K., Yang W.C., van Kammen A., Bisseling T.,
 RA Franssen H.J.;
 RT "Comparison of soybean and pea ENOD40 cDNA clones representing genes
 RT expressed during both early and late stages of nodule development.";
 RL Plant Mol. Biol. 26:487-493(1994).
 CC -!- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
 CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
 CC SIMILARITY).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
 CC DEVELOPMENT.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

```

CC or send an email to license@lsib-sib.ch).
CC -----
CC EMBL: X81064; -, NOT_ANNOTATED_CDS.
CC -----
KW Modulation
SQ SEQUENCE 13 AA; 1565 MW; 3C695B66BD8A26C3 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKF 6
DB 1 MKF 3

RESULT 8
TY13 PHYRO
ID TY13 PHYRO STANDARD; PRT; 13 AA.
AC P04096;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Trypophyllin-13.
OS Phyllomedusa rhodei (Rhode's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OC NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RA Montecucchi P.C., Gozzini L., Erspamer V.;
RT "Primary structure determination of a tryptophan-containing
RT tridecapeptide from Phyllomedusa rhodei."
RL Int. J. Pept. Protein Res. 27:175-182(1986).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC PIR: A05174; A05174.
KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
FT MOD_RES 1
SQ SEQUENCE 13 AA; 1646 MW; 33BF33A21222773 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB 7 PPP 9

RESULT 9
KLPS SCARA
ID KLPS SCARA STANDARD; PRT; 14 AA.
AC P58196;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kinin-like peptide-S (Fragment).
OS Scaptocosa raptorina (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Lycosidae; Scaptocosa.
OC NCBI_TaxID=180440;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98267639; PubMed=9604280;
RA Ferreira L.A.F., Lucas S.M., Alves E.W., Hermann V.V., Reichl A.P.,
RA Habermehl G., Zingali R.B.;
RT "Isolation, characterization and biological properties of two
RT kinin-like peptides (peptide-S and peptide-R) from Scaptocosa
RT raptorina venom."
RL Toxicon 36:31-39(1998).
CC -!- FUNCTION: Has kinin-like biological properties. Causes contraction

```

```

CC on the of mammalian ileum; relaxes the duodenum and increases the
CC capillary permeability.
CC Vasodilator.
KW NON_TER 14
SQ SEQUENCE 14 AA; 1510 MW; E811E2E5D2EE27CA CRC64;

Query Match 20.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 3 VLE 5

RESULT 10
AF2S MALPA
ID AF2S MALPA STANDARD; PRT; 16 AA.
AC P83142;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein-2, small subunit (CW-2) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Malva.
OC NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RX TISSUE=Seed;
RX MEDLINE=20568734; PubMed=1118343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseweed (Malva
RT parviflora)."
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not F.graminearum.
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
CC GO; GO:0003799; F:antifungal peptide activity; IDA.
DR Fungicide; Antibiotic.
KW NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 2027 MW; 9998D9E8F8F7EE65 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11
DB 9 PPQ 11

RESULT 11
IBP4 PIG
ID IBP4 PIG STANDARD; PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1722398;
RA Coleman M.E., Pan Y.-C.E., Ehterton T.D.;

```

```

RT Identification and NH2-terminal amino acid sequence of three
RL insulin-like growth factor-binding proteins in porcine serum."
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 IGFBP domain.
CC -1- SIMILARITY: Contains 1 thyroglobulin type-I domain.
DR PIR: JH0517; JH0517.
DR InterPro: IPR000867; Insl_gro_fac_dr.
DR InterPro: IPR000716; Thyroglobulin_1.
DR PROSITE: PS00222; IGF BINDING; PARTIAL.
DR PROSITE: PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 4098884009655E2 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 12
ID APID_BOMPA STANDARD; PRT; 17 AA.
AC P81464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apidaecin.
OS Bombus pascuorum (Brown bumble bee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=65598;
RN (1)_TaxID=65598;
RP SEQUENCE.
RC TISSUE=Hemolymph; PubMed=9219367;
EX MEDLINE=97362903; PubMed=9219367;
EA Rees J.A., Moniatte M., Bulet P.;
ET "Novel antibacterial peptides isolated from a European bumblebee,
RT Bombus pascuorum (Hymenoptera, Apoidea).";
RL Insect Biochem. Mol. Biol. 27:413-422(1997).
CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
CC BACTERIA.
CC -1- INDUCTION: By bacterial infection.
DR InterPro: IPR004828; Apidaecin.
DR Pfam: PF00807; Apidaecin; 1.
KW Insect immunity; Antibiotic; Hemolymph.
SQ SEQUENCE 17 AA; 1963 MW; CD1D0D02C8BC23D1 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

Qy 7 PPP 9
Db 8 PPP 10

RESULT 13
LUXB KRYAS
ID LUXB KRYAS STANDARD; PRT; 18 AA.
AC P18300;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)

```

```

DE Alkanal monooxygenase beta chain (BC 1.14.14.3) (Bacterial luciferase
DE beta chain) (fragment).
GN LUXB.
OS Kryptophanaron alfredi symbiont.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
CC Vibrionaceae; light emitting symbionts of fish.
OX NCBI_TaxID=28177;
RN (1)_TaxID=28177;
RP SEQUENCE FROM N.A.
EX MEDLINE=91076680; PubMed=2256783;
RA Havgood M.G.;
RT Relationship of the luminous bacterial symbiont of the Caribbean
RT flashlight fish, Kryptophanaron alfredi (family Anomalopidae) to
RT other luminous bacteria based on bacterial luciferase (luxA) genes.";
RL Arch. Microbiol. 154:496-503(1990).
CC -1- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE
CC SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUTELY
CC REQUIRED FOR BIOLUMINESCENCE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: RCHO + FMNH(2) + O(2) = RCOOH + FMN + H(2)O +
CC light.
CC -1- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M36597; AAA91214.1;
DR InterPro: IPR002103; Bac_luciferase.
DR PROSITE: PS00494; BACTERIAL_LUCIFERASE; PARTIAL.
KW Photoprotein; Luminescence; Oxidoreductase; Monooxygenase;
KW Flavoprotein; FMN.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2153 MW; 8CB3B6955CCB2E7A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

Qy 4 MKF 6
Db 1 MKF 3

RESULT 14
ID HI70_RAT STANDARD; PRT; 19 AA.
AC P21794;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Hormone-induced protein 70 kDa (HIP-70) (Fragment).
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10115;
RN (1)_TaxID=10115;
RP SEQUENCE.
EX MEDLINE=90208308; PubMed=2181662;
RA Mobbs C.V., Fink G., Pfaff D.W.;
RT "HIP-70: a protein induced by estrogen in the brain and LH-RH in the
RT pituitary.";
RL Science 247:1477-1479(1990).
CC -1- INDUCTION: MOST PROMINENT PROTEIN INDUCED BY ESTROGEN IN
CC HYPOTHALAMUS AND MOST PROMINENT PROTEIN INDUCED BY LH-RH IN
CC PITUITARY.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2113 MW; F793A98720B68E3C CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;

```

Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 1 VLE 3
|||
Db 2 VLE 4

RESULT 15
PSAE_CUCSA STANDARD; PRT; 19 AA.
AC P42047;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 19.5 kDa protein) [PS I subunit 6] (Fragment).
GN PSAB.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE.
RC ISSUES=Cotyledon; PubMed=183835;
RA MEDLINE=9135209; Iwahara H., Hibino T., Takabe T.;
RA Iwasaki Y., Iwahara H., Hibino T., Takabe T.;
RT "Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing."
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -!- FUNCTION: Stabilizes the interaction between psaC and the PSI core, assists the docking of the ferredoxin to PSI and interacts with ferredoxin-NADP oxidoreductase (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -!- SIMILARITY: BELONGS TO THE PSAE FAMILY.
CC PIR: G56819; G56819.
KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1810 MW; A93B8DD089FB738 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 7 PPP 9
|||
Db 6 PPP 8

RESULT 16
APAL_ERYPA STANDARD; PRT; 20 AA.
AC P18647;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein A-I (Apo-AI) (Fragment).
GN APOA1.
OS Erythrocytes patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; DE Cercopithecinae; Erythrocytes.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RA MEDLINE=76184721; PubMed=178359;
RX Mahley R.W., Weisgraber K.H., Innerarity T., Brewer H.B. Jr.;
RT "Characterization of the plasma lipoproteins and apoproteins of the Erythrocytes patas monkey."
RL Biochemistry 15:1928-1933(1976).
CC -!- FUNCTION: APOA-I PARTICIPATES IN THE REVERSE TRANSPORT OF CHOLESTEROL FROM TISSUES TO THE LIVER FOR EXCRETION BY PROMOTING

CC CHOLESTEROL EFFLUX FROM TISSUES AND BY ACTING AS A COFACTOR FOR THE LECITHIN CHOLESTEROL ACYLTRANSFERASE (LCAT).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MAJOR PROTEIN OF PLASMA HDL, ALSO FOUND IN CHYLOMICRONS.
CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
DR PIR: A05313; A05313.
KW Plasma; Lipid transport; HDL; Cholesterol metabolism.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2387 MW; 9C970997C7FC976A CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 9 PPQ 11
|||
Db 3 PPQ 5

RESULT 17
CS21_STRTR STANDARD; PRT; 20 AA.
AC P81621;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 21 kDa cold-shock induced protein (Fragment).
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE.
RC STRAIN=PB18;
RX MEDLINE=99456673; PubMed=10525839;
RA Perrin C., Guimont C., Bracquart P., Gaillard J.L.;
RA "Expression of a new cold shock protein of 21.5 kDa and of the major cold shock protein by Streptococcus thermophilus after cold shock."
RL Curr. Microbiol. 39:342-347(1999).
CC -!- INDUCTION: By cold shock.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2390 MW; 9C2CA57F266880AD CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 0;

QY 12 ETV 14
|||
Db 10 ETV 12

RESULT 18
DNK_MYCAV STANDARD; PRT; 20 AA.
AC P80462;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) (Fragment).
GN DNK.
OS Mycobacterium avium.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 25291;
RX MEDLINE=97126793; PubMed=8971687;
RA Ratnakar P., Rao S.P., Catanzaro A.;
RA "Isolation and characterization of a 70 kDa protein from

```

RT Mycobacterium avium.;
RL Microb. Pathog. 21:471-486(1996).
CC -1- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -1- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HAMAP; MF_00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; PARTIAL.
KW Chaperone; ATP-binding; Heat shock.
FT VARIANT 17 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 1926 MW; 625A1CBBEP9ADCB7 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 17 VLE 19

RESULT 19
MDH_KIBAR
ID MDH_KIBAR STANDARD; PRT; 20 AA.
AC P19978;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
GN MDH.
OS Kibdelosporangium aridum.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Kibdelosporangium.
OX NCBI_TaxID=2030;
RN [1]
RP SEQUENCE.
RX MEDLINE=89374824; PubMed=2775496;
RA Rommel T.O., Hund H.-K., Speth A.R., Lingens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
dehydrogenases from six actinomycetales strains and from
Phenyllobacterium immobile strain E." (1989).
RL Biol.Chem.Hoppe-Seyler 370:763-768(1989).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
DR InterPro; IPR001252; Mdh.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 20
SQ SEQUENCE 20 AA; 1989 MW; 79587E5F58C00AC9 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 8 TVT 10

RESULT 20
MDH_MICGL
ID MDH_MICGL STANDARD; PRT; 20 AA.
AC P19979;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
GN MDH.

```

```

OS Microtrasporea glauca.
OC Bacteria; Actinobacteridae; Actinobacteridae; Actinomycetales;
OC Streptosporangiaceae; Streptosporangiaceae; Microtrasporea.
OX NCBI_TaxID=1996;
RN [1]
RP SEQUENCE.
RX MEDLINE=89374824; PubMed=2775496;
RA Rommel T.O., Hund H.-K., Speth A.R., Lingens F.;
RT "Purification and N-terminal amino-acid sequences of bacterial malate
dehydrogenases from six actinomycetales strains and from
Phenyllobacterium immobile strain E." (1989).
RL Biol.Chem.Hoppe-Seyler 370:763-768(1989).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
DR InterPro; IPR001252; Mdh.
DR PROSITE; PS00068; MDH; PARTIAL.
KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2065 MW; 740129BE59D01EBE CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 5 TVT 7

RESULT 21
RM01_YEAST
ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285105; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
subunit from yeast mitochondria."
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VT 15
DB 2 VT 3

RESULT 22
EI04_LITRU
ID EI04_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

```

```

DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]_TaxID=104895;
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 5 5
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TV 14
DB 3 TV 4

RESULT 23
PAP2_PAPMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moles sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moles sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 4 PP 5

RESULT 24
ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
RN [1]
RP SEQUENCE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wold F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol_endopep_ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 5 VL 6

RESULT 25
VP19_HSVIK STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

 CC EMBL; M57646; AAA45830.1; -
 DR Capsid assembly; Coat protein; DNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MK 5
 DB 1 MK 2

RESULT 26
 CCF1_ENTFA STANDARD; PRT; 7 AA.
 AC P20104;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone ccf10.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
 RA Adait J.C., Dunny G.M., Suzuki A.;
 RT "Structure of ccf10, a peptide sex pheromone which induces
 RT conjugative transfer of the Streptococcus faecalis tetracycline
 RT resistance plasmid, pCF10."
 RL J. Biol. Chem. 263:14574-14578(1988).
 CC -1- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PCF10.
 DR PIR; A30812; A30812.
 KW Pheromone.
 SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VT 15
 DB 2 VT 3

RESULT 27
 TPFY_PACDA STANDARD; PRT; 7 AA.
 AC P83455;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Trypophyllin-1 (PdT-1).
 OS Pachymedusa dactinolor (Giant mexican leaf frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Phyllomedusinae; Pachymedusa.
 OX NCBI_TaxID=75988;
 RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
 RP PRO-7.
 RC TISSUE=Skin secretion;

RA Chen T.B., Orr D.F., Shaw C.;
 RT "Pachymedusa dactinolor tryptophyllin-1 (pdt-1): structural
 RT characterization, pharmacological activity and cloning of precursor
 RT cDNA."
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.
 CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular
 CC smooth muscle.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
 DR CO; GO:0005576; C:extracellular; NAS.
 DR CO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
 KW Amphibian defense peptide; Amidation; Hydroxylation.
 FT MOD_RES 3 3
 FT MOD_RES 7 7
 FT AMIDATION.
 SQ SEQUENCE 7 AA; 794 MW; 7772D37DC776350 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PP 8
 DB 2 PP 3

RESULT 28
 UF04_MOUSE STANDARD; PRT; 7 AA.
 ID UF04_MOUSE
 AC P38642;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 EX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis."
 RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PP 8
 DB 3 PP 4

RESULT 29
 MWAL_ACHFU STANDARD; PRT; 7 AA.
 ID MWAL_ACHFU
 AC P35919;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Wamide-1.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]


```

RP SEQUENCE.
RX TISSUE=Ganglion;
RA MEDLINE=93765912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR; S33245; G33245.
KW Neuropeptide; Amidation.
FT MOD_RES 7 AMIDATION.
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 3 EM 4

RESULT 30
WMA3_ACHFU ID WMA3_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Wamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigamurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RX TISSUE=Ganglion;
RA MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD_RES 7 AMIDATION.
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EM 4
DB 3 EM 4

RESULT 31
ALI5_CALVO ID ALI5_CALVO STANDARD; PRT; 8 AA.
AC P41841.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calliostatin 5 (Met-calliostatin 1) ([Hyp3]Met-calliostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=93211980; PubMed=8460157;

```

```

RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RA "Calliostatins: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
RC TISSUE=Head;
RA MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-calliostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR; E47393; E47393.
KW Neuropeptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 HYDROXYLATION (20%).
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PP 8
DB 2 PP 3

RESULT 32
CADI_ENTFA ID CADI_ENTFA STANDARD; PRT; 8 AA.
AC P13268;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CADI.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Enteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85051889; PubMed=6437872;
RX Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, CADI, that
RT induces plasmid transfer in Streptococcus faecalis.";
RL FEBS Lett. 178:97-100(1984).
CC -!- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PAD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
DB 5 VL 6

RESULT 33
CLP_THICU ID CLP_THICU STANDARD; PRT; 8 AA.
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)

```

```

DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemiluminophor-specific protein (fragment).
OS Thiomacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]_SEQUENCE.
RP STRAIN=DSM 5494;
RC Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;
RA Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOLITHOTROPHICALLY.
FT NON TER
SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QE 12
Db 5 QE 6

RESULT 34
COW2_CONU STANDARD; PRT; 8 AA.
AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]_SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP STRAIN=Clipperton Island; TISSUE=Venom;
RC MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez B.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RA "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD RES 4 4 D-LEUCINE.
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VL 2
Db 3 VL 4

RESULT 35
NFB_BOVIN STANDARD; PRT; 8 AA.
ID NPB_BOVIN
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

```

DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine";
PL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQ 11
Db 5 PQ 6

RESULT 36
PPK2_PERAM STANDARD; PRT; 8 AA.
ID _PPK2_PERAM
AC P82652;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-EK-2) (EXPRIL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]_SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RP TISSUE=Corpora cardiaca;
RC MEDLINE=9733923; PubMed=9210163;
RA Fredel R., Reilner R., Kaufmann R., Penzlin H., Gaede G.;
RT "Isolation and structural elucidation of two pyrokinins from the
RT retrocerebral complex of the American cockroach.";
RL Peptides 18:473-478(1997).
RN [2]
RP TISSUE SPECIFICITY.
RA MEDLINE=20189894; PubMed=10723010;
RA Fredel R., Eckert M.;
RT "Tagma-specific distribution of EXPRILamides in the nervous system of
RT the American cockroach.";
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 PP 8
DB      2 PP 3

RESULT 37
UH09 RAT
ID      STANDARD;          PRT;          8 AA.
AC      P56575;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS      Rattus norvegicus (Rat)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE.
RC      STRAIN=Wistar; TISSUE=Heart;
RA      Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA      Jungblut P.R.;
RL      Submitted (SEP-1998) to the SWISS-PROT data bank.
CC      -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC      PROTEIN IS: 8.9, ITS MW IS: 42 KDa.
FT      NON TER      8
SQ      SEQUENCE      8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      11 OE 12
DB      1 QE 2

RESULT 38
UPAL HUMAN
ID      STANDARD;          PRT;          8 AA.
AC      P30087;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Plasma;
RC      MEDLINE=93092937; PubMed=1459097;
RA      Hughes G.J., Frutiger S., Faquet N., Ravier F., Pasquali C.,
RA      Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA      Hochstrasser D.F.;
RT      "Plasma protein map: an update by microsequencing.";
RL      Electrophoresis 13:707-714(1992).
CC      -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC      PROTEIN IS: 4.9, ITS MW IS: 65 KDa.
DR      SWISS-2DPAGE; P30087; HUMAN.
FT      NON TER      1
FT      UNSURE      8
FT      NON TER      8
SQ      SEQUENCE      8 AA; 944 MW; C01772C455B06DA CRC64;

Query Match      13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      11 OE 12
DB      2 QE 3

RESULT 39
AL10 CARMA
ID      STANDARD;          PRT;          9 AA.
AC      P81813;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Carcinustatin 10.
OS      Carcinus maenas (Common shore crab) (Green crab).
OC      Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC      Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC      Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX      NCBI_TaxID=6759;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC      MEDLINE=98121193; PubMed=9461295;
RA      Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA      Thorpe A.;
RT      "Isolation and identification of multiple neuropeptides of the
RT      allatostatin superfamily in the shore crab Carcinus maenas.";
RL      Eur. J. Biochem. 250:727-734(1997).
CC      -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC      -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW      Neuropeptide; Amidation; Multigene family.
FT      MOD RES      9
FT      SEQUENCE      9 AA; 963 MW; 372D79CDB476C7 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      10 PQ 11
DB      2 PQ 3

RESULT 40
BS43 SERPL
ID      STANDARD;          PRT;          9 AA.
AC      P83375;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Bacteriocin serracin P 43 kDa subunit (Fragment).
OS      Serratia plymuthica.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Serratia.
OX      NCBI_TaxID=82996;
RN      [1]
RP      SEQUENCE, AND FUNCTION.
RC      STRAIN=DJ7;
RC      MEDLINE=22293561; PubMed=12406768;
RA      Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA      Van Beeumen J., Thonart P.;
RT      "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT      its activity against Erwinia amylovora, the fire blight pathogen.";
RL      Appl. Environ. Microbiol. 68:5704-5710(2002).
CC      -1- FUNCTION: Major component of a prophage tail sheath (Probable).
CC      -1- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC      E. amylovora.
DR      InterPro: IPR006498; Tail tube.
DR      Pfam: PF04985; Phage_tube_1.
KW      Antibiotic; Bacteriocin.
FT      NON TER      9
FT      SEQUENCE      9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match      13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      1 VL 2
      8 VL 9
Db
RESULT 41
ID FARI CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
CX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion; PubMed=1549595;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A41978; A41978.
KW Neuropeptide; Anidation.
FT MOD_RES 5 ANIDATION.
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PQ 11
      2 PQ 3
Db
RESULT 42
ID FIBB ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocebus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
CX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COPACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDP6409C7287B06 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 QE 12
      2 QE 3
Db
RESULT 44
ID FIBB PAPA STANDARD; PRT; 9 AA.

```

```

CC      (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; D24180; D24180.
CC DR InterPro; IPR002181; Fibrinogen C.
CC DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

```

Query Match 13.3%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 VL 2
      4 VL 5
Db

```

RESULT 43

```

ID FIBB PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
CX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COPACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDP6409C7287B06 CRC64;

```

Query Match 13.3%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      11 QE 12
      2 QE 3
Db

```

RESULT 44

```

ID FIBB PAPA STANDARD; PRT; 9 AA.

```

```

CC      (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDP6409C7287B06 CRC64;

```

```

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 QE 12
      2 QE 3
Db

```

RESULT 44

```

ID FIBB PAPA STANDARD; PRT; 9 AA.

```

```

AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR, E28854; E28854.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE: PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1057 MW; DDFE71E9C7287B06 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QE 12
DB 2 QE 3

RESULT 45
FIBB THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Theropithecus.
OX NCBI_TaxID=9565;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

```

```

CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR, E28854; E28854.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE: PS00514; FIBRIN AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QE 12
DB 2 QE 3

RESULT 46
KNL3 BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PP 8
DB 2 PP 3

RESULT 47
LPCA STAAU STANDARD; PRT; 9 AA.
AC P16884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Streptococcus aureus, and
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S. aureus; STRAIN=436; PLASMID=pSCS7;
RX MEDLINE=92027652; PubMed=1929326;

```


DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE Sperm-activating peptide (SAP).
 OS Stomopneustes variolaris (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
 OC Stomopneustes.
 OX NCBI_TaxID=7663;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BOND.
 RC TISSUE=Egg jelly;
 RX MEDLINE=92097763; PubMed=1756858;
 RA Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;
 RT "Determination of the amino acid sequence of an intramolecular
 RT disulfide linkage-containing sperm-activating peptide by tandem mass
 RT spectrometry.";
 RL FEBS Lett. 294:179-182(1991).
 CC -!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
 CC THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF
 CC CAMP, CGMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT
 CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
 CC GUANYLATE CYCLASE.
 FT DISULFID 3
 FT SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;
 SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KF 6
 DB 1 KF 2
 RESULT 51
 ID UHA2 HUMAN STANDARD; PRT; 9 AA.
 AC P40929;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994.";
 RL Electrophoresis 15:1459-1465(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
 FT NON TER 9
 FT SEQUENCE 9 AA; 1104 MW; 8874B1B5B5B01B2CA CRC64;
 SQ SEQUENCE 9 AA; 1104 MW; 8874B1B5B5B01B2CA CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 VT 15
 DB 3 VT 4
 RESULT 52
 ID ULAE HUMAN STANDARD; PRT; 9 AA.
 AC P31931;

DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 115) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1222(1993).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.5, ITS MW IS: 11 kDa.
 FT NON TER 9
 FT SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;
 SQ SEQUENCE 9 AA; 1096 MW; 477B3B173AE729C7 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LE 3
 DB 6 LE 7
 RESULT 53
 ID ULAH HUMAN STANDARD; PRT; 9 AA.
 AC P31934;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 94) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1222(1993).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.5, ITS MW IS: 12 kDa.
 FT NON TER 1
 FT SEQUENCE 9 AA; 990 MW; F1CC7B172AB6DDCA CRC64;
 SQ SEQUENCE 9 AA; 990 MW; F1CC7B172AB6DDCA CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred.No.1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LE 3
 DB 6 LE 7
 RESULT 54
 ID UN19 CLOPA STANDARD; PRT; 9 AA.
 AC P81355;

```

DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 19 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]_TaxID=1501;
RP SEQUENCE
RC STRAIN=W5;
RX MEDLINE=96291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RI "two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC VARIANT 8 6.5, ITS MW IS: 38.0 kDa.
CC NON TER 9 9
FT 3 EM 4
SQ SEQUENCE 9 AA; 1128 MW; E33E9B0AF5B19DA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 EM 4
Db 7 EM 8

RESULT 55
UPA3_HUMAN STANDARD; PRT; 9 AA.
AC P30689;
AT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
CC SWISS-2DPAGE; P30689; HUMAN.
DR NON TER 9 9
FT 6 FP 7
SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FP 7
Db 4 FP 5

RESULT 56
YBFR_AZOVI STANDARD; PRT; 9 AA.
AC P25025;
AT 01-MAY-1992 (Rel. 22, Created)

```

```

DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]_TaxID=354;
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman W.J., Hinton S.W., Minak-Bernero V., Slaughter C.,
RA Sierfel E.I.;
RI "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; M83692; AA322122.1; -
DR PIR; B41983; B41983.
KW Hypothetical Protein.
FT NON TER 9
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PP 8
Db 3 PP 4

RESULT 57
AH3_PRUSE STANDARD; PRT; 10 AA.
AC F29261;
AT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH II) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]_TaxID=23207;
RP SEQUENCE.
RC TISSUE=Seed;
RX Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -|- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
CC glucose.
CC -|- SUBUNIT: Monomer.
CC -|- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -|- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

QY      7 PP 8
Db      3 PP 4

RESULT 56
AXHX LOOMI
ID AXHX LOOMI STANDARD; PRT; 10 AA.
AC P81626;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peptide hormone.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Siebert K.J.;
RL Submitted (DEC-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST
CC -!- INTERMEDIARY METABOLISM. BEHAVIOR AND/OR DEVELOPMENT.
CC -!- SIMILARITY. BELONGS TO THE AXH / HRTH / RPCH FAMILY.
DR Interfero; IPR002047; AXH.
DR PROSITE; PS00256; AXH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 VT 15
Db      2 VT 3

RESULT 59
BPP2 BOTIN
ID BPP2 BOTIN STANDARD; PRT; 10 AA.
AC P30422;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; B37196; B37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1213 MW; 30C53546C761F773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PP 8
Db      9 PP 10

RESULT 60
BPP2 BOTJA
ID BPP2 BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-II).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
RA Kocy O.;
RL "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RL jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01255; XAVI6B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PP 8
Db      9 PP 10

RESULT 61
BPP8 BOTIN
ID BPP8 BOTIN STANDARD; PRT; 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 8S,1 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).

```

CC -1- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.

DR PIR: H37196; H37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1173 MW; 2FF83545761F6D8 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PP 8

Db 9 PP 10

RESULT 62

BRK_ONCMY ID -BPP_VIPAS STANDARD; PRT; 10 AA.

AC P31351;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Bradykinin-potentiating peptide (Angiotensin-converting

DE enzyme inhibitor).

OS Vipera aspis (Aspic viper).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidogaulia; Squamata; Scleroglossa; Serpentes; Colubroidae;

OC Viperidae; Viperinae; Vipera.

OX NCBI_TaxID=8706;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=90382616; PubMed=2169439;

RA Komori Y., Sugihara H.;

RT "Characterization of a new inhibitor for angiotensin converting

RT enzyme from the venom of Vipera aspis aspis.";

RL Int. J. Biochem. 22:767-771(1990).

CC -1- FUNCTION: This peptide both inhibits the activity of the

CC angiotensin-converting enzyme and enhances the action of

CC bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.

CC PIR: A60377; XASNPC.

DR Hypotensive agent; Pyrrolidone carboxylic acid.

KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT SEQUENCE 10 AA; 1062 MW; 35A827C327686773 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PP 8

Db 9 PP 10

RESULT 63

BRK_ONCMY ID -BRK_ONCMY STANDARD; PRT; 10 AA.

AC Q9PZL1;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lysyl-bradykinin-like.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE.

RX MEDLINE=94039817; PubMed=8224232;

RA Conlon J.M., Olson K.R.;

RT "Purification of a vasoactive peptide related to lysyl-bradykinin from

RT trout plasma.";

RL FEBS Lett. 334:75-78(1993).

CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR

CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.

DR PIR: S39030; S39030.

KW Bradykinin; Vasodilator.

SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PP 8

Db 3 PP 4

RESULT 64

COXA_ONCMY ID -COXA_ONCMY STANDARD; PRT; 10 AA.

AC P80328;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8022;

RN [1]

RP SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=94237150; PubMed=8181469;

RA Freund R., Kadenbach B.;

RT "Identification of tissue-specific isoforms for subunits Vb and Vlla

RT of cytochrome c oxidase isolated from rainbow trout.";

RL Eur. J. Biochem. 221:1111-1116(1994).

CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C

CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.

CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome

CC c + 2 H(2)O.

CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.

DR PIR: S43625; S43625.

KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ET 13

Db 6 ET 7

RESULT 65

ESL_LACCA ID -ESL_LACCA STANDARD; PRT; 10 AA.

AC P81758;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Putative esterase/lipase (EC 3.1.-.-) (Fragment).

OS Lactobacillus casei.

QC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1592;
 RN [1] _SEQUENCE
 RC STRAIN=IPPL731;
 RA Lopez de Felipe F.;
 RL Submitted (MAR-1999) to the SWISS-PROT data bank.
 KW Hydrolase; Serine esterase.
 PT NON_TER
 SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
 ||
 Db 6 VL 7

RESULT 66

PAR6_PANRE
 ID _PAR6_PANRE STANDARD; PRT; 10 AA.
 AC P82620;
 DT 18-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE FMRamide-like neuropeptide PF6 (NGAPQFVRP-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1] _SEQUENCE, FUNCTION, AND AMIDATION.
 RP Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRamide-related
 RT peptides (PARPs) from free-living nematode, Panagrellus redivivus";
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -!- FUNCTION: MYOACTIVE.
 CC -!- SIMILARITY: BELONGS TO THE PARP (FMRPAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1132 MW; CH13B4C9D776C76D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQ 11
 ||
 Db 4 PQ 5

RESULT 67

GON1_PETWA
 ID _GON1_PETWA STANDARD; PRT; 10 AA.
 AC P04376;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (gonadotropin-releasing hormone I) (GNRH-I)
 DE (Luliberin I).
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1] _SEQUENCE.
 RP TISSUE=Brain;
 RC MEDLINE=86158192; PubMed=3514603;

RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
 RT "Primary structure of gonadotropin-releasing hormone from lamprey
 RT brain";
 RL J. Biol. Chem. 261:4812-4819(1986).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GNRH family.

DR PIR: A01412; ERLWGS.

DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH; 1.

DR PROSITE: PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3
 ||
 Db 5 LE 6

RESULT 68

LABA_JATMU
 ID _LABA_JATMU STANDARD; PRT; 10 AA.
 AC F13270;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Labaditin.
 OS Jatropha multifida (Physic nut).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Jatropha.
 OX NCBI_TaxID=3996;
 RN [1] _SEQUENCE

RP TISSUE=Latex;

RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;

RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha

RT multifida L. (Euphorbiaceae). Isolation and sequence determination

RT by means of two-dimensional NMR";

RL FEBS Lett. 256:91-96(1989).

CC -!- FUNCTION: LABADITIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE

CC CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY

CC SEEMS TO BE BASED ON AN INTERACTION WITH C1.

CC -!- PTM: This is a cyclic peptide.

CC -!- DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR

CC TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.

SQ SEQUENCE 10 AA; 1089 MW; D98AAD632D1B362 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TV 14
 ||
 Db 5 TV 6

RESULT 69

ODP2_BOVIN
 ID _ODP2_BOVIN STANDARD; PRT; 10 AA.
 AC P11180;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase

```

DE complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=86024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aicken A., James L.A., Yeaman S.J.;
RT "Primary structure around the lipote attachment site on the E2
RT component of bovine heart pyruvate dehydrogenase complex.";
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL
CC COPACITOR.
CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
DR InterPro: IPR003016; Lipoyl
KW Glycolysis; Transferase; Acyltransferase; Repeat; Mitochondrion;
KW Lipoyl.
FT NON_TER 1 1
FT BINDING 5 5 LIPOYL.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1066 MW; 889BECDDIADD33AB1 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ET 13
DB 2 ET 3

RESULT 70
PVK_LOCOMI
ID PVK_LOCOMI STANDARD; PRT; 10 AA.
AC P83382;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Periviscerokinin (lom-PVK-1).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=21896327; PubMed=11897380;
RA Predel R., Gaede G.;
RT "Identification of the abundant neuropeptide from abdominal
RT perisymphathetic organs of locusts.";
RL Peptides 23:621-627(2002).
CC -!- FUNCTION: Myotropic peptide; increases the frequency of
CC contraction of the heart and stimulates amplitude and tonus of the
CC foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
DR GO; GO:0005576; C:extracellular; IDA.

DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 7 PP 8

RESULT 71
SLAP_BACTG
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. Galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045; PubMed=2592346;
RX MEDLINE=90078111;
RA Luckeovich M.D., Beveridge T.O.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
DR PIR; A60476; A60476.
KW Cell wall; S-layer.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769DIA3 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PP 7
DB 5 PP 6

RESULT 72
TKL3_LOCOMI
ID TKL3_LOCOMI STANDARD; PRT; 10 AA.
AC P30249;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin III (TK-III).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91219696; PubMed=2132575;
RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,
RA de Loof A.;
RT "Locustatachykinin III and IV: two additional insect neuropeptides
RT with homology to peptides of the vertebrate tachykinin family.";
RL Regul. Pept. 31:199-212(1990).

```

CC -I- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR; A60073; ECLQ3M.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;
QY 10 PQ 11 5 KF 6
DB 2 PQ 3 2 KF 3
RESULT 73
ID TKN1 SCYCA STANDARD; PRT; 10 AA.
AC P08608;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Scyllorhinin I.
OS Scyllorhinus canicula (Spotted dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=86192829; PubMed=2422058;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyllorhinin I and II: two novel tachykinins from dogfish gut.";
RL FEBS Lett. 200:111-116(1986).
RN [2]
RP SEQUENCE.
RC TISSUE=Brain;
EX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazen N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
peptides from the brain of the dogfish, Scyllorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A24867; A24867.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C33AA9 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;
QY 5 KF 6 5 KF 6
DB 2 KF 3 2 KF 3
RESULT 74
ID TKN1 AEDAE STANDARD; PRT; 10 AA.
AC P42634;
DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialokinin I.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
mosquito Aedes aegypti.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -I- FUNCTION: VASODILATORY PEPTIDE. MAY ACTIVATE MACROPHAGES AT THE
SITE OF FEEDING.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; A49581; A49581.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1145 MW; 3DCFDE6B59C33AA8 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;
QY 5 KF 6 5 KF 6
DB 5 KF 6 5 KF 6
RESULT 75
ID TKN2 AEDAE STANDARD; PRT; 10 AA.
AC P42635;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Sialokinin II.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE.
RC STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
mosquito Aedes aegypti.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -I- FUNCTION: VASODILATORY PEPTIDE. MAY ACTIVATE MACROPHAGES AT THE
SITE OF FEEDING.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR; B49581; B49581.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33AA8 CRC64;
Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;
QY 5 KF 6 5 KF 6
DB 5 KF 6 5 KF 6

Search completed: November 25, 2003, 18:17:27
Job time : 8.26064 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 36.1436 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLENKFPFPQETWT 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 810525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL_23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.protist:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriaph:*
17: sp.archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	26.7	12	4	Q9BZ49
2	4	26.7	15	6	Q9T814
3	4	26.7	15	10	P82439
4	4	26.7	17	6	Q9TR22
5	4	26.7	17	10	Q49225
6	4	26.7	17	10	Q41400
7	4	26.7	18	4	Q9UCT9
8	4	26.7	20	11	Q64619
9	3	20.0	7	2	Q54248
10	3	20.0	8	4	Q81UB8
11	3	20.0	9	4	Q9UCS8
12	3	20.0	9	4	Q9H4M8
13	3	20.0	9	5	Q96417
14	3	20.0	9	10	P82429
15	3	20.0	10	4	Q9H121
16	3	20.0	10	4	Q9UMK9

17	3	20.0	10	4	Q9UCP3
18	3	20.0	10	8	Q94VG5
19	3	20.0	10	8	Q9TG95
20	3	20.0	10	10	P81898
21	3	20.0	10	12	Q9Q0W9
22	3	20.0	10	12	Q8JV70
23	3	20.0	10	12	Q9Q0W1
24	3	20.0	10	12	Q8JV68
25	3	20.0	10	12	Q9Q0V9
26	3	20.0	10	12	Q9Q0W7
27	3	20.0	10	12	Q8JV66
28	3	20.0	10	12	Q9Q0V7
29	3	20.0	10	12	Q8JV82
30	3	20.0	10	12	Q8JV76
31	3	20.0	10	12	Q8JV74
32	3	20.0	10	12	Q9Q0W5
33	3	20.0	10	12	Q9Q0X3
34	3	20.0	10	12	Q9Q0X5
35	3	20.0	10	12	Q9Q0W3
36	3	20.0	10	12	Q8JV80
37	3	20.0	10	12	Q9Q0X1
38	3	20.0	10	12	Q9Q0X9
39	3	20.0	10	12	Q8JV72
40	3	20.0	11	2	Q44237
41	3	20.0	11	10	P82436
42	3	20.0	11	12	Q8S083
43	3	20.0	11	13	P83168
44	3	20.0	12	4	Q9UGS1
45	3	20.0	12	7	Q77879
46	3	20.0	12	10	Q93X21
47	3	20.0	13	6	Q9BDQ8
48	3	20.0	13	6	Q98YX1
49	3	20.0	14	2	Q9ZB42
50	3	20.0	14	4	Q96K99
51	3	20.0	14	5	P82216
52	3	20.0	14	10	Q94IT6
53	3	20.0	14	10	P82335
54	3	20.0	14	11	Q94JUS
55	3	20.0	14	12	Q9S0N0
56	3	20.0	14	12	Q9E0N1
57	3	20.0	14	12	Q995W2
58	3	20.0	15	2	Q9R533
59	3	20.0	15	3	Q96V23
60	3	20.0	15	4	Q15344
61	3	20.0	15	4	Q9UCJ8
62	3	20.0	15	5	Q9TWC7
63	3	20.0	15	6	Q28822
64	3	20.0	15	10	Q9S8Q8
65	3	20.0	15	10	Q9S8N8
66	3	20.0	15	11	Q9QVB6
67	3	20.0	15	11	Q9QVK9
68	3	20.0	15	11	Q9QVT2
69	3	20.0	15	11	Q9QVY3
70	3	20.0	15	11	Q9QVB7
71	3	20.0	15	13	Q9FTM6
72	3	20.0	15	13	Q9SP61
73	3	20.0	15	13	P83102
74	3	20.0	15	15	Q85713
75	3	20.0	16	2	Q9R4D1
76	3	20.0	16	6	Q9BG68
77	3	20.0	16	6	Q9TQ27
78	3	20.0	16	6	Q9TRD1
79	3	20.0	16	8	Q8SLF0
80	3	20.0	16	10	P82161
81	3	20.0	16	12	P83511
82	3	20.0	16	12	Q89560
83	3	20.0	16	13	Q9PRU6
84	3	20.0	17	2	Q9R528
85	3	20.0	17	2	Q9R512
86	3	20.0	17	6	Q9ZYW0
87	3	20.0	17	8	Q8H8Z4
88	3	20.0	17	11	Q9QVK3
89	3	20.0	17	11	Q920M0

Q9UCP3	homo sapien
Q94VG5	varanus gri
Q9TG95	annella ge
P81898	prunus dulc
Q9Q0W9	polymaviru
Q8JV70	polymaviru
Q9Q0W1	polymaviru
Q8JV68	polymaviru
Q9Q0V9	polymaviru
Q9Q0W7	polymaviru
Q8JV66	polymaviru
Q9Q0V7	polymaviru
Q8JV82	polymaviru
Q8JV76	polymaviru
Q8JV74	polymaviru
Q9Q0W5	polymaviru
Q9Q0X3	polymaviru
Q9Q0X5	polymaviru
Q9Q0W3	polymaviru
Q8JV80	polymaviru
Q9Q0X1	polymaviru
Q9Q0X9	polymaviru
Q8JV72	polymaviru
Q44237	anaeana sp
P82436	nicotiana t
Q8S083	leucania se
P83168	struthio ca
Q9UGS1	homo sapien
Q77879	oreochromis
Q93X21	zea mays (m
Q9BDQ8	sus scrofa
Q98YX1	human immun
Q9ZB42	streptococc
Q96K99	homo sapien
P82216	bombyx mori
Q94IT6	fragaria ru
P82335	pisum sativ
Q94JUS	mus musculus
Q9S0N0	human herpe
Q9E0N1	human herpe
Q995W2	human herpe
Q9R533	pseudomonas
Q96V23	cryptococcu
Q15344	homo sapien
Q9UCJ8	homo sapien
Q9TWC7	dirofilaria
Q28822	oryctolagus
Q9S8Q8	ricinus com
Q9S8N8	hordeum vul
Q9QVB6	rattus sp.
Q9QVK9	mus sp. nep
Q9QVT2	rattus norv
Q9QVY3	rattus sp.
Q9QVB7	rattus sp.
Q9FTM6	poephila gu
Q9SP61	galus gall
P83102	scyllorhinu
Q85713	rous sarcom
Q9R4D1	naemophilus
Q9BG68	sorex arane
Q9TQ27	bos taurus
Q9TRD1	bos taurus
Q8SLF0	sus scrofa
P82161	taraxacum (
P83511	spinacia ol
Q89560	kaposi's sa
Q9PRU6	gallus gall
Q9R528	escherichia
Q9R512	porphyromon
Q9ZYW0	bettybracco
Q8H8Z4	sphedra sin
Q9QVK3	rattus sp.
Q920M0	rattus norv

90 Q9PRU7
91 Q8X4A4
92 Q96V21
93 Q96V22
94 Q01672
95 Q9UCG7
96 Q16173
97 Q9UC58
98 Q9NFB4
99 Q9TWV6
100 Q9TRD8

3 20.0 17 13
3 20.0 17 16
3 20.0 18 3
3 20.0 18 3
3 20.0 18 3
3 20.0 18 4
3 20.0 18 4
3 20.0 18 4
3 20.0 18 4
3 20.0 18 5
3 20.0 18 6

Q9PRU7 gallus gall
Q8X4A4 escherichia
Q96V21 cryptococcus
Q96V22 cryptococcus
Q01672 pneumocysti
Q9UCG7 homo sapien
Q16173 homo sapien
Q9UC58 homo sapien
Q9NFB4 homo sapien
Q9TWV6 aplysia cal
Q9TRD8 oryctolagus

ALIGNMENTS

RESULT 1
Q9BZ49 PRELIMINARY; PRT; 12 AA.

ID Q9BZ49
AC Q9BZ49
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Glycophorin C (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Patel S.S., Mehlotra R.K., Kastens W., Mgone C.S., Kazura J.W.,
RA Zimmerman P.A.;
RT "the association of the glycoprotein C exon 3 deletion with
RT ovalocytosis and malaria susceptibility in the Wosera, Papua New
RT Guinea";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF342984; AAK01459.1; -;
FT NON TER 1
FT NON TER 12
SQ SEQUENCE 12 AA; 1361 MW; 2A07044DB8377378 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQ 11
DB 9 PPPQ 12

RESULT 2
Q9TR14 PRELIMINARY; PRT; 15 AA.

ID Q9TR14
AC Q9TR14
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Troponin-T homolog/proteolysis CONDITIONING INDICATOR peptide
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96187584; PubMed=8611748;
RA Nakai Y., Nishimura T., Shimizu M., Arai S.;
RT "Effects of freezing on the proteolysis of beef during storage at 4
RT degrees C";
RL Biosci. Biotechnol. Biochem. 59:2255-2258(1995).
SQ SEQUENCE 15 AA; 1597 MW; C38A5B4A79E4777 CRC64;

Query Match 26.7%; Score 4; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
DB 2 PPPP 5

RESULT 3
P82439 PRELIMINARY; PRT; 15 AA.

ID P82439
AC P82439
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 200 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture";
RL Planca O:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
KW Cell wall; Hydroxylation.
FT MOD_RES 6 HYDROXYLATION.
FT NON TER 15
FT NON TER 15
SQ SEQUENCE 15 AA; 1870 MW; 3E1E05A20A3C5681 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
DB 6 PPPP 9

RESULT 4
Q9TR22 PRELIMINARY; PRT; 17 AA.

ID Q9TR22
AC Q9TR22
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE NONAMELOGENIN glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96126798; PubMed=8564801;
RA Punzi J.S., DenBesten P.K.;
RT "Purification of nonamelogenin proteins from bovine secretory
RT enamel";
RL Calif. Tissue Int. 57:379-384(1995).
SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;

Query Match 26.7%; Score 4; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10

Db 8 PPPP 11
||||

RESULT 5

O49225 O49225 PRELIMINARY; PRT; 17 AA.
AC O49225;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hydroxyproline-rich glycoprotein (Fragment).
GN HRGP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Essex; TISSUE=Root;
RX MDLINE=94211912; PubMed=8159793;
RA Hong J.C., Cheong Y.H., Nagao R.T., Baik J.D., Cho M.J., Key J.L.;
RT "Isolation and characterization of three soybean extensin cDNAs.";
RL Plant Physiol. 104:793-796(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Essex; TISSUE=Root;
RA Mahalingam K., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
FT EMBL; AF047052; AAC03558.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 PPPP 10
||||

RESULT 6

O41400 O41400 PRELIMINARY; PRT; 17 AA.
AC Q41400;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Hydroxyproline-rich protein (Fragment).
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OX NCBI_TaxID=3895;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sesbania rostrata;
RC TISSUE=Bacterial infected stem located root primordia;
RX MDLINE=96113737; PubMed=8664492.
RA Goormachtig S., Valerio-Lepiniec M., Szczylowski K., Van Montagu M.,
RA Holsters M., De Bruijn F.;
RT "Use of differential display to identify novel Sesbania rostrata genes
RT enhanced by Azorhizobium caulinodans infection.";
RL Mol. Plant Microbe Interact. 8:816-824(1995).
DR EMBL; Z48673; CAA88592.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 26.7%; Score 4; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 PPPP 10
||||

Db 10 PPPP 13

RESULT 7

OSUCT9 OSUCT9 PRELIMINARY; PRT; 18 AA.
AC OSUCT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PRG=PROLINE-rich glycoprotein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MDLINE=91373355; PubMed=1894623;
RA Gilless-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
RA Fisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein.";
RL J. Biol. Chem. 266:17358-17368(1991).
RN [2]
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 26.7%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 PPPQ 11
||||

RESULT 8

O64619 O64619 PRELIMINARY; PRT; 20 AA.
AC O64619;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Polymerase-beta (EC 2.7.7.7) (Fragment).
GN POLB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MDLINE=87257910; PubMed=3600656;
RA Yamaguchi M., Hirose F., Hayashi Y., Nishimoto Y., Matsukage A.;
RT "Murine DNA polymerase beta gene: Mapping of transcription initiation
RT sites and the nucleotide sequence of the putative promoter region.";
RL Mol. Cell. Biol. 7:2012-2018(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MDLINE=88294046; PubMed=3042024;
RA Date T., Yamaguchi M., Hirose F., Nishimoto Y., Tanihara K.,
RA Matsukage A.;
RT "Expression of active rat DNA polymerase beta in Escherichia coli.";
RL Biochemistry 27:2983-2990(1988).
DR EMBL; M19679; AAA41902.1; -.
DR HSSP; P06766; IENO.
FT Nucleotidyltransferase; Transferase.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2190 MW; B7D8F9A3C5801825 CRC64;

```

Query Match      25.7%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 PQET 13
DB      7 PQET 10

RESULT 9
Q54248      PRELIMINARY;      PRT;      7 AA.
AC Q54248;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RplO protein (Fragment).
GN RPL0.
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=20011291; PubMed=10542330;
RA Poshling S., Siepersberg W., Wenmeier U.F.;
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
RT N2-3-11 and interaction of the SecY protein with the SecA protein.";
RL Biochim. Biophys. Acta 1447:298-302(1999).
DR EMBL; X95915; CAA65160.1; -.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TVT 15
DB      2 TVT 4

RESULT 10
Q81UB8      PRELIMINARY;      PRT;      8 AA.
AC Q81UB8;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CD95 antigen (Fragment).
GN CD95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kuth J., Pernik A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kuipers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; AJ509178; CAD48928.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 846 MW; 34B724405DC2D1AB CRC64;

Query Match      20.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 8; Gaps 0;

QY      13 TVT 15
DB      2 TVT 4

RESULT 11
Q9UCS8      PRELIMINARY;      PRT;      9 AA.
AC Q9UCS8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92075698; PubMed=1742116;
RA Ehnholm C., Bozas S.E., Tenkanen H., Kirezbaum L., Metso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT protein of human blood are different proteins which both bind to
RT apolipoprotein A-I";
RL Biochim. Biophys. Acta 1086:255-260(1991).
FT NON TER 1 1
SQ SEQUENCE 9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match      20.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 PQQ 11
DB      3 PQQ 5

RESULT 12
Q9H4M8      PRELIMINARY;      PRT;      9 AA.
AC Q9H4M8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PAR2 (fragment).
GN NR112.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Periphereal blood;
RA Pentecost B.T., King G.;
RT "The human pregnane X receptor promoter complex provides
RT transcriptional starts for a number of PXR related transcripts.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY007189; AAG23345.1; -.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1129 MW; 82F8B1F1B411B2D1 CRC64;

Query Match      20.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TVT 15
DB      2 TVT 4

```

```

RESULT 13
O96417 ID O96417 PRELIMINARY; PRT; 9 AA.
AC O96417;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE SXL E1 form (Fragment).
GN SXL.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96337843; PubMed=9671597;
RA Erickson J.W., Cline T.W.;
RT "Key aspects of the primary sex determination mechanism are conserved
RT across the genus Drosophila."
RL Development 125:3259-3268(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Bell M., Cline T.W.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF046045; AAC97605.1; -.
DR FlyBase; FBgn0016470; Dvir\Xsl.
FT NON TER 9
SQ SEQUENCE 9 AA; 1089 MW; 9A8BD1AA9C449CA CRC64;

Query Match 20.0%; Score 3; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 7 TVT 9

RESULT 14
P82429 ID P82429 PRELIMINARY; PRT; 9 AA.
AC P82429;
DT 01-JUN-2000 (TEMBLrel. 14, Created)
DT 01-JUN-2000 (TEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE 44 kDa cell wall protein (fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco cultures."
RL Planta 210:6(2000);
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON TER 9
SQ SEQUENCE 9 AA; 986 MW; C22CCAADC6C7776 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPQ 11
DB 11

RESULT 15
O9H121 ID O9H121 PRELIMINARY; PRT; 10 AA.
AC O9H121;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE DJ309P20.1.2 (Isoform 2 of guanine nucleotide binding protein (G
DE protein), alpha stimulating activity polypeptide 1) (Fragment).
GN GNAS1 (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Laird G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121917; CAC18783.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1095 MW; 7809E3D322C7244B CRC64;

Query Match 20.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 1 VLE 3

RESULT 16
Q9UMK9 ID Q9UMK9 PRELIMINARY; PRT; 10 AA.
AC Q9UMK9;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Dystrophin (Fragment).
GN DAG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Saad F.A., Moatacciulo M.L., Merlini L., Trevisan C., Tomelleri G.,
RA Angelini C., Danieli G.A.;
RT "Novel point mutations in the human dystrophin gene detected by double
RT strand conformation analysis."
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; L41643; AAB59464.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1223 MW; 5D3C9185A2CAB6D7 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MKF 6
DB 8 MKF 10

RESULT 17
Q9UCP3 ID Q9UCP3 PRELIMINARY; PRT; 10 AA.
AC Q9UCP3;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)

```

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE COMP-inhibited LOW K(M) cAMP phosphodiesterase PEAK 37, CGI-PDE
 OS (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1] _SEQUENCE.
 RP MEDLINE=92283180; PubMed=1317779;
 RA LeBon T.R., Kasuya J., Paxton R.J., Belfrage P., Hockman S.,
 RA Manganiello V.C., Fujita Yamaguchi Y.;
 RT "Purification and characterization of guanosine 3',5'-monophosphate-
 RT inhibited low K(M) adenosine 3',5'-monophosphate phosphodiesterase
 RT from human placental cytosolic fractions.";
 RL Endocrinology 130:3265-3274(1992).
 FT NON_TER 1 10
 FT NON_TER 1 10
 SQ SEQUENCE 10 AA; 1272 MW; C80C440B549C046 CRC64;

 Query Match 20.0%; Score 3; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 ENK 5
 DB 8 ENK 10

 RESULT 18
 ID Q94VG5 PRELIMINARY; PRT; 10 AA.
 AC Q94VG5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Col.
 OS Varanus griseus griseus.
 OG Mitochondrion.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OK NCBI_TaxID=169828;
 RN [1] _SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407503; AAL10063.1; -.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1219 MW; C97C0CB7336411B2 CRC64;

 Query Match 20.0%; Score 3; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 13 TVT 15
 DB 2 TVT 4

 RESULT 19
 ID Q9TG95 PRELIMINARY; PRT; 10 AA.
 AC Q9TG95;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Anniella geronimensis.
 OS Anniella geronimensis.
 OG Mitochondrion.

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguillidae;
 CC Anniellinae; Anniella.
 OK NCBI_TaxID=52220;
 RN [1] _SEQUENCE FROM N.A.
 RP MEDLINE=9343613; PubMed=10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tunney B.S., Orlov N.,
 RA Papenfuss T.J.;
 RT "Molecular phylogenetics, rRNA evolution, and historical biogeography
 RT in anguillid lizards and related taxonomic families.";
 RL Mol. Phylogenet. Evol. 12:250-272(1999).
 DR EMBL; AF085605; AAD51505.1; -.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1241 MW; DFEE80C7336411B2 CRC64;

 Query Match 20.0%; Score 3; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 13 TVT 15
 DB 2 TVT 4

 RESULT 20
 ID P81898 PRELIMINARY; PRT; 10 AA.
 AC P81898;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, small
 DE chain (Subunit B) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
 DE glycosidase) (N-glycanase) (Fragment).
 OS Prunus dulcis (Almond) (Prunus amygdalus).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC Eurosidia I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 OK NCBI_TaxID=3755;
 RN [1] _SEQUENCE, AND CHARACTERIZATION.
 RP SEQUENCE, AND CHARACTERIZATION.
 RA Altman F., Faschinger K., Dalik T., Vorauer K.;
 RT "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
 RT amidase A and its N-glycans.";
 RL Eur. J. Biochem. 252:118-123(1998).
 CC -|- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
 CC GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
 CC GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
 CC (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
 CC CONTAINING AN ASPARTIC RESIDUE.
 CC -|- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
 CC -|- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
 CC DEGLYCOSYLATION.
 CC -|- MASS SPECTROMETRY: MW=21247; METHOD=MALDI.
 KW Hydrolyase; Glycoprotein.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1149 MW; 863278CA1E73771 CRC64;

 Query Match 20.0%; Score 3; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 6 FPP 8
 DB 8 FPP 10

 RESULT 21
 ID Q9Q0W9 PRELIMINARY; PRT; 10 AA.

```

AC Q9QW9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UMEA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119350; AAF24106.1; -.
FT NON-TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 22
Q8JV70
ID Q8JV70 PRELIMINARY; PRT; 10 AA.
AC Q8JV70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 5;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
  Girones R.;
RT "Potential transmission of human polyomaviruses through the
  gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1; -.
FT NON-TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 23
Q9QW1
ID Q9QW1 PRELIMINARY; PRT; 10 AA.
AC Q9QW1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFB;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119354; AAF24114.1; -.
FT NON-TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 24
Q8JV68
ID Q8JV68 PRELIMINARY; PRT; 10 AA.
AC Q8JV68;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
  Girones R.;
RT "Potential transmission of human polyomaviruses through the
  gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304388; AAM97806.1; -.
FT NON-TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPP 9
Db 7 PPP 9

RESULT 25
Q9QV9
ID Q9QV9 PRELIMINARY; PRT; 10 AA.
AC Q9QV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFE;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).

```

DR EMBL; AF119355; AAF24116.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
 |||
 Db 7 PPP 9

RESULT 26

Q9Q0W7 PRELIMINARY; PRT; 10 AA.

AC Q9Q0W7;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119351; AAF24108.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
 |||
 Db 7 PPP 9

RESULT 27

Q8JV66 PRELIMINARY; PRT; 10 AA.

AC Q8JV66;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF304389; AAM97808.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
 |||
 Db 7 PPP 9

QY 7 PPP 9
 |||
 Db 7 PPP 9

RESULT 28

Q9Q0V7 PRELIMINARY; PRT; 10 AA.

AC Q9Q0V7;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 RT populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119356; AAF24118.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
 |||
 Db 7 PPP 9

RESULT 29

Q8JV82 PRELIMINARY; PRT; 10 AA.

AC Q8JV82;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF303944; AAM97792.1; -.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
 |||
 Db 7 PPP 9

RESULT 30

Q8JV76 PRELIMINARY; PRT; 10 AA.

```

AC Q8JVV76;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
  Girones R.;
RT "Potential transmission of human polyomaviruses through the
  gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR ENBL; AF303947; AAM97798.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

  Query Match      20.0%; Score 3; DB 12; Length 10;
  Best Local Similarity 100.0%; Pred. No. 5.8e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 7 PPP 9
D/ 7 PPP 9

RESULT 31
Q8JVV74
ID Q8JVV74 PRELIMINARY; PRT; 10 AA.
AC Q8JVV74;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA3;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
  Girones R.;
RT "Potential transmission of human polyomaviruses through the
  gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR ENBL; AF303948; AAM97800.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

  Query Match      20.0%; Score 3; DB 12; Length 10;
  Best Local Similarity 100.0%; Pred. No. 5.8e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 7 PPP 9
D/ 7 PPP 9

RESULT 32
Q9QOW5
ID Q9QOW5 PRELIMINARY; PRT; 10 AA.
AC Q9QOW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

```

```

OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR ENBL; AF119352; AAF24110.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

  Query Match      20.0%; Score 3; DB 12; Length 10;
  Best Local Similarity 100.0%; Pred. No. 5.8e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 7 PPP 9
D/ 7 PPP 9

RESULT 33
Q9QOX3
ID Q9QOX3 PRELIMINARY; PRT; 10 AA.
AC Q9QOX3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN8;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR ENBL; AF119348; AAF24102.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

  Query Match      20.0%; Score 3; DB 12; Length 10;
  Best Local Similarity 100.0%; Pred. No. 5.8e+03;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q/ 7 PPP 9
D/ 7 PPP 9

RESULT 34
Q9QOX5
ID Q9QOX5 PRELIMINARY; PRT; 10 AA.
AC Q9QOX5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN16;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
  populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).

```

```

DR EMBL; AF119347; AAF24100.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB |||
7 PPP 9

RESULT 35
Q9Q0W3 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W3
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA1;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB |||
7 PPP 9

RESULT 36
Q8JV80 PRELIMINARY; PRT; 10 AA.
AC Q8JV80
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA "Girones R.;
RT "Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF303945; AAW97794.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB |||
7 PPP 9

RESULT 37
Q9Q0X1 PRELIMINARY; PRT; 10 AA.
AC Q9Q0X1
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN15;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119349; AAF24104.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB |||
7 PPP 9

RESULT 38
Q9Q0X9 PRELIMINARY; PRT; 10 AA.
AC Q9Q0X9
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCNU;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119345; AAF24096.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB |||
7 PPP 9

RESULT 39
Q8JV72 PRELIMINARY; PRT; 10 AA.
AC Q8JV72

```


DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA 4;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions or viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL; AF304386; AAM97802.1; -;
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

 Query Match 20.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 PPP 9
 Db 7 PPP 9

 RESULT 40
 ID Q44237 PRELIMINARY; PRT; 11 AA.
 AC Q44237;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Glutamine synthetase (Fragment).
 GN GLNA.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 7120;
 RA Warner L.B., Ligon P.J., Stahl A.W., Curtis S.E.;
 RT "The apcF gene of Anabaena sp. strain PCC 7120 is regulated by
 RT nitrogen and the apcF and glbA promoters overlap.";
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 7120;
 RA Scappino L.A.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U21853; AAA5652.1; -;
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1316 MW; 2000580E32CB06C7 CRC64;

 Query Match 20.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 10 PQE 12
 Db 4 PQE 6

 RESULT 41
 ID P82436 PRELIMINARY; PRT; 11 AA.
 AC P82436;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

DE 65 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Wojtaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco cultures.";
 RL Planta 0:0-0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -1- TISSUE SPECIFICITY: XYLEM.
 KW Cell wall.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B867 CRC64;

 Query Match 20.0%; Score 3; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 7 PPP 9
 Db 2 PPP 4

 RESULT 42
 ID Q83083 PRELIMINARY; PRT; 11 AA.
 AC Q83083;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P13 mini peptide.
 OS Leucania separata nuclear polyhedrosis virus (LanPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OX Nucleopolyhedrovirus.
 OX NCBI_TaxID=41714;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96140622; PubMed=8572949;
 RA Wang J.W., Qi Y.P., Huang Y.X., Li S.D.;
 RT "Nucleotide sequence of a 1446 base pair SalI fragment and structure
 RT of a novel early gene of Leucania separata nuclear polyhedrosis
 RT virus.";
 RL Arch. Virol. 140:2283-2291(1995).
 DR EMBL; U30303; AAA99737.1; -;
 SQ SEQUENCE 11 AA; 1339 MW; F7BDBE0BD40DC401 CRC64;

 Query Match 20.0%; Score 3; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 VLE 3
 Db 8 VLE 10

 RESULT 43
 ID P83168 PRELIMINARY; PRT; 11 AA.
 AC P83168;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Alpha-2-antiplasmin (Alpha-2-plasmin inhibitor) (Alpha-2-Pi) (Alpha-2-
 DE AP) (Fragment).
 OS Struthio camelus (Ostrich).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Palaeognathae; Struthioniformes; Struthionidae;

```

OC Struthio.
OX NCBI_TaxID=8801;
RN [1]_
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Plasma;
RX MEDLINE=21328857; PubMed=11435135;
RA Thomas A.R., Naude R.J., Oelofsen W., Naganuma T., Muramoto K.;
RT "Purification and partial characterisation of alpha(2)-antiplasmin and
RL plasmin(ogen) from ostrich plasma.";
RL Comp. Biochem. Physiol. 129B:809-820(2001).
CC -1- FUNCTION: THE MAJOR TARGETS OF THIS INHIBITOR ARE PLASMIN AND
CC TRYPSIN. BUT IT ALSO INACTIVATES CHYMOTRYPSIN.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
KW Serpin; Serine protease inhibitor.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1261 MW; 9E08C06B32C73B5A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 11;
Best Local Similarity 100.0%; Pred.No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 7 VLE 9

RESULT 44
Q9UGS1
ID Q9UGS1 PRELIMINARY; PRT; 12 AA.
AC Q9UGS1;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE D0796117.4 (Novel protein similar to GS2) (Fragment).
GN D0796117.4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035398; CAB63074.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69A46 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred.No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEW 4
DB 3 LEW 5

RESULT 45
O77879
ID O77879 PRELIMINARY; PRT; 12 AA.
AC O77879;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MHC class II B locus 2 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]_
RP SEQUENCE FROM N.A.
RA Shi X.W., Tuglie C.K.;
RL "Genetic linkage and physical mapping of porcine cholesterol ester
RL transfer protein (CETP) gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333037; AAK16584.1; -.

RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF049988; AAC41327.1; -.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1214 MW; 86535979D0B879CE CRC64;

Query Match 20.0%; Score 3; DB 7; Length 12;
Best Local Similarity 100.0%; Pred.No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 10 TVT 12

RESULT 46
Q93X21
ID Q93X21 PRELIMINARY; PRT; 12 AA.
AC Q93X21;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Polynubiquitin homolog (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD; Clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=cv. INRA 258; TISSUE=Leaf;
RX MEDLINE=96236829; PubMed=8680303;
RA Didierjean L., Frendo P., Nasser W., Genot G., Marivet J., Burkard G.;
RT "Heavy-metal-responsive genes in maize: identification and comparison
RT of their expression upon various forms of abiotic stress.";
RL Planta 199:1-8(1996).
DR EMBL; S82313; AAB47175.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1277 MW; 250D2D2F6F340DD8 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred.No. 6.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPP 9
DB 2 PPP 4

RESULT 47
Q9BDQ8
ID Q9BDQ8 PRELIMINARY; PRT; 13 AA.
AC Q9BDQ8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Cholesteryl ester transfer protein (Fragment).
OS CETP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]_
RP SEQUENCE FROM N.A.
RA Shi X.W., Tuglie C.K.;
RL "Genetic linkage and physical mapping of porcine cholesterol ester
RL transfer protein (CETP) gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333037; AAK16584.1; -.

```

```

FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1551 MW; 779D9C94B9A742CB CRC64;

Query Match 20.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13
DB 2 QET 4

RESULT 48
Q98YM1 PRELIMINARY; PRT; 13 AA.
AC Q98YM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=991043;
RA Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E., Korn X.;
RT "Recovery of HIV-1 pol gene sequences by direct sequencing of RT amplification products derived from plasma samples.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF347446; AAK32523.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1390 MW; 805408704623D1AA CRC64;

Query Match 20.0%; Score 3; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 8 VLE 10

RESULT 49
Q9ZB42 PRELIMINARY; PRT; 14 AA.
AC Q9ZB42;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Ssba (fragment).
GN SSBA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]_SEQUENCE FROM N.A.
RC STRAIN=CS101;
RA Rodieleski A., Wolschnik M., Leonard B.A.B., Schmidt K.H.;
RT "Characterization of nra, a global negative regulator gene in group A Mol. Microbiol. 31:0-0(1999).
RL EMBL; U49397; AAC97153.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1618 MW; 47074E277A834F17 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VLE 3
DB 6 VLE 8

RESULT 50
Q96KF9 PRELIMINARY; PRT; 14 AA.
AC Q96KF9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative magnesium transporter (fragment).
GN MRS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=21295035; PubMed=11401429;
RA Zsurka G., Gregan J., Schweyen R.J.;
RT "The human mitochondrial MRS2 protein functionally substitutes for its yeast homologue, a candidate magnesium transporter.";
RL Genomics 72:158-168(2001).
DR EMBL; AF293077; AAK38616.1; -.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1537 MW; C6344FF1E984AFB2 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTV 15
DB 6 TTV 8

RESULT 51
P82216 PRELIMINARY; PRT; 14 AA.
AC P82216;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]_SEQUENCE.
RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of silkworm";
RL 1 Chuan Hsueh Pao 28:217-224(2001).
CC 1- SIMILARITY: TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1619 MW; 86C639958983BC45 CRC64;

Query Match 20.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
DB 10 ETV 12

```

RESULT 52

Q94176 PRELIMINARY; PRT; 14 AA.
 AC Q94176
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Regulator of anthocyanin biosynthesis pathway (Fragment).
 OS Fragaria nubicola.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
 OX NCBI_TaxID=60188;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. FRA520;
 RA Deng C., Davis T.;
 RT "Molecular identification of the yellow fruit color (c) locus in
 RT diploid strawberry: a candidate gene approach.";
 RL Theor. Appl. Genet. 0:0-0(2001).
 DR EMBL; AY017488; AAK33145.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1533 MW; C2862EA5812DC832 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3

Db 7 VLE 9

RESULT 53

P82335 PRELIMINARY; PRT; 14 AA.
 AC P82335
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid (SPOT119) (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320;
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 RT targeting analysis of luminal and peripheral thylakoid proteins.";
 RL Plant Cell 12:319-341(2000).
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST STROMAL SIDE OF THE THYLAKOID
 CC MEMBRANE.
 CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.9, ITS MW IS: 29.9 KDA.
 KW Chloroplast; Thylakoid membrane.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1477 MW; 9397654E0784A231 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14

Db 12 ETV 14

Db 12 ETV 14

RESULT 54

Q91JUS PRELIMINARY; PRT; 14 AA.
 AC Q91JUS
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE B-Raf protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barnier J.V.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Barnier J.V., Papin C., Eyche A., Jacq O.;
 RT "The mouse B-Raf gene encodes multiple protein isoforms with tissue-
 RT specific expression.";
 RL J. Biochem. 270:23381-23389(1995).
 DR EMBL; A0276308; CAB81556.1; -.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFP 7

Db 3 KFP 5

RESULT 55

Q9E0N0 PRELIMINARY; PRT; 14 AA.
 AC Q9E0N0
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Immediate early protein ICP47 (Fragment).
 GN US12.
 OS Human herpesvirus 1.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10298;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maertzdorf J., Van der lelij A., Baarma G.S., Osterhaus A.D.M.E.,
 RA Verjans G.M.G.M.;
 RT "Herpes Simplex Virus type 1 (HSV-1) Induced Retinitis Following
 RT Herpes Simplex Encephalitis: Indications for Brain-to-Eye Transmission
 RT of HSV-1.";
 RL Ann. Neurol. 48:0-0(2000).
 DR EMBL; AF290018; AAG33134.1; -.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4

Db 5 LEM 7

```

RESULT 56
ID Q9E0N1 PRELIMINARY; PRT; 14 AA.
AC Q9E0N1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Varusae; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RA Maertzdorf J., Van der lელი A., Baarma G.S., Osterhaus A.D.M.E.,
RA Verjans G.M.G.M.;
RT "Herpes Simplex Virus type 1 (HSV-1) Induced Retinitis Following
RT Herpes Simplex Encephalitis: Indications for Brain-to-Eye Transmission
RT of HSV-1.";
RL Ann. Neurol. 48:0-0(2000).
DR EMBL; AF290017; AAG3133.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
DB 5 LEM 7

RESULT 57
ID Q99BW2 PRELIMINARY; PRT; 14 AA.
AC Q99BW2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Immediate early protein ICP47 (Fragment).
GN US12.
OS Human herpesvirus 1.
OC Varusae; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RA Reweijer L., Maertzdorf J., Doornenbal P., Verjans G.M.G.M.,
RA Osterhaus A.D.M.E.;
RT "Herpes simplex virus type 1 transmission through corneal
RT transplantation.";
RL Lancet 357:442-442(2001).
DR EMBL; AF324428; AAK12110.1; -.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1631 MW; BDE58B6F5C2A94D6 CRC64;

Query Match 20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEM 4
DB 5 LEM 7

RESULT 58
ID Q9R533 PRELIMINARY; PRT; 15 AA.
AC Q9R533;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Integration host factor-like protein beta subunit (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE.
RA MEDLINE=94030028; PubMed=8216322;
RA Tousseint B., Delic-Attree I., Vignais P.M.;
RT "Pseudomonas aeruginosa contains an IHF-like protein that binds to the
RT aigD promoter.";
RL Biochem. Biophys. Res. Commun. 196:416-421(1993).
SQ SEQUENCE 15 AA; 1703 MW; 7315E3A63536EF32 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 10 TVT 12

RESULT 59
ID Q96V23 PRELIMINARY; PRT; 15 AA.
AC Q96V23;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Pheromone alpha (Fragment).
GN MFALPHA1A.
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IUM 89-3369;
RX MEDLINE=21538945; PubMed=11682503;
RA Cogliati M., Esposito M.C., Clarke D.L., Wickes B.L., Viviani M.A.;
RT "Origin of Cryptococcus neoformans var. neoformans Diploid Strains.";
RL J. Clin. Microbiol. 39:3889-3894(2001).
DR EMBL; AF376995; AAK5591.1; -.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1563 MW; 9AE1F336ACF0E29B CRC64;

Query Match 20.0%; Score 3; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TVT 15
DB 11 TVT 13

RESULT 60
ID Q15344 PRELIMINARY; PRT; 15 AA.
AC Q15344;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Aml1 protein (Fragment).
GN AML1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN  SEQUENCE FROM N.A.
RP  MEDLINE=96226397; PubMed=8634147;
RX  Levanon D., Bernstein Y., Negraru V., Ghazi M.C., Bar-Am I.,
RA  Alevy R., Goldenberg D., Lotem J., Groner Y.,
RT  "A large variety of alternatively spliced and differentially expressed
RL  mRNAs are encoded by the human acute myeloid leukemia gene AML1."
DR  DNA Cell Biol. 13:175-185(1996).
EMBL; X90980; CAA62467.2; -.
FT  NON_TER 1
FT  SEQUENCE 15 AA; 1931 MW; 228A48BEE675423 CRC64;
SQ  SEQUENCE 20.0%; Score 3; DB 4; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.1e+03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 FPP 8
    |||
Db  7 FPP 9

RESULT 61
O9UCJ8  PRELIMINARY; PRT; 15 AA.
ID  O9UCJ8
AC  Q9UCJ8
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE  01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE  Type IV PROCOLLAGENASE (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE
RX  MEDLINE=93125366; PubMed=1480041;
RA  Sterler-Stevenson W.G., Krutzsch H.C., Liotta L.A.;
RT  "TMP-2: identification and characterization of a new member of the
RT  metalloproteinase inhibitor family.";
RL  Matrix Suppl. 1:299-306(1992).
SQ  SEQUENCE 15 AA; 1537 MW; D5DA1AA9C32276C CRC64;

Query Match 20.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 KFP 7
    |||
Db  7 KFP 9

RESULT 62
O9TWC7  PRELIMINARY; PRT; 15 AA.
ID  O9TWC7
AC  Q9TWC7
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-MAY-2000 (TrEMBLrel. 20, Last annotation update)
DE  20 kDa excretory-secretory protein (Fragment).
OS  Dirofilaria immitis (Canine heartworm).
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC  Onchocercidae; Dirofilaria.
OX  NCBI_TaxID=6287;
RN  [1]
RP  SEQUENCE
RX  MEDLINE=96258562; PubMed=8992320;
RA  Frank G.R., Griewe R.B.;
RT  "Purification and characterization of three larval excretory-secretory
RT  proteins of Dirofilaria immitis.";
RL  Mol. Biochem. Parasitol. 75:221-229(1996).
SQ  SEQUENCE 15 AA; 1801 MW; F074BFEBE0E48CB CRC64;

Query Match 20.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  12 ETV 14
    |||
Db  8 ETV 10

RESULT 63
Q28622  PRELIMINARY; PRT; 15 AA.
ID  Q28622
AC  Q28622
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE  Voltage-dependent dihydropyridine-sensitive calcium channel alpha 1
DE  subunit 155 kDa isoform (Fragment).
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92265303; PubMed=1316766;
RA  Malouf N.N., McMahon D.K., Hainsworth C.N., Kay B.K.;
RT  "A two-motif isoform of the major calcium channel subunit in skeletal
RT  muscle.";
RL  Neuron 8:899-906(1992).
DR  EMBL; S36895; AAB22180.1; -.
FT  NON_TER 1
FT  SEQUENCE 15 AA; 1796 MW; 841B2DB08BF99DB CRC64;

Query Match 20.0%; Score 3; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 LEM 4
    |||
Db  13 LEM 15

RESULT 64
Q9S8Q8  PRELIMINARY; PRT; 15 AA.
ID  Q9S8Q8
AC  Q9S8Q8
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE  Phospholipase D (EC 3.1.4.4) (Fragment).
OS  Ricinus communis (Castor bean).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX  NCBI_TaxID=3988;
RN  [1]
RP  SEQUENCE
RX  MEDLINE=94029022; PubMed=8215453;
RA  Wang X., Dyer J.H., Zheng L.;
RT  "Purification and immunological analysis of phospholipase D from
RT  castor bean endosperm.";
RL  Arch. Biochem. Biophys. 306:486-494(1993).
SQ  SEQUENCE 15 AA; 1620 MW; 7C3849DA9B2F50C CRC64;

Query Match 20.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  12 ETV 14
    |||
Db  8 ETV 10

```

RESULT 65

Q9S8N8 PRELIMINARY; PRT; 15 AA.
AC Q9S8N8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Protein E-22 (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE
RX MEDLINE=94170739; PubMed=8125056;
RA Flengsrud R.;
RT "Separation of acidic barley endosperm proteins by two-dimensional electrophoresis.";
RL Electrophoresis 14:1060-1066(1993).
SQ SEQUENCE 15 AA; 1752 MW; C7D693937E908B9E CRC64;

Query Match 20.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PPO 11
|||

DB 5 PPO 7
|||

RESULT 66

Q9QVB6 PRELIMINARY; PRT; 15 AA.
AC Q9QVB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Plasma T-kinin isoform II (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE
RX MEDLINE=23348359; PubMed=1639765;
RA Enyoji K.; Kato H.;
RT Purification and Characterization of two isoforms of T-kininogens from rat liver microsomes.";
RL J. Biochem. 111:670-675(1992).
SQ SEQUENCE 15 AA; 1717 MW; 82BE84AE486A0AAB CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
|||

DB 12 ETV 14
|||

RESULT 67

Q9QVK9 PRELIMINARY; PRT; 15 AA.
AC Q9QVK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 21, Last annotation update)
DE MEPRIN-METALLOENDOPEPTIDASE (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;

RN [1]

RP SEQUENCE.
RX MEDLINE=91363409; PubMed=1888759;
RA Flannery A.V.; Macadam G.C.; Beynon R.J.;
RT "Immunological characterisation of different meprin species in mice.";
RL Biochim. Biophys. Acta 1079:119-122(1991).
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1662 MW; FF7E0C2A04A388F2 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
|||

DB 2 ETV 4
|||

RESULT 68

Q9QWT2 PRELIMINARY; PRT; 15 AA.
AC Q9QWT2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Nitric oxide synthase 1 (Fragment).
GN NOS1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98368654; PubMed=9705156;
RA Oberbaumer I.; Moser D.; Bachmann S.;
RT "Nitric oxide synthase 1 mRNA: Tissue-specific variants with new alternative first exons from rat.";
RL Biol. Chem. 379:913-919(1998).
DR EMBL; AJ005845; CAA06740.1; -.
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1560 MW; 42DE978DAF21ED38 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 BMK 5
|||

DB 6 BMK 8
|||

RESULT 69

Q9QUY3 PRELIMINARY; PRT; 15 AA.
AC Q9QUY3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE L-glutamate/aspartate NEUROTRANSMITTER transporter (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96085162; PubMed=8521863;
RA Schulte S.; Stoffel W.;
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter. Copurification, separation and characterization of the two glycoproteins.";
RL Eur. J. Biochem. 233:947-953(1995).

SQ SEQUENCE 15 AA; 1724 MW; CBS53AD02748CA16 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5
DB 13 EMK 15

RESULT 70

Q9QV7 PRELIMINARY; PRT; 15 AA.

AC Q9QV7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE Plasma T-kinin isoform I (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92348359; PubMed=1639765;
RA Enyoji K., Kato H.;
RT "Purification and characterization of two isoforms of T-kininogens
from rat liver microsomes.";
RL J. Biochem. 111:670-675(1992).
SQ SEQUENCE 15 AA; 1698 MW; 01FB84AE486A0A5 CRC64;

Query Match 20.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ETV 14
DB 12 ETV 14

RESULT 71

Q9PTM6 PRELIMINARY; PRT; 15 AA.

AC Q9PTM6;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE Aromatase (Fragment).
GN AROMATASE.
OS Poephilia guttata (Zebra finch) (Taeniopygia guttata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Estrilidae;
OC Estrilidae; Taeniopygia.
OX NCBI_TaxID=59729;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20033564; PubMed=10564828;
RA Ramachandran B., Schlinger B.A., Arnold A.P., Campagnoni A.T.;
RT "Zebra finch aromatase gene expression is regulated in the brain
through an alternate promoter.";
RL Gene 240:209-216(1999).
DR EMBL: AF170273; AAF20041.1; --
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1745 MW; 25099C05146F360E CRC64;

Query Match 20.0%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 2 VLE 4

RESULT 72

Q9PS61 PRELIMINARY; PRT; 15 AA.

AC Q9PS61;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Factor XA light CHAIN. VAPAM light CHAIN=23 kDa PARAMYXOVIRUS-
DE activating endoprotease light chain (Fragment).
OS Gallus gallus (Chicken)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92164779; PubMed=1537403;
RA Gotoh B., Yamauchi F., Ogasawara T., Nagai Y.;
RT "Isolation of factor Xa from chick embryo as the amniotic endoprotease
RT responsible for paramyxovirus activation.";
RL FEBS Lett. 296:274-278(1992).
FT NON TER 1 1
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1766 MW; B84F5F7ED0E57533 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EMK 5
DB 7 EMK 9

RESULT 73

P83012 PRELIMINARY; PRT; 15 AA.

AC P83012;
DT 01-OCT-2001 (Tremblrel. 18, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
DE Cytochrome C oxidase polypeptide VA, mitochondrial (EC 1.9.3.1)
(Fragment).
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcariniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP TISSUE=Rectal gland;
RC Schuurmans Stekhoven F.M.A.H., Flik G., Wendelaar Bonga S.E.;
RA "Phospholeman in the rectal gland of sharks.";
RL submitted (JUN-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICCYTOCHROME C.
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (BY
SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR InterPro: IPR003204; Cyt_c_ox5a.
DR Pfam: PF02284; COX5A; 1_ox5a.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 1720 MW; 937518D7590B3C5 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QET 13
|
|
|
Db 5 QET 7

RESULT 74

Q85713
ID Q85713 PRELIMINARY; PRT; 15 AA.
AC Q85713
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 29 (RSV-29) src (Fragment).
OS Rous sarcoma virus.
OC Viruses; Retrovird viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85265036; PubMed=2991593;
RA Dutta A., Wang L.-H., Hanafusa T., Hanafusa H.;
RT "Partial nucleotide sequence of Rous sarcoma virus-29 provides
RT evidence that the original rous sarcoma virus was replication
RT defective.";
RL J. Virol. 55:728-735(1985).
DR EMBL: M11117; AAA42556.1; -.
FT NON TER 1
SQ SEQUENCE 15 AA; 1597 MW; DB53E0F31273C5C1 CRC64;

Query Match 20.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred.No. 8.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
|
|
|
Db 10 VLE 12

RESULT 75

Q9R4D1
ID Q9R4D1 PRELIMINARY; PRT; 16 AA.
AC Q9R4D1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE 30 kDa IGA NEPHROPATHY-associated outer membrane antigen (Fragment).
OS Haemophilus parainfluenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=729;
RN [1]
RP SEQUENCE.
RX MEDLINE=96215401; PubMed=8625525;
RA Suzuki S., Nakatomi Y., Odani S., Sato H., Gejyo F., Arakawa M.;
RT "Circulating IGA, IgG, and IGM class antibody against Haemophilus
RT parainfluenzae antigens in patients with IGA nephropathy.";
RL Clin. Exp. Immunol. 104:306-311(1996).
SQ SEQUENCE 16 AA; 1645 MW; D19D462569AFF83D CRC64;

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred.No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PQE 12
|
|
|
Db 2 PQE 4

Search completed: November 25, 2003, 18:25:23
Job time : 38.1936 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 48,5904 Seconds
(without alignments)
48,999 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKRPPPPQETVT 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03.*

```

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	Colostrinin derive
2	15	100.0	15	22	Colostrinin peptid
3	15	100.0	15	22	Colostrinin peptid
4	15	100.0	15	22	Ewe colostrinin pe
5	15	100.0	15	23	Colostrinin consti
6	15	100.0	15	23	Colostrinin consti
7	15	100.0	15	23	Neural cell regula
8	15	100.0	16	22	Ewe colostrinin pe
9	6	40.0	10	11	Smooth muscle myos

10	5	33.3	5	19	AAW37157	EVH1 ligand motif.
11	5	33.3	5	20	AAW89423	Moraxella lactofer
12	5	33.3	5	22	AAW79177	Amino acid sequenc
13	5	33.3	5	22	AAU09140	Ena/VASP homology
14	5	33.3	5	23	AAO17762	Zyxine VASP bindin
15	5	33.3	6	19	AAW31441	Transcriptional ac
16	5	33.3	7	22	AAW72259	Colostrinin derive
17	5	33.3	7	22	AAW72512	Colostrinin peptid
18	5	33.3	7	22	AAW72544	Colostrinin peptid
19	5	33.3	7	22	AAW59315	Ewe colostrinin pe
20	5	33.3	7	23	AAW51048	Colostrinin consti
21	5	33.3	7	23	AAW51048	Colostrinin consti
22	5	33.3	7	23	AAO14590	Neural cell regula
23	5	33.3	9	21	AAW35516	S. cerevisiae RNA
24	5	33.3	9	21	AAW35516	Motif A of RNA tri
25	5	33.3	9	22	AAU09144	Ena/VASP homology
26	5	33.3	9	23	AAU09144	Peptide motif of R
27	5	33.3	9	24	ABR27236	Human cancer-relat
28	5	33.3	9	24	ABR28248	Human cancer-relat
29	5	33.3	9	24	ABR28254	Human cancer-relat
30	5	33.3	9	24	ABR28437	Human cancer-relat
31	5	33.3	10	22	AAU09138	Ena/VASP homology
32	5	33.3	10	24	ABR27336	Human cancer-relat
33	5	33.3	10	24	ABR27737	Human cancer-relat
34	5	33.3	10	24	ABR27891	Human cancer-relat
35	5	33.3	10	24	ABR28332	Human cancer-relat
36	5	33.3	10	24	ABR28354	Human cancer-relat
37	5	33.3	10	24	ABR28537	Human cancer-relat
38	5	33.3	14	22	AAW79174	Peptide derived fr
39	5	33.3	14	22	AAW85935	2A11 seed storage
40	5	33.3	15	14	AAW42641	N-terminal sequenc
41	5	33.3	15	18	AAW39038	Peptide resembling
42	5	33.3	15	18	AAW39006	Peptide resembling
43	5	33.3	15	18	AAW39070	Peptide resembling
44	5	33.3	15	18	AAW38976	Peptide resembling
45	5	33.3	15	18	AAW38942	Peptide resembling
46	5	33.3	15	18	AAW38952	Peptide resembling
47	5	33.3	15	21	AAW93014	Transforming growt
48	5	33.3	15	21	AAW93015	Transforming growt
49	5	33.3	15	22	AAW79166	Synthetic antigen
50	5	33.3	15	23	ABG72860	Human ribosomal pr
51	5	33.3	15	23	ABP59535	Human ribonucleoti
52	5	33.3	15	24	ABR38294	Human cancer-relat
53	5	33.3	15	24	ABR38351	Human cancer-relat
54	5	33.3	15	24	ABR38352	Human cancer-relat
55	5	33.3	15	24	ABR38391	Human cancer-relat
56	5	33.3	15	24	ABR38392	Human cancer-relat
57	5	33.3	17	19	AAW83113	LRPS protein fragm
58	5	33.3	18	17	AAW05469	SH3-binding peptid
59	5	33.3	18	18	AAW37677	PPPPY motif contai
60	5	33.3	18	18	AAW38909	Peptide resembling
61	5	33.3	18	19	AAW47567	Exendin agonist (1
62	5	33.3	18	19	AAW47569	Exendin agonist (2
63	5	33.3	18	19	AAW47571	Exendin agonist (2
64	5	33.3	18	19	AAW47577	Exendin agonist (2
65	5	33.3	18	19	AAW47562	Exendin agonist (1
66	5	33.3	18	19	AAW47564	Exendin agonist (1
67	5	33.3	18	19	AAW47550	Exendin agonist (1
68	5	33.3	18	19	AAW47552	Exendin agonist (3
69	5	33.3	18	20	AAW03721	Exendin agonist co
70	5	33.3	18	20	AAW03723	Exendin agonist co
71	5	33.3	18	20	AAW03733	Exendin agonist co
72	5	33.3	18	20	AAW03735	Exendin agonist co
73	5	33.3	18	20	AAW03738	Exendin agonist co
74	5	33.3	18	20	AAW03740	Exendin agonist co
75	5	33.3	18	20	AAW03742	Exendin agonist co
76	5	33.3	18	21	AAW52873	Exendin agonist c
77	5	33.3	18	21	AAW52876	Exendin agonist c
78	5	33.3	18	21	AAW52878	Exendin agonist c
79	5	33.3	18	21	AAW52880	Exendin agonist c
80	5	33.3	18	21	AAW52885	Exendin agonist c
81	5	33.3	18	21	AAW52886	Exendin agonist c
82	5	33.3	18	22	AAW19823	PAK-related sterol

83 Peptide resembling
84 ActA peptide (aa29
85 PEST-like amino ac
86 Peptidase substrat
87 Peptidase substrat
88 Peptidase substrat
89 BOP activated pept
90 Cyclic polymer der
91 WW domain ligand P
92 PPPV motif found
93 Peptide #67 from P
94 Daucus carota SERK
95 Mammalian Ena (Men
96 FAM-(Pro)4-Lys(eps
97 Hepatitis GB virus
98 Ena/VASP homology
99 "L domain" amino a
100 Amino acid sequenc

5 33.3 20 18 AAW38971
5 33.3 20 19 AAW37154
5 33.3 20 22 AAB83376
4 26.7 4 16 AAR80051
4 26.7 4 16 AAR80057
4 26.7 4 16 AAR80048
4 26.7 4 19 AAW59261
4 26.7 4 24 ABUS6778
4 26.7 5 17 AAR97694
4 26.7 5 18 AAW37648
4 26.7 5 19 AAW65842
4 26.7 5 19 AAW47014
4 26.7 5 19 AAW37156
4 26.7 5 20 AAW98982
4 26.7 5 21 AAB09480
4 26.7 5 22 AAU09141
4 26.7 5 22 AAG78309
4 26.7 5 22 AAG63123

ALIGNMENTS

RESULT 1

AAB72252
ID AAB72252 standard; peptide; 15 AA.

AC AAB72252;

DT 14-MAY-2001 (first entry)

DE Colostrinin derived cytokine inducing peptide SEQ ID 7.

KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

OS Synthetic.

PV WO200111937-A2.

XX 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22818.

PR 17-AUG-1999; 99US-0149311.

PA (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -

PS Claim 1; Page 34; 50pp; English.

CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15
| | | | | | | | | | | | | | |
Db 1 VLEMKFPPPPQETVT 15

RESULT 2

AAB72506

ID AAB72506 standard; Peptide; 15 AA.

XX AC AAB72506;

DT 09-MAY-2001 (first entry)

XX Colostrinin peptide #7.

XX Dermatological; oxidative stress regulator; colostrinin.

OS Unidentified.

PN WO200112650-A2.

PD 22-FEB-2001.

PF 17-AUG-2000; 2000WO-US22665.

PR 17-AUG-1999; 99US-0149310.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Stanton GJ, Hughes TK, Boldogh I;

DR WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -

PS Claim 6; Page 25; 48pp; English.

CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.7e-08;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15

| | | | | | | | | | | | | | |

Db 1 VLEMKFPPPPQETVT 15

RESULT 3

AAB72538

ID AAB72538 standard; Peptide; 15 AA.

XX AC AAB72538;

DT 09-MAY-2001 (first entry)

XX

```

DE Colostrinin peptide #7.
XX
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW Colostrum.
XX
OS Unidentified.
XX
PN WO200112651-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22774.
XX
PR 17-AUG-1999; 99US-0149633.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Boldogh I;
XX
XX WPI; 2001-226545/23.
XX
PT Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
XX
PS Claim 6; Page 21; 35pp; English.
XX
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKFPPPPQETVT 15
Db 1 VLEMKFPPPPQETVT 15

RESULT 4
AAB59312
ID AAB59312 standard; Peptide; 15 AA.
XX
AC AAB59312;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment A-3.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB02128.
XX
PR 02-JUN-1999; 99GB-0012852.
XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
XX WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders, such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX Sequence 15 AA;
SQ

Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKFPPPPQETVT 15
Db 1 VLEMKFPPPPQETVT 15

RESULT 5
AAE20234
ID AAE20234 standard; peptide; 15 AA.
XX
AC AAE20234;
XX
DT 18-JUN-2002 (first entry)
XX
XX Colostrinin constituent peptide #7.
DE
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 15
FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX
XX 21-FEB-2002.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX 17-AUG-2000; 2000WO-US22776.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Stanton GJ, Hughes TK, Boldogh I;
XX
XX WPI; 2002-269151/31.
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 25; 51pp; English.
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15
 |||||
 Db 1 VLEMKFPPPPQETVT 15

RESULT 6

AA051042
 ID AAM51042 standard; Peptide; 15 AA.

AC AAM51042;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; human.

OS Homo sapiens.

Key Location/Qualifiers

FT Modified-site 15 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patient. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide. Cytokines induced by this peptide in human
 CC leucocyte cultures include interferon-gamma, tumour necrosis
 CC factor-alpha, interleukin-4, interleukin-6 and interleukin-10.

XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEMKFPPPPQETVT 15
 |||||
 Db 1 VLEMKFPPPPQETVT 15

RESULT 7

AA014583

ID AAO14583 standard; peptide; 15 AA.

XX AAO14583;

XX 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 7.

XX Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 15 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKPPPPQETVT 15
 |||||
 Db 1 VLEMKPPPPQETVT 15

RESULT 8

AAB59343
 ID AAB59343 standard; Peptide; 16 AA.

XX AC AAB59343;

XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment derived sequence #3.

XX DR Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX

OS Ovis sp.

XX WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 2000WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REGF-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from
 PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX

PS Claim 8; Page 27; 63pp; English.

XX CC The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 15; DB 22; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.9e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEMKPPPPQETVT 15
 |||||
 Db 2 VLEMKPPPPQETVT 16

RESULT 9

AAR07284
 ID AAR07284 standard; protein; 10 AA.

XX AAR07284;

XX DT 31-JAN-1991 (first entry)

XX DE Smooth muscle myosin-2 immunogen for antibody prodn.

XX KW Smooth muscle myosin isoform 2; monoclonal antibody; immunogen;
 KW diagnosis; arteriosclerosis.

XX OS Homo sapiens.

XX PN WO9011520-A.

XX PD 04-OCT-1990.

XX PF 26-MAR-1990; 90WO-JP00398.

XX PR 28-MAR-1989; 89JP-0075884.

XX PA (YAMS) YAMASA SHOYU KK.

XX PI Nagai R, Kuroo M, Kato H;

XX DR WPI; 1990-320366/42.

XX PT Antibody against heavy chain of smooth muscle myosin - as reagent
 PT for histological staining of smooth muscle or diagnosis of blood
 PT vessel disorders

XX PS Claim 7; Page 42; 61pp; Japanese.

XX CC The oligopeptide is used as immunogen for the prodn. of monoclonal
 CC antibodies recognising isoform SM-2 of the heavy chain of smooth
 CC muscle myosin, pref. from heart or skeletal muscle, esp. human.
 CC The peptide contains the part which differs between isoforms SM1-3.
 CC The antibodies may be obtained by immunisation with the immunogen,
 CC followed by cell fusion to produce a hybridoma, cloning and for
 CC culturing the chosen hybridoma clone. The Ab is a reagent for
 CC the histological staining of smooth muscle, and is useful in the
 CC diagnosis of arteriosclerosis, blood vessel disorders etc.
 XX See also AAR07283-5.

SQ Sequence 10 AA;

Query Match 40.0%; Score 6; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPQET 13
 |||||
 Db 3 PPPQET 8

RESULT 10

AAR37157

ID AAR37157 standard; Peptide; 5 AA.

XX AC AAR37157;

XX DT 06-JUL-1998 (first entry)

XX DE EVH1 ligand motif.

XX KW Mena protein; mammalian Ena; Enabled; Evi protein; cytoskeleton;
 KW cell morphology; cell adhesion; cell differentiation; cell growth;
 KW cell motility; mouse; EVH1 ligand.

XX OS Synthetic.

XX PN WO9801755-A1.

XX PD 15-JAN-1998.

XX PF 03-JUL-1997; 97WO-US11669.
 XX PR 05-JUL-1996; 96US-0675815.
 XX PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 XX PI Gertler FB, Niebuhr K, Soriano P, Wehland J;
 XX DR WPI; 1998-101197/09.
 XX PT Detection of modulators of Mena and Ena-VASP-like genes and proteins
 PT - used in control of cytoskeletal dynamic events in normal and
 PT abnormal cell morphology, adhesion, motility, growth and
 PT differentiation
 XX PS Example 7; Page 44; 77pp; English.
 XX CC This peptide motif is found in zyxin, vinculin and other focal
 CC adhesion proteins containing an ActA-like motif. The N-terminal
 CC portion of novel murine Mena (mammalian Ena) protein (see AAW37148)
 CC contains an Ena-VASP homology domain (EVH1) that directs the proper
 CC localisation of Mena to focal contacts via directed protein-protein
 CC interactions with zyxin, vinculin etc. This suggests that the
 CC FPPPP motif may comprise the core recognition site in EVH1 ligands.
 CC Based on the disclosed Mena and Evi genes (see AAV02996-98) and
 CC proteins (see AAW37148-53), a variety of methods and compositions are
 CC provided for screening, isolating and characterising endogenous and
 CC exogenous factors, drugs and therapeutic agents useful to evaluate
 CC and/or control cytoskeletal dynamic events involved in normal and
 CC abnormal cell morphology, adhesion, motility, growth and/or
 CC differentiation.
 XX SQ Sequence 5 AA;
 Query Match 33.3%; Score 5; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 FPPPP 10
 Db 1 FPPPP 5
 RESULT 11
 AAW89423
 ID AAW89423 standard; Peptide; 5 AA.
 XX AC AAW89423;
 XX DT 21-JUN-1999 (first entry)
 XX DE Moraxella lactoferrin binding protein 1 (Lbp1) C-terminal peptide.
 XX KW Lactoferrin receptor; lactoferrin binding protein; Lbp1;
 KW lbpA gene; infection; otitis media; sinusitis; conjunctivitis;
 KW pneumonia; bronchitis; tracheitis; emphysema; diagnosis; therapy;
 KW vaccine; Branhamella catarrhalis.
 XX OS Moraxella catarrhalis.
 XX PN WO9855606-A2.
 XX PD 10-DEC-1998.
 XX PF 02-JUN-1998; 98WO-CA00544.
 XX PR 08-MAY-1998; 98US-0074658.
 XX PR 03-JUN-1997; 97US-0867941.
 XX PA (CONN-) CONNAUGHT LAB LTD.

PI Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;
 XX WPI; 1999-070266/06.
 XX PT Lactoferrin receptor genes from Moraxella, especially M. catarrhalis
 PT - useful to diagnose Moraxella infection e.g. to detect otitis media
 PT due to M. catarrhalis infection and to immunise against such
 PT infections
 XX PS Example 1; Page 37; 202pp; English.
 XX CC This is a conserved C-terminal pentapeptide found in all known
 CC examples of lactoferrin binding protein 1 (Lbp1). PCR primers (see
 CC AAV82030-31) based on this peptide have been designed for use in the
 CC PCR amplification of M. catarrhalis lbpA genes that code for Lbp1.
 CC The invention provides immunogenic compositions, including vaccines,
 CC based upon expressed recombinant Lbp1 and/or Lbp2 and/or ORF3
 CC proteins (see AAW89413-21) for use in the prevention of diseases
 CC (e.g. Otitis media) caused by Moraxella. The genes and DNA
 CC sequences of the Moraxella lactoferrin receptor (lfr) locus (see
 CC AAV82019-21) are useful for diagnosis, immunisation, and the
 CC generation of diagnostic and immunological reagents.
 XX SQ Sequence 5 AA;
 Query Match 33.3%; Score 5; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LEMKF 6
 Db 1 LEMKF 5
 RESULT 12
 AAG79177
 ID AAG79177 standard; peptide; 5 AA.
 XX AC AAG79177;
 XX DT 03-JAN-2002 (first entry)
 XX DE Amino acid sequence of a Fyb/SLAP complex inhibitor.
 XX KW Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
 KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;
 KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
 KW infectious disease; cancer; autoimmune disease; inflammation;
 KW platelet aggregation; wound healing; clotting.
 XX OS Homo sapiens.
 XX PN WO200174858-A2.
 XX PD 11-OCT-2001.
 XX PF 03-APR-2001; 2001WO-US10753.
 XX PR 03-APR-2000; 2000US-194215P.
 XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 XX (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
 XX PI Krause M, Sechi AS, Gertler FB, Wehland J;
 XX WPI; 2001-616686/71.
 XX PT Modulating cytoskeletal rearrangement to regulate T cell and macrophage
 PT activation for treating cancer, autoimmune disease, and infectious
 PT disease, comprises contacting with a Fyb/SLAP complex modulator -
 XX PS Claim 4; Page 56; 79pp; English.

DR WPI; 2002-463650/49.

XX Identifying compounds that modulate Ena-vasodilator-stimulated

PT phosphoprotein homolog (EVH)-1 binding interactions, useful e.g. for

PT treating cardiovascular disease, comprises using antibodies -

XX

XX Example 4; Page 18; 34pp; German.

XX

CC The present invention relates to a method of identifying compounds which

CC modulate the interaction between an EVH-1 (Ena-vasodilator-stimulated

CC phosphoprotein (VASP) homologue) binding domain and an EVH-1 domain. Such

CC compounds can be used for treating cardiovascular diseases, inflammation

CC and neoplastic cell/tissue alterations such as cancer. The present

CC sequence is a VASP binding domain from zyxine described in the

CC exemplification of the invention.

XX

SQ Sequence 5 AA;

Query Match 33.3%; Score 5; DB 23; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10

Db 1 FPPPP 5

RESULT 15

AAW31441

ID AAW31441 standard; Protein; 6 AA.

XX

AC AAW31441;

XX

DT 04-AUG-1998 (first entry)

XX

DE Transcriptional activator peptide fragment LS46.

XX

XX Activating sequence; Gal4; transcriptional activator; RNA polymerase;

KW Protein-protein interaction; gene therapy; therapeutic; holoenzyme;

KW Gal1; DNA binding domain.

XX

OS Synthetic.

OS

XX WO9744447-A2.

PN

XX 27-NOV-1997.

PD

XX

XX 02-MAY-1997; 97WO-US07338.

PF

XX

XX 01-MAY-1997; 97US-0017016.

PR

XX 03-MAY-1996; 96US-0017016.

ER

XX (HARD) HARVARD COLLEGE.

PA

XX Lu X, Ptashne M, Wu Y;

PI

XX

XX WPI; 1998-018502/02.

DR

DR N-ESDB; AAV02536.

XX

PT New transcriptional activator containing DNA binding domain bound to

PT peptide - useful for controlling gene expression, especially in gene

PT therapy, and in protein-protein interaction assays, does not inhibit

PT other transcription activators

XX

XX Example 1; Page 24; 55pp; English.

PS

XX AAW31412-W31459, AAW31461-W31481, AAW31483-W31493 and AAW39053-W39076

CC are fragments used in an assay to determine novel transcriptional

CC activators. The method involves the production of transcriptional

CC activators comprising of a DNA-binding group and a 6-25 amino acid

CC peptide that is covalently bonded to the DNA binding group and does not

CC represent a fragment of a natural transcription activator.

CC Protein-protein interactions are identified in the assay by fusing a

CC

CC DNA-binding domain to a library of DNA fragments and introducing this and

CC a fusion of target protein and a polypeptide containing a region of Gal4

CC which interacts with Gal1p into a cell containing Gal1p and identifying

CC members of the library that interact with the target transcription in a

CC transcription. Such constructs are used to activate transcription in a

CC cell, e.g. for controlling gene activity, particularly in gene therapy

CC (e.g. recognizing a site close to a selected therapeutic gene).

CC Transcription can be activated without blocking other transcriptional

CC activators. They probably act by interacting with a component of the RNA

CC polymerase II holoenzyme, Gal11, the strongest known yeast activator,

CC which provides a more sensitive assay allowing detection of even weak

CC protein-protein interactions. Such activators do not create toxicity

CC problems even when overexpressed.

XX

SQ Sequence 6 AA;

Query Match 33.3%; Score 5; DB 19; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10

Db 1 FPPPP 5

RESULT 16

AAW72259

ID AAW72259 standard; peptide; 7 AA.

XX

AC AAW72259;

XX

DT 14-MAY-2001 (first entry)

XX

DE Colostrinin derived cytokine inducing peptide SEQ ID 14.

XX

XX Colostrinin; immune response; cytokine; blood cell proliferation;

KW central nervous system disorder; neurological disorder; mental disorder;

KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;

KW neurosis; infection.

XX

OS Synthetic.

OS

XX WO200111937-A2.

PN

XX 22-FEB-2001.

PD

XX 17-AUG-2000; 2000WO-US22818.

PF

XX 17-AUG-1999; 99US-0149311.

PR

XX (TEXA) UNIV TEXAS SYSTEM.

PA

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

PI

XX WPI; 2001-202804/20.

DR

XX

PT Inducing a cytokine and modulating an immune response, useful for

PT treating central nervous system diseases and bacterial and viral

PT infections, comprises administering colostrinin as an immunological

PT regulator -

XX

XX Claim 1; Page 34; 50pp; English.

PS

XX Sequences AAW72246 - AAW72275 represent peptides derived from colostrinin,

CC a proline rich polypeptide aggregate contained in colostrum. The

CC peptides have immune response modulatory activity, and are capable of

CC inducing cytokines. Colostrinin and its derived peptides are useful for

CC inducing cytokine production, for modulating an immunological response

CC and for inducing blood cell proliferation. The peptides are useful in the

CC treatment of disorders of the central nervous system, neurological

CC disorders, mental disorders, dementia, neurodegenerative diseases,

CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic

CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.
 XX
 SQ Sequence 7 AA;
 Query Match 33.3%; Score 5; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 PPPPQ 11
 |||||
 Db 2 PPPPQ 6
 RESULT 17
 AAB72512
 ID AAB72512 standard; Peptide; 7 AA.
 XX
 AC AAB72512;
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #13.
 XX
 KW Dermatological; oxidative stress regulator; colostrinin.
 KW Unidentified.
 OS
 XX WO200112650-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22665.
 XX
 PR 17-AUG-1999; 99US-0149310.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 WPI; 2001-218342/22.
 DR
 XX
 PT Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -
 XX
 PS Claim 6; Page 25; 48pp; English.
 XX
 CC The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.
 XX
 SQ Sequence 7 AA;
 Query Match 33.3%; Score 5; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 PPPPQ 11
 |||||
 Db 2 PPPPQ 6
 RESULT 18
 AAB72544
 ID AAB72544 standard; Peptide; 7 AA.
 XX
 AC AAB72544;
 XX

DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #13.
 XX
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22774.
 XX
 PR 17-AUG-1999; 99US-0149633.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 XX
 SQ Sequence 7 AA;
 Query Match 33.3%; Score 5; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 PPPPQ 11
 |||||
 Db 2 PPPPQ 6
 RESULT 19
 AAB59315
 ID AAB59315 standard; Peptide; 7 AA.
 XX
 AC AAB59315;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Ewe colostrinin peptide fragment A-7.
 XX
 KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-GB02128.
 XX
 PR 02-JUN-1999; 99GB-0012852.
 XX
 PA (REGG-) REGEN THERAPEUTICS PLC.
 XX
 PI Georgiades JA;
 XX
 DR WPI; 2001-071058/08.

XX Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
XX
XX Claim 7; Page 27; 63pp; English.
PS
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX
SQ Sequence 7 AA;
Query Match 33.3%; Score 5; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PPPPQ 11
Db 2 PPPPQ 6
RESULT 20
AAE20241
ID AAE20241 standard; peptide; 7 AA.
XX
XX AAE20241;
AC
XX
XX 18-JUN-2002 (first entry)
DT
XX
XX Colostrinin constituent peptide #13.
DE
XX
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnary.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 7 /note= "Optionally C-terminal amide"
FT
FT
XX
XX WO200213850-A1.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2000; 2000WO-US22776.
PF
XX
XX 17-AUG-2000; 2000WO-US22776.
PR
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX
XX Stanton GJ, Hughes TK, Boldogh I;
PI
XX
XX WPI; 2002-269151/31.
DR
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
PT
XX
XX Claim 6; Page 25; 51pp; English.
PS
XX
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,

CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.
XX
XX
SQ Sequence 7 AA;
Query Match 33.3%; Score 5; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PPPPQ 11
Db 2 PPPPQ 6
RESULT 21
AAM51048
ID AAM51048 standard; Peptide; 7 AA.
XX
XX AAM51048;
AC
XX
XX 30-MAY-2002 (first entry)
DT
XX
XX Colostrinin constituent peptide.
DE
XX
XX Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; human.
KW
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 7 /note= "optional C-terminal amidation"
FT
FT
XX
XX WO200213849-A1.
PN
XX
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2000; 2000WO-US22775.
PF
XX
XX 17-AUG-2000; 2000WO-US22775.
PR
XX
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX
XX (REGG-) REGEN THERAPEUTICS PLC.
XX
XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
PI
XX
XX WPI; 2002-269150/31.
DR
XX
XX Modulation of blood cell proliferation in a patient involves use of
PT blood cell regulator selected from colostrinin, its constituent peptide
PT and/or analogue -
PT
XX
XX Claim 1; Page 34; 54pp; English.
PS
XX
XX The present sequence is that of a colostrinin constituent peptide
CC that is used as an immunological regulator and as a blood cell
CC regulator in claimed methods of the invention. Methods are
CC claimed for: inducing a cytokine in a cell by contact with an
CC immunological regulator, where the cell is present in a cell
CC culture, a tissue, an organ or an organism, and the cell is
CC mammalian, including human; modulating an immune response in a cell

CC by contact with the immunological regulator under conditions
 CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patient. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide.

XX SQ Sequence 7 AA;
 Query Match 33.3%; Score 5; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
 Db 2 PPPPQ 6
 |||||

RESULT 22
 AA014590
 ID AA014590 standard; peptide; 7 AA.
 AC AA014590;
 XX 27-MAY-2002 (first entry)
 DT
 DE Neural cell regulatory colostrinin peptide 13.
 XX
 KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.
 XX Unidentified.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 7 /note= "Optional C-terminal amide"
 FT
 XX WO200213851-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22777.
 PF
 XX 17-AUG-2000; 2000WO-US22777.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I, Stanton JG, Hughes TK;
 PI WPI; 2002-269152/31.
 DR
 XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 FT analog -
 XX
 XX Claim 7; Page 21; 37pp; English.
 CC The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.

XX SQ Sequence 7 AA;
 Query Match 33.3%; Score 5; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
 Db 2 PPPPQ 6
 |||||

RESULT 23
 AAB35516
 ID AAB35516 standard; Peptide; 9 AA.
 XX
 AC AAB35516;
 XX 14-FEB-2001 (first entry)
 DT
 DE S. cerevisiae RNA triphosphatase motif A.
 XX
 KW mRNA cap formation inhibition; RNA guanylyltransferase;
 KW RNA triphosphatase; growth inhibition; antiviral agent;
 KW antiparasitic agent.
 XX
 OS Saccharomyces cerevisiae.
 XX WO2000063433-A1.
 PN
 XX 26-OCT-2000.
 PD
 XX 09-NOV-1999; 99WO-US26520.
 PF
 XX 09-NOV-1998; 98US-0189579.
 PR
 XX 20-MAY-1999; 99US-0315444.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Shuman S;
 XX WPI; 2000-656425/63.
 DR
 XX Screening for a compound that inhibits formation of an organism's 5'
 PT mRNA cap structure for use as e.g. antiviral or antiparasitic agents,
 PT comprises comparing the inhibition of different organism's capping
 PT apparatus in a test organism -
 XX
 XX Disclosure; Page 132; 146pp; English.
 CC The present invention describes a novel method for use in identifying
 CC compounds which inhibit the formation of an organism's 5' mRNA cap
 CC structure. The cap-forming enzymes differ between organisms, enabling the
 CC inhibitors to be specific to particular viruses, parasites or eukaryotes.
 CC Inhibitors prevent the growth of the organism as the cap is essential,
 CC and so they can be used in disease treatment.

XX SQ Sequence 9 AA;
 Query Match 33.3%; Score 5; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEWKF 6
 Db 5 LEWKF 9
 |||||

RESULT 24
 AAB32219
 ID AAB32219 standard; Peptide; 9 AA.

```

XX AC AAB32219;
XX XX
XX DT 08-JAN-2001 (first entry)
XX AC
XX DE Motif A of RNA triphosphatase.
XX XX
XX KW RNA guanylyltransferase; mRNA capping; growth inhibition; antiviral;
XX KW antineoplastic agent; antiparasitic; triphosphatase.
XX XX
XX OS Saccharomyces cerevisiae.
XX XX
XX PN US6107040-A.
XX XX
XX PD 22-AUG-2000.
XX XX
XX PF 09-NOV-1998; 98US-0188579.
XX XX
XX PR 09-NOV-1998; 98US-0188579.
XX XX
XX PA (SHUM/) SHUMAN S.
XX XX
XX PI Shuman S;
XX XX
XX DR WPI; 2000-578532/54.
XX XX
XX PT Screening for 5' mRNA cap inhibitors comprising treating host organisms
XX PT with capping apparatus from two different organisms with test compounds
XX PT and comparing growth inhibition -
XX XX
XX PS Example 9; Figure 4; 62pp; English.
XX XX
XX CC This invention relates to a method of screening for compounds that
XX CC inhibit the formation of a 5' mRNA cap. The m7GpppN cap is the first
XX CC modification of the 5' terminus of a nascent transcript that occurs
XX CC during the processing of eukaryotic mRNA, and involves the RNA
XX CC triphosphatase and guanylyltransferase enzymes. The method comprises
XX CC replacing the hosts genes encoding 5' mRNA capping functions with genes
XX CC encoding mRNA capping functions from two different organisms, treating
XX CC the modified host cells with a test compound and comparing growth
XX CC inhibition in the two host cells with different modifications. Also
XX CC included in the invention is a method of screening for a compound that
XX CC inhibits the catalytic activity of fungal 5' triphosphatase. The methods
XX CC are used for screening for a compound that inhibits the formation of an
XX CC organisms 5' mRNA cap structure. The method is useful in gene
XX CC biochemical pharmacology and drug discovery. Compounds identified as
XX CC specific inhibitors of capping in mammalian cells are capable of being
XX CC developed as potential antineoplastic agents. The methods also allow for
XX CC the identification of antiviral and antiparasitic agents. Sequences
XX CC AAB32132-B32209 represent peptide motifs of RNA guanylyltransferase
XX CC proteins. RNA guanylyltransferase motif 1 contains a conserved element
XX CC which is involved in the transfer of GMP from GTP by the enzyme. Motifs
XX CC III, IIIa, IV, V and VI are conserved in the same order and with similar
XX CC spacing in the capping enzymes from fungi, metazoans, DNA viruses and
XX CC trypanosomes. Sequences AAB32210-B32218 represent RNA
XX CC guanylyltransferase proteins. These sequences are used in the
XX CC identification of essential enzymic functional groups used in the capping
XX CC process. Sequences AAB32219-B32242 represent RNA triphosphatase peptide
XX CC motifs, and AAB32243-B32245 represent methyltransferase protein
XX CC sequences. The peptides and proteins are used in examples of the method
XX CC of the invention.
XX XX
XX SQ Sequence 9 AA;
    Query Match 33.3%; Score 5; DB 21; Length 9;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEMKF 6
Db 5 LEMKF 9

```

```

RESULT 25
AAU09144
ID AAU09144 standard; peptide; 9 AA.
XX AC
XX AC AAU09144;
XX DT
XX DT 19-DEC-2001 (first entry)
XX DE
XX DE Ena/VASP homology (EVH) proline-rich motif #3.
XX KW
XX KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
XX KW cell migration; Ena/VASP; wound healing; actin polymerisation;
XX KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;
XX KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;
XX KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;
XX KW Tourettes syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;
XX KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;
XX KW inflammatory disorder; arthritis; allergy; gout; organ transplant;
XX KW cancer; ischaemia.
XX OS
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT Misc-difference 9 /label= OTHER
XX FT /note= "Other = any amino acid"
XX PN WO200174853-A2.
XX XX
XX PD 11-OCT-2001.
XX PF
XX PF 30-MAR-2001; 2001WO-US10249.
XX PR
XX PR 03-APR-2000; 2000US-194564P.
XX PA (WASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX PI
XX PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;
XX DR WPI; 2001-626380/72.
XX XX
XX XX Regulating cell motility for promoting wound healing and tissue
XX PT regeneration, treating, neurodegenerative disease and metastasis, by
XX PT inducing or depleting a functional enabled/vasodilator-stimulated
XX PT phosphoprotein -
XX XX
XX PS Example 6; Page 66; 107pp; English.
XX XX
XX CC The invention relates to a method of preventing mammalian cell migration,
XX CC comprising inducing a functional Ena(enabled)/vasodilator-stimulated
XX CC phosphoprotein (VASP) or promoting cell migration comprising depleting
XX CC functional Ena/VASP protein in the mammalian cell. The method is useful
XX CC for preventing or promoting mammalian cell migration, preferably tumour
XX CC cell migration in vitro or in vivo and to prevent tumour cell metastasis
XX CC in a subject. An Ena/VASP activator or inhibitor is useful for promoting
XX CC wound healing, preferably fibroblasts or nerve cells of a tissue type
XX CC with the inhibitor to promote actin polymerisation and tissue formation
XX CC on a scaffold. The inhibitor is also useful for preventing
XX CC neurodegeneration such as in Alzheimer's disease, Down Syndrome,
XX CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct
XX CC trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia
XX CC complex, progressive supranuclear palsy, progressive bulbar palsy,
XX CC spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Rett's
XX CC cerebellar degeneration, Tourettes syndrome, hypoglycaemia, hypoxia,
XX CC Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP
XX CC inhibitor is further useful for enhancing learning and memory in a
XX CC subject having or at risk of developing a learning disorder such as
XX CC Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile
XX CC dementia, Korsakow's disorder and age-related memory loss. The inhibitor
XX CC is administered in an amount for inhibiting the activity of Ena in a
XX CC synapse. Ena/VASP activator is useful for disrupting learning and memory
XX CC and the activator is administered in an amount to promote Ena/VASP

```

CC protein-FE65 interaction. Inducing the activity of Ena/VASP protein
 CC in immune or haematopoietic cells reduces the ability of the cells to
 CC migrate and this is useful for treating and preventing inflammatory
 CC disorders such as arthritis, allergy, gout, organ transplant,
 CC ulcerative colitis and ischaemic diseases and also for treating cancer
 CC metastasis. The present sequence represents the amino acid sequence
 CC of Ena/VASP homology (EVH) proline-rich motif #3.
 XX
 SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
 Db 1 FPPPP 5
 |||||
 |||||

RESULT 26
 ABJ05692
 ID ABJ05692 standard; Peptide; 9 AA.
 XX
 AC ABJ05692;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Peptide motif of RNA triphosphatase SEQ ID No 88.
 XX
 KW Antimicrobial; fungicide; transformed host organism; 5' mRNA capping;
 KW eukaryotic gene expression; mRNA 5' cap m7GpppN; enzyme.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PI US6420163-B1.
 XX
 PD 16-JUL-2002.
 XX
 PF 22-NOV-2000; 2000US-0721362.
 XX
 PR 09-NOV-1998; 98US-0188579.
 XX
 FA (SHUM/) SHUMAN S.
 XX
 PI Shuman S;
 XX
 DR WPI; 2002-654639/70.
 XX
 PT Transformed host organism for drug screening assays to identify
 PT candidate drugs, e.g. anti-fungal agents, comprises genes from a second
 PT organism replacing genes involved in 5' mRNA capping -
 XX
 PS Disclosure; Fig 4; 82pp; English.
 XX
 CC The invention relates to a transformed host organism, in which the host
 CC organism's genes encoding entire 5' mRNA capping functions have been
 CC replaced with replacement genes encoding 5' mRNA capping functions from
 CC another organism (therefore producing a host organism expressing the
 CC another organism's complete capping apparatus). The transformed host
 CC organism may be used to screen for drugs which target an essential aspect
 CC of eukaryotic gene expression, the formation of the mRNA 5' cap m7GpppN.
 CC For example, if the transformed host organism was an isogenic yeast
 CC strain that derived all its capping activities from fungal sources
 CC rather than mammalian sources it may be used to identify molecules that
 CC specifically target the fungal capping apparatus. This sequence
 CC represents a peptide relating to the formation of the mRNA 5' cap m7GpppN
 CC of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
 Db 1 FPPPP 5
 |||||
 |||||

RESULT 27
 ABR27236
 ID ABR27236 standard; Peptide; 9 AA.
 XX
 AC ABR27236;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 187P3F2 HLA peptide #71.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WC200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US11654.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 10-APR-2001; 2001US-283112P.
 PR 25-APR-2001; 2001US-286630P.
 XX
 FA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 PS Claim 13; Page 401; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
 Db 4 PPPPQ 8
 |||||
 |||||

RESULT 28
 ABR28248
 ID ABR28248 standard; Peptide; 9 AA.
 XX

```

AC ABR28248;
XX
XX 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 187P3F2 HLA peptide #1083.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
PR
XX 10-APR-2001; 2001US-283112P.
PR
XX 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 413; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 33.3%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 1 PPPPQ 5

RESULT 29
ABR28254
ID ABR28254 standard; Peptide; 9 AA.
XX
XX ABR28254;
AC
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 187P3F2 HLA peptide #1089.
DE
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS

```

```

XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US11654.
XX
XX 10-APR-2001; 2001US-282739P.
PR
XX 10-APR-2001; 2001US-283112P.
PR
XX 25-APR-2001; 2001US-286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
XX Claim 13; Page 413; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
XX Sequence 9 AA;
SQ
Query Match 33.3%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 4 PPPPQ 8

RESULT 30
ABR28437
ID ABR28437 standard; Peptide; 9 AA.
XX
XX ABR28437;
AC
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 187P3F2 HLA peptide #1272.
DE
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US11654.
PR
XX 10-APR-2001; 2001US-282739P.
PR
XX 10-APR-2001; 2001US-283112P.
PR
XX 25-APR-2001; 2001US-286630P.
PR

```

```

XX PA (AGEN-) AGENSYS INC.
XX PA
XX PI Jakovovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR
XX DR WPI; 2003-075555/07.
XX PT
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients
XX PS
XX PS Claim 13; Page 415; 1021pp; English.
XX CC
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 9 AA;
XX
XX Query Match 33.3%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 PPPPQ 11
XX Db 1 PPPPQ 5
XX
XX RESULT 31
XX ID AAU09138 standard; peptide; 10 AA.
XX AC AAU09138;
XX DT 19-DEC-2001 (first entry)
XX DE
XX DE Ena/VASP homology (EVH) consensus binding site.
XX KW Enabled protein; Ena; vasodilator stimulated phosphoprotein; VASP;
XX KW cell migration; Ena/VASP; wound healing; actin polymerisation;
XX KW neurodegeneration; Alzheimer's disease; Down Syndrome; trauma; stroke;
XX KW Parkinson's disease; amyotrophic lateral sclerosis; ALS; epilepsy;
XX KW Huntington's disease; ALS-Parkinsonism-dementia complex; bulbar palsy;
XX KW Tourette's syndrome; hypoglycaemia; hypoxia; Creutzfeldt-Jakob disease;
XX KW Korsakoff's syndrome; learning; memory; brain damage; senile dementia;
XX KW inflammatory disorder; arthritis; allergy; gout; organ transplant;
XX KW cancer; ischaemia.
XX OS
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 1 /label= Asp, Gly
XX FT Misc-difference 7 /label= OTHER
XX FT /note= "Other = any amino acid"
XX
XX FN WO200174853-A2.
XX PD
XX PD 11-OCT-2001.
XX XX
XX PF 30-MAR-2001; 2001WO-US10249.

```

```

XX PA 03-APR-2000; 2000US-194564P.
XX PA (NASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX PI
XX PI Gertler FB, Bear JE, Wehland J, Loureiro JJ;
XX DR
XX DR WPI; 2001-626380/72.
XX PT
XX PT Regulating cell motility for promoting wound healing and tissue
XX PT regeneration, treating, neurodegenerative disease and metastasis, by
XX PT inducing or depleting a functional enabled/vasodilator-stimulated
XX PT phosphoprotein
XX PS
XX PS Example 2; Page 59; 107pp; English.
XX
XX CC The invention relates to a method of preventing mammalian cell migration,
XX CC comprising inducing a functional Ena(enabled)/vasodilator-stimulated
XX CC phosphoprotein (VASP) or promoting cell migration comprising depleting
XX CC functional Ena/VASP protein in the mammalian cell. The method is useful
XX CC for preventing or promoting mammalian cell migration, preferably tumour
XX CC cell migration in vitro or in vivo and to prevent tumour cell metastasis
XX CC in a subject. An Ena/VASP activator or inhibitor is useful for promoting
XX CC wound healing, preferably fibroblasts or nerve cells of a tissue type
XX CC with the inhibitor to promote actin polymerisation and tissue formation
XX CC on a scaffold. The inhibitor is also useful for preventing
XX CC neurodegeneration such as in Alzheimer's disease, Down Syndrome,
XX CC Parkinson's disease, amyotrophic lateral sclerosis (ALS), stroke, direct
XX CC trauma, Huntington's disease, epilepsy, ALS-Parkinsonism-dementia
XX CC complex, progressive supranuclear palsy, progressive bulbar palsy,
XX CC spinomuscular atrophy, cerebral amyloidosis, Pick's atrophy, Retts
XX CC cerebellar degeneration, Tourette's syndrome, hypoglycaemia, hypoxia,
XX CC Creutzfeldt-Jakob disease and Korsakoff's syndrome. The Ena/VASP
XX CC inhibitor is further useful for enhancing learning and memory in a
XX CC subject having or at risk of developing a learning disorder such as
XX CC Alzheimer's disease, Creutzfeldt-Jakob disease, brain damage, senile
XX CC dementia, Korsakow's disorder and age-related memory loss. The inhibitor
XX CC is administered in an amount for inhibiting the activity of Mena in a
XX CC synapse. Ena/VASP activator is useful for disrupting learning and memory
XX CC and the activator is administered in an amount to promote Ena/VASP
XX CC protein-FB65 interaction. Inducing the activity of Ena/VASP protein
XX CC in immune or haematopoietic cells reduces the ability of the cells to
XX CC migrate and this is useful for treating and preventing inflammatory
XX CC disorders such as arthritis, allergy, gout, organ transplant,
XX CC ulcerative colitis and ischaemic diseases and also for treating cancer
XX CC metastasis. The present sequence represents the amino acid sequence
XX CC of Ena/VASP homology (EVH) consensus binding site.
XX SQ Sequence 10 AA;
XX
XX Query Match 33.3%; Score 5; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 FPPPP 10
XX Db 2 FPPPP 6
XX
XX RESULT 32
XX ID ABR27336 standard; Peptide; 10 AA.
XX AC ABR27336;
XX DT 19-MAY-2003 (first entry)
XX DE
XX DE Human cancer-related protein 187B3F2 HLA peptide #171.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.

```


PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX
 XX Claim 13; Page 409; 1021pp; English.
 PS
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
 |||||
 Db 1 PPPPQ 5

RESULT 35

ABR28332
 ID ABR28332 standard; Peptide; 10 AA.

AC ABR28332;

DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 187P3F2 HLA peptide #1167.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

XX human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 10-APR-2001; 2001US-283112P.

XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX

XX Claim 13; Page 414; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX
 SQ Sequence 10 AA;

Query Match 33.3%; Score 5; DB 24; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
 |||||
 Db 2 PPPPQ 6

RESULT 36

ABR28354
 ID ABR28354 standard; Peptide; 10 AA.

XX ABR28354;

XX 19-MAY-2003 (first entry)

XX Human cancer-related protein 187P3F2 HLA peptide #1189.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

XX human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 10-APR-2001; 2001US-283112P.

XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;

XX Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response
 PT in cancer patients -
 XX

XX Claim 13; Page 414; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention.
 XX

SQ Sequence 10 AA;

```
Query Match      33.3%; Score 5; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
DB 4 PPPPQ 8

RESULT 37
ABR28537
ID ABR28537 standard; Peptide; 10 AA.
XX AC ABR28537;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 187P3F2 HLA peptide #1372.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients -
XX PS Claim 13; Page 416; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 10 AA;

Query Match      33.3%; Score 5; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
DB 2 PPPPQ 6
```

RESULT 38

```
AAG79174
ID AAG79174 standard; peptide; 14 AA.
XX AC AAG79174;
XX DT 03-JAN-2002 (first entry)
XX DE Peptide derived from ActA, and containing EVH1-binding site.
XX KW ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
XX KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;
XX KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
XX KW infectious disease; cancer; autoimmune disease; inflammation;
XX KW platelet aggregation; wound healing; clotting.
XX OS Listeria monocytogenes.
XX PN WO200174858-A2.
XX PD 11-OCT-2001.
XX PF 03-APR-2001; 2001WO-US10753.
XX PR 03-APR-2000; 2000US-194215P.
XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PA (GBFB ) GBS BIOTECHNOLOGISCHE FORSCHUNG MBH.
XX PI Krause M, Sechi AS, Gertler FB, Wehland J;
XX DR WPI; 2001-616686/71.
XX PT Modulating cytoskeletal rearrangement to regulate T cell and macrophage
XX PT activation for treating cancer, autoimmune disease, and infectious
XX PT disease, comprises contacting with a Fyb/SLAP complex modulator -
XX PS Example 5; Page 43; 79pp; English.
XX CC The specification describes Fyb/SLAP proteins. Fyb/SLAP proteins are
XX CC ligands for the EVH1 domains of Ena(enabled)/vasodilator-stimulated
XX CC phosphoprotein (VASP) proteins. The specification describes a method for
XX CC modulating cytoskeletal rearrangement in a cell, or T cell response to T
XX CC cell receptor stimulation. The method comprises contacting the cell or T
XX CC cell with a Fyb/SLAP complex modulator sufficient to modulate the
XX CC formation of a complex of an Ena/VASP protein and a Fyb/SLAP protein.
XX CC The method is useful for modulating cytoskeletal rearrangement in a cell
XX CC such as a lymphocyte, preferably a T cell, a macrophage or a cell
XX CC fragment such as a platelet and for modulating T cell response to a
XX CC T cell receptor stimulation. T cell response is increased in a subject
XX CC having or at risk of developing infectious disease or cancer and T cell
XX CC response is inhibited in a subject having or is at risk of developing an
XX CC autoimmune disease or a condition characterized by inflammation. A
XX CC composition comprising a Fyb/SLAP complex inhibitor is useful for
XX CC increasing platelet aggregation for promoting wound healing or
XX CC clotting. The present sequence represents a peptide derived from
XX CC ActA, which is used in the course of the invention.
XX SQ Sequence 14 AA;

Query Match      33.3%; Score 5; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
DB 3 FPPPP 7

RESULT 39
AAB85935
ID AAB85935 standard; peptide; 14 AA.
XX
```

AC AAB85935;
 DT 30-NOV-2001 (first entry)
 XX
 DE 2A11 seed storage protein fragment.
 XX
 KW Napin gene; promoter; Brassica; phenotype; transcription; EA9; 3H11;
 KW 2A11.
 XX
 OS Lycopersicon esculentum.
 XX
 PN US6281410-B1.
 XX
 PD 28-AUG-2001.
 XX
 XX 15-JAN-1999; 99US-0232861.
 XX
 PR 29-APR-1988; 88US-0188361.
 PR 02-NOV-1988; 88US-0267685.
 PR 10-AUG-1993; 93US-0105852.
 PR 07-JUN-1995; 95US-0484941.
 PR 07-MAR-1997; 97US-0812665.
 PR 31-JUL-1986; 86US-0891529.
 PR 26-MAY-1987; 87US-0054369.
 PR 28-JUL-1987; 87US-0078538.
 PR 25-JAN-1988; 87US-0147781.
 PR 15-MAR-1988; 88US-0168190.
 XX
 PA (CALJ) CALGENE LLC.
 XX
 XX Knauf VC, Kridl JC;
 PI
 XX WPI; 2001-564354/63.
 DR
 XX
 PT Obtaining a plant that produces a seed with a modified phenotype or
 PT altering a seed phenotype, comprises transforming a plant cell with a
 PT DNA construct consisting of operably linked components in the direction
 PT of transcription -
 XX
 PS Example 9; Fig 6; 68pp; English.
 XX
 CC The invention provides a method for obtaining a plant which produces
 CC at least one seed having a modified phenotype. The method involves
 CC transforming a host plant cell with a DNA construct which consists of
 CC operably linked components in the direction of transcription, a promoter
 CC region from a Brassica plant gene, a DNA sequence of interest other than
 CC the native coding sequence, and a transcription termination region. The
 CC method is useful for obtaining plants having modified phenotype or for
 CC altering the phenotype of a plant seed or tissue. The DNA constructs are
 CC used in manipulating plant cells to provide for regulated transcription,
 CC such as light inducible transcription, in a plant tissue or plant part of
 CC interest at particular stages of plant growth or in response to external
 CC control. These constructs are also used for modulation of expression of
 CC endogenous products as well as production of exogenous products in the
 CC seed. The present sequence represents an amino acid fragment of the
 CC seed storage protein 2A11.
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 33.3%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 PPQET 13
 Db 8 PPQET 12
 XX
 RESULT 40
 AAR42641
 ID AAR42641 standard; peptide; 15 AA.
 XX
 AC AAR42641;

XX 25-MAR-2003 (updated)
 DT 22-APR-1994 (first entry)
 XX
 DE N-terminal sequence of protein from BCG culture supernatant.
 XX
 KW Tuberculosis; delayed hypersensitivity; antigen; immunogen; vaccine;
 KW T lymphocyte stimulation; BCG.
 XX
 OS Mycobacterium tuberculosis BCG.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4
 FT /label= OTHER
 FT /note= "defined only as modified amino acid"
 FT Modified-site 6
 FT /label= OTHER
 FT /note= "defined only as modified amino acid"
 FT Modified-site 12
 FT /label= OTHER
 FT /note= "defined only as modified amino acid"
 FT Modified-site 14
 FT /label= OTHER
 FT /note= "defined only as modified amino acid"
 XX
 PN WO9319093-A1.
 XX
 PD 30-SEP-1993.
 XX
 PF 17-MAR-1993; 93WO-FR00268.
 XX
 PR 19-MAR-1992; 92FR-0003286.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Marchal G, Romain F;
 XX
 XX WPI; 1993-320686/40.
 DR
 XX
 PT New peptide inducing intense delayed hypersensitivity reaction -
 PT in presence of live, but not dead, Mycobacterium tuberculosis,
 PT useful diagnostically and in therapeutic immunogens
 XX
 PS Claim 2; Page 17; 31pp; French.
 XX
 CC A peptide which can initiate delayed hypersensitivity reactions of
 CC different intensity in the presence of live or dead Mycobacterium
 CC tuberculosis complex bacteria is isolated from supernatant of BCG
 CC cell culture. The N-terminal sequence of the peptide has been
 CC determined.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 15 AA;
 Query Match 33.3%; Score 5; DB 14; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PPPPQ 11
 Db 7 PPPPQ 11
 XX
 RESULT 41
 AAW39038
 ID AAW39038 standard; peptide; 15 AA.
 XX
 AC AAW39038;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:439.
 XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 XX WO9730074-A1.
 XX 21-AUG-1997.
 XX 14-FEB-1997; 97WO-US02298.
 XX 16-FEB-1996; 96US-0602999.
 XX (CYTO-) CYTOGEN CORP.
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 XX Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 XX tyrosine kinase(s) and to stimulate immune response by increasing
 XX production of certain lymphokine(s), e.g. interleukin-1
 XX Claim 22; Page 94; 131pp; English.
 XX The present sequence represents a peptide which resembles a Src homology
 XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 XX binding peptides can be used in the method to identify inhibitors of
 XX their binding to their respective SH3 domains, which could be used to
 XX modulate the pharmacological activity of proteins or polypeptide
 XX containing the SH3 domain. The peptides can also be used to activate
 XX Src or Src-related protein tyrosine kinases, to stimulate the immune
 XX response by increasing the production of certain lymphokines, e.g.
 XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
 XX conjugated molecule to certain cellular compartments containing Src or
 XX Src related proteins.
 XX Sequence 15 AA;
 SQ Query Match 33.3%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PPPPQ 11
 Db 6 PPPPQ 10
 RESULT 42
 AAW39006
 ID AAW39006 standard; peptide; 15 AA.
 XX AAW39006;
 XX 27-MAR-1998 (first entry)
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:405.
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.

XX WO9730074-A1.
 XX 21-AUG-1997.
 XX 14-FEB-1997; 97WO-US02298.
 XX 16-FEB-1996; 96US-0602999.
 XX (CYTO-) CYTOGEN CORP.
 XX (UYNC-) UNIV NORTH CAROLINA.
 XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
 XX Sparks AB, Thorn JM;
 XX WPI; 1997-424972/39.
 XX Src homology region 3 binding peptide - used to activate Src
 XX tyrosine kinase(s) and to stimulate immune response by increasing
 XX production of certain lymphokine(s), e.g. interleukin-1
 XX Claim 22; Page 93; 131pp; English.
 XX The present sequence represents a peptide which resembles a Src homology
 XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
 XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
 XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
 XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
 XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
 XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
 XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
 XX binding peptides can be used in the method to identify inhibitors of
 XX their binding to their respective SH3 domains, which could be used to
 XX modulate the pharmacological activity of proteins or polypeptide
 XX containing the SH3 domain. The peptides can also be used to activate
 XX Src or Src-related protein tyrosine kinases, to stimulate the immune
 XX response by increasing the production of certain lymphokines, e.g.
 XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
 XX conjugated molecule to certain cellular compartments containing Src or
 XX Src related proteins.
 XX Sequence 15 AA;
 SQ Query Match 33.3%; Score 5; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PPPPQ 11
 Db 6 PPPPQ 10
 RESULT 43
 AAW38970
 ID AAW38970 standard; peptide; 15 AA.
 XX AAW38970;
 XX 27-MAR-1998 (first entry)
 XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:367.
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
 KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.
 XX Synthetic.
 XX WO9730074-A1.
 XX 21-AUG-1997.

DR WPI; 1997-424972/39.

XX Src homology region 3 binding peptide - used to activate Src

PT tyrosine kinase(s) and to stimulate immune response by increasing

PT production of certain lymphokine(s), e.g. interleukin-1

XX

PS Claim 22; Page 91; 131pp; English.

XX

CC The present sequence represents a peptide which resembles a Src homology

CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:

CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which

CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3

CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)

CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind

CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3

CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)

CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified

CC binding peptides can be used in the method to identify inhibitors of

CC their binding to their respective SH3 domains, which could be used to

CC modulate the pharmacological activity of proteins or polypeptide

CC containing the SH3 domain. The peptides can also be used to activate

CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.

CC tumour necrosis factor-alpha and interleukin-1, or to deliver a

CC conjugated molecule to certain cellular compartments containing Src or

CC Src related proteins.

XX

SQ Sequence 15 AA;

Query Match 33.3%; Score 5; DB 18; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPPQ 11

DB 6 PPPPQ 10

RESULT 46

AAW38952

ID AAW38952 standard; peptide; 15 AA.

XX

AC AAW38952;

XX

DT 27-MAR-1998 (first entry)

XX

DE Peptide resembling an SH3 domain binding peptide SRQ ID NO:349.

XX

KW Cortactin; SH3 domain; binding peptide; Src homology region 3;

KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;

KW Abl; PLCgamma; p53bp2; Crk; Yes; Grb2.

XX

OS Synthetic.

XX

PN WO9730074-A1.

XX

PD 21-AUG-1997.

XX

PF 14-FEB-1997; 97WO-US02298.

XX

PR 16-FEB-1996; 96US-0602999.

XX

PA (CYTO-) CYTOGEN CORP.

XX

PA (UNIV NORTH CAROLINA.

XX

PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;

PI Sparks AB, Thorn JM;

XX

DR WPI; 1997-424972/39.

XX

PT Src homology region 3 binding peptide - used to activate Src

PT tyrosine kinase(s) and to stimulate immune response by increasing

PT production of certain lymphokine(s), e.g. interleukin-1

XX

PS Claim 22; Page 91; 131pp; English.

CC

CC The present sequence represents a peptide which resembles a Src homology

CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:

CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which

CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3

CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)

CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind

CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3

CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)

CC binding peptides which bind the amino-terminal SH3 domain of Grb2. The purified

CC binding peptides can be used in the method to identify inhibitors of

CC their binding to their respective SH3 domains, which could be used to

CC modulate the pharmacological activity of proteins or polypeptide

CC containing the SH3 domain. The peptides can also be used to activate

CC Src or Src-related protein tyrosine kinases, to stimulate the immune

CC response by increasing the production of certain lymphokines, e.g.

CC tumour necrosis factor-alpha and interleukin-1, or to deliver a

CC conjugated molecule to certain cellular compartments containing Src or

CC Src related proteins.

XX

SQ Sequence 15 AA;

Query Match 33.3%; Score 5; DB 18; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 PPPPQ 11

DB 6 PPPPQ 10

RESULT 47

AAV93014

ID AAV93014 standard; peptide; 15 AA.

XX

AC AAV93014;

XX

DT 08-NOV-2000 (first entry)

XX

DE Transforming growth factor inhibitory peptide P60.

XX

KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;

KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;

KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX

OS Rattus sp.

XX

PN WO200031135-A1.

XX

PD 02-JUN-2000.

XX

PF 23-NOV-1999; 99WO-ES00375.

XX

PR 24-NOV-1998; 98ES-0002465.

XX

PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX

PI Ezquerro Saenz J, Lasarte Sagastibelza JJ, Prieto Valtuena J;

PI Borras Cuesta F;

XX

DR WPI; 2000-411935/35.

XX

PT Peptides that antagonize binding of transforming growth factor beta1,

PT useful for treatment of liver disease, especially cirrhosis, are

PT partial sequences of the factor or its receptors

XX

PS Disclosure; Page 27; 86pp; Spanish.

XX

CC The invention relates to synthetic peptides that antagonise the binding

CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor

CC in vivo which have partial amino acid sequences identical, or similar,

CC with those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133
 CC represent examples of the peptides of the invention. The peptides act
 CC by competitive inhibition of the binding of TGF- β 1 to its receptors,
 CC e.g. they are inhibitors of stimulation of collagen synthesis in liver
 CC cells and inhibitors of synthesis of proteolytic enzymes able to degrade
 CC the extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of
 CC liver disease, specifically cirrhosis.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
 Db 10 PPPPQ 14

RESULT 48
 AAY93015
 ID AAY93015 standard; peptide; 15 AA.

XX AAY93015;

AC AC
 DT 08-NOV-2000 (first entry)
 XX

DE Transforming growth factor inhibitory peptide P61.

XX Hepatotropic; antagonist; transforming growth factor beta1; TGF- β 1;
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.

XX WO200031135-A1.

PN 02-JUN-2000.

PD 23-NOV-1999; 99WO-ES00375.

PF 24-NOV-1998; 98ES-0002465.

PR (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor beta1,
 PT useful for treatment of liver disease, especially cirrhosis, are
 PT partial sequences of the factor or its receptors -

PS Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor
 CC in vivo which have partial amino acid sequences identical or similar,
 CC with those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133
 CC represent examples of the peptides of the invention. The peptides act
 CC by competitive inhibition of the binding of TGF- β 1 to its receptors,
 CC e.g. they are inhibitors of stimulation of collagen synthesis in liver
 CC cells and inhibitors of synthesis of proteolytic enzymes able to degrade
 CC the extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of
 CC liver disease, specifically cirrhosis.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 7 PPPPQ 11
 Db 5 PPPPQ 9

RESULT 49

AAG79166
 ID AAG79166 standard; peptide; 15 AA.

XX AC AAG79166;

XX DT 03-JAN-2002 (first entry)

XX Synthetic antigenic peptide derived from ActA.

XX ActA; Fyb/SLAP protein; EVH1 domain; cytoskeletal rearrangement;
 KW enabled/vasodilator-stimulated phosphoprotein protein; T cell;
 KW T cell receptor; Ena/VASP protein; lymphocyte; macrophage; platelet;
 KW infectious disease; cancer; autoimmune disease; inflammation;
 KW platelet aggregation; wound healing; clotting.

XX Synthetic.

OS Listeria monocytogenes.

XX WO200174858-A2.

XX PD 11-OCT-2001.

XX PF 03-APR-2001; 2001WO-US10753.

XX PR 03-APR-2000; 2000US-194215P.

XX (WASI) MASSACHUSETTS INST TECHNOLOGY.

PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.

XX Krause M, Sechi AS, Gertler FB, Wehland J;

XX WPI; 2001-616686/71.

XX Modulating cytoskeletal rearrangement to regulate T cell and macrophage
 PT activation for treating cancer, autoimmune disease, and infectious
 PT disease, comprises contacting with a Fyb/SLAP complex modulator -

XX Example 1; Page 36; 79pp; English.

XX The present sequence represents an antigenic peptide derived from ActA.
 CC polyclonal antibodies raised against this peptide were used to screen
 CC mouse embryo expression library to isolate Fyb/SLAP clones. Fyb/SLAP
 CC proteins are ligands for the EVH1 domains of
 CC Ena(enabled)/vasodilator-stimulated phosphoprotein (VASP) proteins.
 CC The specification describes a method for modulating cytoskeletal
 CC rearrangement in a cell, or T cell response to T cell receptor
 CC stimulation. The method comprises contacting the cell or T cell with a
 CC Fyb/SLAP complex modulator sufficient to modulate the formation of a
 CC complex of an Ena/VASP protein and a Fyb/SLAP protein. The method is
 CC useful for modulating cytoskeletal rearrangement in a cell such as a
 CC lymphocyte, preferably a T cell, a macrophage or a cell fragment such
 CC as a platelet and for modulating T cell response to a T cell receptor
 CC stimulation. T cell response is increased in a subject having or at
 CC risk of developing infectious disease or cancer and T cell response
 CC is inhibited in a subject having or is at risk of developing an
 CC autoimmune disease or a condition characterized by inflammation. A
 CC composition comprising a Fyb/SLAP complex inhibitor is useful for
 CC increasing platelet aggregation for promoting wound healing or
 CC clotting.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
 DB 4 FPPPP 8

RESULT 50

ABG72860
 ID ABG72860 standard; Peptide; 15 AA.

AC ABG72860;

DT 26-FEB-2003 (first entry)

XX Human ribosomal protein 17.05 N-terminal.

XX Human; ribosomal protein 17.05; malignant tumour; haemopathy;
 KW human immunodeficiency virus; HIV; immunological disease;
 XX inflammation.

OS Homo sapiens.

PN CN1352106-A.

PD 05-JUN-2002.

XX 06-NOV-2000; 2000CN-0127235.

XX 06-NOV-2000; 2000CN-0127235.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-683308/74.

XX New human ribosomal protein 17.05 polypeptide for treating malignant
 PT tumors, hemopathy, human immunodeficiency virus infection,
 PT immunological diseases and various inflammations -

XX Example 5; Page 18 (Disclosure); 33pp; Chinese.

XX The present invention discloses a new kind of polypeptide, human
 CC ribosomal protein 17.05, polynucleotides encoding the polypeptide and a
 CC DNA recombination process to produce the polypeptide. The present
 CC invention also describes applying the polypeptide in treating various
 CC diseases, such as malignant tumors, haemopathy, human immunodeficiency
 CC virus (HIV) infection, immunological diseases and various inflammations.
 CC Also discloses is the antagonist resisting the polypeptide and its
 CC treatment effect, and the application of the polynucleotides encoding
 CC human ribosomal protein 17.05. This is the amino acid sequence of the
 CC novel human ribosomal protein 17.05 N-terminal.

QY 6 FPPPP 10

DB 5 FPPPP 9

Query Match 33.3%; Score 5; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 51

ABP59535
 ID ABP59535 standard; Peptide; 15 AA.

AC ABP59535;

DT 03-MAR-2003 (first entry)

XX Human ribonucleotide protein RBM856.43 N-terminal peptide.

XX

KW Human; ribonucleotide protein RBM856.43; infection; cancer; diabetes;
 KW arrhythmia; hyperthyroidism.

OS Homo sapiens.

PN CN1345752-A.

PD 24-APR-2002.

XX 29-SEP-2000; 2000CN-0125516.

XX 29-SEP-2000; 2000CN-0125516.

XX (SHAN-) SHANGHAI BIOWINDOM GENE DEV INC.

PI Mao Y, Xie Y;

DR WPI; 2002-675774/73.

XX Novel polypeptide-ribonucleotide protein RBM 856.43 for curing several
 PT diseases, such as diabetes, hyperthyroidism, arrhythmic, tumor and
 PT various infections -

XX Example 5; Page 18 (disclosure); 33pp; Chinese.

XX The present invention provides the protein and coding sequences of human
 CC ribonucleotide protein RBM856.43. The sequences are useful in the
 CC treatment of diabetes, hyperthyroidism, arrhythmia, cancer and
 CC infections. The present sequence is the N-terminus of the protein of the
 CC invention.

QY 6 FPPPP 10

DB 7 FPPPP 11

Query Match 33.3%; Score 5; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 52

ABR38294
 ID ABR38294 standard; Peptide; 15 AA.

AC ABR38294;

DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 187P3P2 HLA peptide #1425.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.

OS Homo sapiens.

PN WO200283921-A2.

PD 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 10-APR-2001; 2001US-283112P.

XX 25-APR-2001; 2001US-286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;

CC from the invention.

XX Sequence 15 AA;

Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11

DB 4 PPPPQ 8
 |||||

RESULT 55

ABR38391
 ID ABR38391 standard; Peptide; 15 AA.

AC ABR38391;
 XX

DT 19-MAY-2003 (first entry)
 XX

DE Human cancer-related protein 187P3F2 HLA peptide #1522.
 XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX

OS Homo sapiens.
 XX

PN WO200283921-A2.
 XX

PD 24-OCT-2002.
 XX

PF 10-APR-2002; 2002WO-US11654.
 XX

PR 10-APR-2001; 2001US-282739P.
 PR

PR 10-APR-2001; 2001US-283112P.
 PR

PR 25-APR-2001; 2001US-286630P.
 XX

PA (AGEN-) AGENSYS INC.
 XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX

WPI; 2003-075555/07.
 XX

XX New composition comprising a substance that modulates the structure of
 proteins and polynucleotides, useful for therapeutic, prognostic and
 diagnostic reagents for eliciting cellular or humoral immune response
 in cancer patients -
 XX

Claim 13; Page 618; 1021pp; English.
 XX

XX The present invention relates to novel human cancer-related genes and
 proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 proteins are useful for eliciting a humoral or cellular immune response.
 XX The genes are useful as probes and primers for the amplification and/or
 detection of genes, mRNAs or their fragments, as reagents for the
 diagnosis and/or prognosis of cancer, as coding sequences capable of
 directing the expression of the protein, as tools for modulating or
 inhibiting the expression of genes and/or translation of transcripts, and
 as therapeutic agents. The proteins and peptides are useful as
 therapeutic, prognostic and diagnostic reagents for cancer. The present
 sequence is a human leukocyte antigen (HLA) peptide, used in an example
 from the invention.
 XX

Sequence 15 AA;
 XX

Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11

|||||

Db 11 PPPPQ 15

RESULT 56

ABR38392
 ID ABR38392 standard; Peptide; 15 AA.

AC ABR38392;
 XX

DT 19-MAY-2003 (first entry)
 XX

DE Human cancer-related protein 187P3F2 HLA peptide #1523.
 XX

KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX

OS Homo sapiens.
 XX

PN WO200283921-A2.
 XX

PD 24-OCT-2002.
 XX

PF 10-APR-2002; 2002WO-US11654.
 XX

PR 10-APR-2001; 2001US-282739P.
 PR

PR 10-APR-2001; 2001US-283112P.
 PR

PR 25-APR-2001; 2001US-286630P.
 XX

PA (AGEN-) AGENSYS INC.
 XX

PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX

WPI; 2003-075555/07.
 XX

XX New composition comprising a substance that modulates the structure of
 proteins and polynucleotides, useful for therapeutic, prognostic and
 diagnostic reagents for eliciting cellular or humoral immune response
 in cancer patients -
 XX

Claim 13; Page 618; 1021pp; English.
 XX

XX The present invention relates to novel human cancer-related genes and
 proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 proteins are useful for eliciting a humoral or cellular immune response.
 XX The genes are useful as probes and primers for the amplification and/or
 detection of genes, mRNAs or their fragments, as reagents for the
 diagnosis and/or prognosis of cancer, as coding sequences capable of
 directing the expression of the protein, as tools for modulating or
 inhibiting the expression of genes and/or translation of transcripts, and
 as therapeutic agents. The proteins and peptides are useful as
 therapeutic, prognostic and diagnostic reagents for cancer. The present
 sequence is a human leukocyte antigen (HLA) peptide, used in an example
 from the invention.
 XX

Sequence 15 AA;
 XX

Query Match 33.3%; Score 5; DB 24; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11

|||||

DB 9 PPPPQ 13

RESULT 57

AAW83313
 ID AAW83313 standard; peptide; 17 AA.

XX AC
 XX AAW83313;
 XX

DT 10-FEB-1999 (first entry)
 XX

XX LRP5 protein fragment #1.
 DE
 XX
 KW LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis;
 KW endocytosis; insulin dependent diabetes mellitus; autoimmune disease;
 KW glomerulonephritis; inflammation; viral infection; osteoporosis;
 KW hypercholesterolemia; Alzheimer's disease; low density lipoprotein.
 XX
 OS Homo sapiens.
 XX
 PN WO9846743-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-GB01102.
 XX
 PR 05-JUN-1997; 97US-0048740.
 PR 15-APR-1997; 97US-0043553.
 XX
 PA (MERI) MERCK & CO INC.
 PA (WELL) WELLCOME TRUST LTD.
 XX
 PI Caskey CT, Cox RD, Gerhold D, Hammond H, Hess JW;
 PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y;
 PI Phillips MS, Todd JA, Twells RCJ;
 XX
 DR WPI; 1998-594573/50.
 XX
 PT New isolated LDL-receptor related protein - used to develop products
 PT for treating, e.g. elevated triglyceride levels, diabetes,
 PT autoimmune disorders, inflammation or Alzheimer's disease
 XX
 XX Claim 20; Page 126; 200pp; English.
 PS
 XX The present invention describes LRP5 (low density lipoprotein (LDL)
 CC receptor related protein, previously designated LRP-3). The present
 CC sequence represents a specifically claimed LRP5 protein fragment.
 CC Nucleic acid molecules (NAMS) encoding LRP5 can be used for determining
 CC if an individual is susceptible to insulin dependent diabetes mellitus
 CC (IDDM). The NAMS or proteins can be used for reducing triglyceride levels
 CC in the serum of an individual. Therapies that affect LRP5 may also be
 CC useful in the treatment of autoimmune diseases such as
 CC glomerulonephritis, diseases and disorders involving disruption of
 CC endocytosis and/or antigen presentation, cytokine clearance and/or
 CC inflammation, viral infection, pathogenic bacterial toxin contamination,
 CC elevation of free fatty acids or hypercholesterolemia, type 2 diabetes,
 CC osteoporosis, Alzheimer's disease and cardiovascular disease. Products
 CC from the present invention can also be used for detection, diagnosis and
 CC drug screening.
 XX
 SQ Sequence 17 AA;
 Query Match 33.3%; Score 5; DB 19; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 FPPPP 10
 Db 6 FPPPP 10
 RESULT 58
 AAW05469
 ID AAW05469 standard; Peptide; 18 AA.
 XX
 AC AAW05469;
 XX
 DT 24-FEB-1998 (first entry)
 XX
 DE SH3-binding peptide bSH3020.
 XX
 KW Src-homology region 3 domain; human; mouse; SH3 domain; cell growth;
 KW cellular signalling element; cellular structural element; malignancy;

KW protein identification; functional domain; protein screening;
 KW cellular signal transduction process; binding peptide.
 XX Synthetic.
 XX WO9631625-A1.
 XX 10-OCT-1996.
 XX 04-APR-1996; 96WO-US04454.
 XX 03-APR-1996; 96US-0630915.
 PR 07-APR-1995; 95US-0417872.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UVNC-) UNIV NORTH CAROLINA.
 XX
 PI Fowlkes DM, Hoffman N, Kay BK, McConnell SJ, Sparks AB;
 XX
 DR WPI; 1996-465045/46.
 XX
 PT Identifying polypeptide(s) having specific functional domain (esp.
 PT SH3 domain) - comprises detecting selective binding to recognition
 PT unit, regardless of sequence homology
 XX
 PS Example; Fig 12b; 174pp; English.
 XX
 CC AAW05445-W05492 represent Src-homology region 3 (SH2) domain binding
 CC peptides. These sequences were used as parts of multivalent recognition
 CC unit complexes used in the method of the invention. The method of the
 CC invention is for identifying polypeptides containing functional domains
 CC of interest (especially SH3 domains). It comprises contacting a
 CC multivalent recognition unit (RU) complex with a number of peptides and
 CC identifying polypeptides having a selective binding affinity for the RU
 CC complex. The method is based on functional similarities and does not
 CC rely on sequence similarities. Prior methods only gave limited success
 CC for identifying proteins containing an SH3 domain due to the minimal
 CC sequence homology among known SH3 proteins. Multivalent RU complexes are
 CC particularly suited to screening for polypeptides containing functional
 CC domains that are similar to, but not identical in sequence to, the
 CC original target functional domain. The new method enables proteins
 CC having a common function to be identified. Identification of novel SH3
 CC proteins will be useful for a better understanding of cell growth,
 CC malignancy, signal transduction processes, etc. New candidate drugs can
 CC be identified, and their specificities (e.g. pharmacological activities)
 CC can be assessed using the method of the invention.
 XX
 SQ Sequence 18 AA;
 Query Match 33.3%; Score 5; DB 17; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 FPPPP 10
 Db 10 FPPPP 14
 RESULT 59
 AAW37677
 ID AAW37677 standard; Peptide; 18 AA.
 XX
 AC AAW37677;
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE PPPPY motif containing peptide bSH3020 used to bind WW domains.
 XX
 KW Peptide recognition unit; WW domain; cell signalling; growth regulation;
 KW cytoskeleton organisation; targeted drug screening; modulator;
 KW WW domain interaction; YAP protein; dystrophin.
 XX
 OS Synthetic.

```

XX WO9737223-A1.
XX
XX PD 09-OCT-1997.
XX
XX PF 03-APR-1997; 97WO-US05547.
XX
XX PR 03-APR-1996; 96US-0630916.
XX
XX PA (CYTO-) CYTOGEN CORP.
XX (UYNC-) UNIV NORTH CAROLINA.
XX
XX PI Fowlkes DM, Kay BK, Firozzi G;
XX
XX DR WPI; 1997-503234/46.
XX
XX PT Identifying cell signalling and growth regulatory polypeptides by
XX reaction with multivalent recognition complex - polypeptides are
XX useful in targetted drug selection
XX
XX PS Example 6.3; Fig 7; 220pp; English.
XX
XX CC Peptides AAW37653-77 contain PPPY-like motifs. The PPPY motif is
XX found in the proline rich regions of WBP-1 and WBP-2 proteins. Peptides
XX containing this residue have been shown to bind the YAP WW domain, but
XX not the WW domain from dystrophin or to a panel of SH3 domains. Peptides
XX AAW37653-77 were biotinylated and complexed with alkaline streptavidin,
XX and used in a cross affinity mapping experiment. They were tested for
XX their ability to bind to the 12 individual novel WW domains of WWP1
XX (AAW36794), WWP2 (AAW36795), WWP3 (AAW37696) and WWP4 (AAW36797), which
XX were expressed as glutathione-S-transferase expression proteins. The
XX present peptide, derived from a vinculin protein, does not bind to
XX WW domains of the novel proteins. The WW domain is a small functional
XX domain. Its name is derived from the observation that two tryptophan
XX residues, one in the amino terminal portion of the WW domain and one in
XX the carboxyl terminal portion, are conserved. Most proteins containing
XX WW domains have a function involving cell signalling and growth
XX regulation or the organisation of the cytoskeleton. Polypeptides
XX containing a WW domain are identified by treating a multivalent
XX recognition unit complex that has selective binding affinity for a WW
XX domain, with many polypeptides and identifying those with selective
XX affinity for the complex. Proteins containing WW domains are used for
XX targeted drug screening, i.e. to identify potential modulators of
XX specific WW domain interactions.
XX
XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 18; Length 18;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
DB 10 FPPPP 14

RESULT 60
AAW38909
ID AAW38909 standard; peptide; 18 AA.
XX
XX AC AAW38909;
XX
XX DT 27-MAR-1998 (first entry)
XX
XX DE Peptide resembling an SH3 domain binding peptide SEQ ID NO:305.
XX
XX KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
XX tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
XX Ah1; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX OS Synthetic.
XX
XX PN WO9730674-A1.

```

```

XX
XX PD 21-AUG-1997.
XX
XX PF 14-FEB-1997; 97WO-US02298.
XX
XX PR 16-FEB-1996; 96US-0602999.
XX
XX PA (CYTO-) CYTOGEN CORP.
XX (UYNC-) UNIV NORTH CAROLINA.
XX
XX PI Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JB;
XX Sparks AB, Thorn JM;
XX
XX DR WPI; 1997-424972/39.
XX
XX PT Src homology region 3 binding peptide - used to activate Src
XX tyrosine kinase(s) and to stimulate immune response by increasing
XX production of certain lymphokine(s), e.g. interleukin-1
XX
XX PS Claim 22; Page 90; 131pp; English.
XX
XX CC The present sequence represents a peptide which resembles a Src homology
XX region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
XX (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
XX bind the middle SH3 domain of Nck; (c) peptides which bind the SH3
XX domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)
XX peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind
XX the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3
XX domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)
XX peptides which bind the amino-terminal SH3 domain of Grb2. The purified
XX binding peptides can be used in the method to identify inhibitors of
XX their binding to their respective SH3 domains, which could be used to
XX modulate the pharmacological activity of proteins or polypeptide
XX containing the SH3 domain. The peptides can also be used to activate
XX Src or Src-related protein tyrosine kinases, to stimulate the immune
XX response by increasing the production of certain lymphokines, e.g.
XX tumour necrosis factor-alpha and interleukin-1, or to deliver a
XX conjugated molecule to certain cellular compartments containing Src or
XX Src related proteins.
XX
XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 18; Length 18;
Best Local Similarity 100.0%; Pred.No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
DB 7 FPPPP 11

RESULT 61
AAW47567
ID AAW47567 standard; peptide; 18 AA.
XX
XX AC AAW47567;
XX
XX DT 03-JUL-1998 (first entry)
XX
XX DE Exendin agonist (18).
XX
XX KW Exendin agonist; gastric motility; gastric emptying; treatment;
XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX obesity; Gila monster venom.
XX
XX OS Synthetic.
XX
XX PF Key Location/Qualifiers
XX Modified-site 18
XX /note= "amidated"
XX
XX PN WO9805351-A1.

```

```

XX PD 12-FEB-1998.
XX PF
XX PR 08-AUG-1997; 97WO-US14199.
XX PP
XX PR 08-AUG-1996; 96US-0694954.
XX PA
XX PI (AMYL-) AMYLIN PHARM INC.
XX PI Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX DR
XX PT Regulating gastrointestinal motility using extendins or their
XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX PT impaired glucose tolerance etc., also in diagnostic investigations
XX PS
XX PS Example 21; Fig 8; 70pp; English.
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm
XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX SQ Sequence 18 AA;
XX Query Match 33.3%; Score 5; DB 19; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 6 FPPPP 10
XX DB |||||
XX 13 FPPPP 17
XX
XX RESULT 62
XX AAW47569
XX ID AAW47569 standard; peptide; 18 AA.
XX AC
XX AC AAW47569;
XX DT 03-JUL-1998 (first entry)
XX DE
XX DE Extendin agonist (20).
XX KW
XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX KW obesity; Gila monster venom.
XX OS
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT Modified-site 11
XX FT /note= "tert-butylglycine"
XX FT Modified-site 18
XX FT /note= "amidated"
XX XX
XX XX WO9805351-A1.
XX XX 12-FEB-1998.
XX XX
XX XX 08-AUG-1997; 97WO-US14199.
XX XX
XX XX 08-AUG-1996; 96US-0694954.
XX XX
XX XX (AMYL-) AMYLIN PHARM INC.

```

```

PF 08-AUG-1997; 97WO-US14199.
XX
XX PR 08-AUG-1996; 96US-0694954.
XX
XX PA (AMYL-) AMYLIN PHARM INC.
XX
XX PI Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX PT Regulating gastrointestinal motility using extendins or their
XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX PT impaired glucose tolerance etc., also in diagnostic investigations
XX PS
XX PS Example 23; Fig 8; 70pp; English.
XX CC The present sequence is an extendin agonist, which reduces gastric
XX CC motility and delays gastric emptying. It can be used to treat spasm
XX CC (where associated with acute diverticulitis or disorders of the
XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX CC extendin agonist is administered to prevent stomach contents passing
XX CC into the intestines, then the stomach pumped) and obesity. It can
XX CC also be administered to subjects undergoing gastrointestinal
XX CC diagnostic investigation, particularly radiological or by magnetic
XX CC resonance imaging.
XX CC Extendins, components of Gila monster venom, have some sequence
XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
XX CC and have been suggested (US5424286) for treatment of diabetes and
XX CC prevention of hyperglycaemia.
XX SQ Sequence 18 AA;
XX Query Match 33.3%; Score 5; DB 19; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 6 FPPPP 10
XX DB |||||
XX 13 FPPPP 17
XX
XX RESULT 63
XX AAW47571
XX ID AAW47571 standard; peptide; 18 AA.
XX AC
XX AC AAW47571;
XX DT 03-JUL-1998 (first entry)
XX DE
XX DE Extendin agonist (22).
XX KW
XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX KW obesity; Gila monster venom.
XX OS
XX OS Synthetic.
XX FH
XX FH Key Location/Qualifiers
XX FT Modified-site 18
XX FT /note= "amidated"
XX XX
XX XX WO9805351-A1.
XX XX 12-FEB-1998.
XX XX
XX XX 08-AUG-1997; 97WO-US14199.
XX XX
XX XX 08-AUG-1996; 96US-0694954.
XX XX
XX XX (AMYL-) AMYLIN PHARM INC.

```

```

XX
PI PI Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX DR WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
PT impaired glucose tolerance etc., also in diagnostic investigations
XX Example 25; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
CC motility and delays gastric emptying. It can be used to treat spasm
CC (where associated with acute diverticulitis or disorders of the
CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
CC and hyperglycaemia (particularly associated with type 2 diabetes),
CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
CC extendin agonist is administered to prevent stomach contents passing
CC into the intestines, then the stomach pumped) and obesity. It can
CC also be administered to subjects undergoing gastrointestinal
CC diagnostic investigation, particularly radiological or by magnetic
CC resonance imaging.
CC Extendins, components of Gila monster venom, have some sequence
CC similarity to glucagon-like peptides (GLP). They are GLP agonists
CC and have been suggested (US5424286) for treatment of diabetes and
CC prevention of hyperglycaemia.
XX Sequence 18 AA;
XX
Query Match 33.3%; Score 5; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
DB 13 FPPPP 17

RESULT 64
AAW47577
ID AAW47577 standard; peptide; 18 AA.
AC AAW47577;
XX
XX 03-JUL-1998 (first entry)
DE Extendin agonist (28).
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment;
KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
KW obesity; Gila monster venom.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 14 /label= Hyp
FT Modified-site 15 /label= Hyp
FT Modified-site 16 /label= Hyp
FT Modified-site 17 /label= Hyp
FT Modified-site 18 /label= Hyp
FT Modified-site 18 /note= "amidated"
XX
XX WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AWYL-) AMYLIN PHARM INC.
XX

```

```

PR 08-AUG-1996; 96US-0694954.
XX
XX (AWYL-) AMYLIN PHARM INC.
XX
XX Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX WPI; 1998-145351/13.
XX
XX Regulating gastrointestinal motility using extendins or their
PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
PT impaired glucose tolerance etc., also in diagnostic investigations
XX Example 31; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
CC motility and delays gastric emptying. It can be used to treat spasm
CC (where associated with acute diverticulitis or disorders of the
CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
CC and hyperglycaemia (particularly associated with type 2 diabetes),
CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
CC extendin agonist is administered to prevent stomach contents passing
CC into the intestines, then the stomach pumped) and obesity. It can
CC also be administered to subjects undergoing gastrointestinal
CC diagnostic investigation, particularly radiological or by magnetic
CC resonance imaging.
CC Extendins, components of Gila monster venom, have some sequence
CC similarity to glucagon-like peptides (GLP). They are GLP agonists
CC and have been suggested (US5424286) for treatment of diabetes and
CC prevention of hyperglycaemia.
XX Sequence 18 AA;
XX
Query Match 33.3%; Score 5; DB 19; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
DB 13 FPPPP 17

RESULT 65
AAW47562
ID AAW47562 standard; peptide; 18 AA.
XX
XX AAW47562;
XX
XX 03-JUL-1998 (first entry)
DE Extendin agonist (13).
XX
XX Extendin agonist; gastric motility; gastric emptying; treatment;
KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
KW obesity; Gila monster venom.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 8 /note= "pentylglycine"
FT Modified-site 18 /note= "amidated"
XX
XX WO9805351-A1.
XX
XX 12-FEB-1998.
XX
XX 08-AUG-1997; 97WO-US14199.
XX
XX 08-AUG-1996; 96US-0694954.
XX
XX (AWYL-) AMYLIN PHARM INC.
XX

```

XX Pl Beeley NRA, Gedulin B, Prickett KS, Young AA;
 XX DR WPI; 1998-145351/13.
 XX PT Regulating gastrointestinal motility using extendins or their
 XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
 XX PT impaired glucose tolerance etc., also in diagnostic investigations
 XX PS Example 16; Fig 8; 70pp; English.
 XX CC The present sequence is an extendin agonist, which reduces gastric
 XX CC motility and delays gastric emptying. It can be used to treat spasm
 XX CC (where associated with acute diverticulitis or disorders of the
 XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
 XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
 XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
 XX CC extendin agonist is administered to prevent stomach contents passing
 XX CC into the intestines, then the stomach pumped) and obesity. It can
 XX CC also be administered to subjects undergoing gastrointestinal
 XX CC diagnostic investigation, particularly radiological or by magnetic
 XX CC resonance imaging.
 XX CC Extendins, components of Gila monster venom, have some sequence
 XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
 XX CC and have been suggested (US5424286) for treatment of diabetes and
 XX CC prevention of hyperglycaemia.
 XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
 Db 13 FPPPP 17

RESULT 66

AAW47564
 ID AAW47564 standard; peptide; 18 AA.

AC AAW47564;

DT 03-JUL-1998 (first entry)

DE Extendin agonist (15).

XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
 XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
 XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
 XX KW obesity; Gila monster venom.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 9 /note= "pentylglycine"

FT Modified-site 18 /note= "amidated"

FT WO9805351-A1.

PN 12-FEB-1998.

PD 08-AUG-1997; 97WO-US14199.

XX 08-AUG-1996; 96US-0694954.

PA (AMYL-) AMYLIN PHARM INC.

PI Beeley NRA, Gedulin B, Prickett KS, Young AA;

XX

DR WPI; 1998-145351/13.
 XX PT Regulating gastrointestinal motility using extendins or their
 XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
 XX PT impaired glucose tolerance etc., also in diagnostic investigations
 XX PS Example 18; Fig 8; 70pp; English.
 XX CC The present sequence is an extendin agonist, which reduces gastric
 XX CC motility and delays gastric emptying. It can be used to treat spasm
 XX CC (where associated with acute diverticulitis or disorders of the
 XX CC biliary tract or sphincter of Oddi), postprandial dumping syndrome
 XX CC and hyperglycaemia (particularly associated with type 2 diabetes),
 XX CC type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
 XX CC extendin agonist is administered to prevent stomach contents passing
 XX CC into the intestines, then the stomach pumped) and obesity. It can
 XX CC also be administered to subjects undergoing gastrointestinal
 XX CC diagnostic investigation, particularly radiological or by magnetic
 XX CC resonance imaging.
 XX CC Extendins, components of Gila monster venom, have some sequence
 XX CC similarity to glucagon-like peptides (GLP). They are GLP agonists
 XX CC and have been suggested (US5424286) for treatment of diabetes and
 XX CC prevention of hyperglycaemia.
 XX SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
 Db 13 FPPPP 17

RESULT 67

AAW47550

ID AAW47550 standard; peptide; 18 AA.

AC AAW47550;

DT 03-JUL-1998 (first entry)

DE Extendin agonist (1).

XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
 XX KW spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
 XX KW type 1 diabetes; impaired glucose tolerance; toxin ingestion;
 XX KW obesity; Gila monster venom.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 18 /note= "amidated"

PN WO9805351-A1.

XX 12-FEB-1998.

XX 08-AUG-1997; 97WO-US14199.

XX 08-AUG-1996; 96US-0694954.

XX (AMYL-) AMYLIN PHARM INC.

XX Beeley NRA, Gedulin B, Prickett KS, Young AA;

XX WPI; 1998-145351/13.

XX PT Regulating gastrointestinal motility using extendins or their
 XX PT agonists - for treating spasm, diabetic postprandial hyperglycaemia,
 XX PT impaired glucose tolerance etc., also in diagnostic investigations


```

XX Example 4; Fig 8; 70pp; English.
XX
XX The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm
XX (where associated with acute diverticulitis or disorders of the
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX and hyperglycaemia (particularly associated with type 2 diabetes),
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX extendin agonist is administered to prevent stomach contents passing
XX into the intestines, then the stomach pumped) and obesity. It can
XX also be administered to subjects undergoing gastrointestinal
XX diagnostic investigation, particularly radiological or by magnetic
XX resonance imaging.
XX Extendins, components of Gila monster venom, have some sequence
XX similarity to glucagon-like peptides (GLP). They are GLP agonists
XX and have been suggested (US5424286) for treatment of diabetes and
XX prevention of hyperglycaemia.
XX Sequence 18 AA;
XX
XX Query Match 33.3%; Score 5; DB 19; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 FPPPP 10
XX Db 13 FPPPP 17
XX
XX RESULT 68
XX AAW47552
XX ID AAW47552 standard; peptide; 18 AA.
XX AC AAW47552;
XX
XX DT 03-JUL-1998 (first entry)
XX DE Extendin agonist (3).
XX
XX KW Extendin agonist; gastric motility; gastric emptying; treatment;
XX spasm; postprandial dumping syndrome; postprandial hyperglycaemia;
XX type 1 diabetes; impaired glucose tolerance; toxin ingestion;
XX obesity; Gila monster venom.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 18
XX FT /note= "amidated"
XX
XX PN WO9805351-A1.
XX
XX PD 12-FEB-1998.
XX
XX PF 08-AUG-1997; 97WO-US14199.
XX
XX PR 08-AUG-1996; 96US-0694954.
XX
XX PA (AMYL-) AMYLIN PHARM INC.
XX
XX PI Beeley NRA, Gedulin B, Prickett KS, Young AA;
XX DR WPI; 1998-145351/13.
XX
XX PT Regulating gastrointestinal motility using extendins or their
XX agonists - for treating spasm, diabetic postprandial hyperglycaemia,
XX impaired glucose tolerance etc., also in diagnostic investigations
XX
XX PS Example 6; Fig 8; 70pp; English.
XX
XX CC The present sequence is an extendin agonist, which reduces gastric
XX motility and delays gastric emptying. It can be used to treat spasm

```

```

XX (where associated with acute diverticulitis or disorders of the
XX biliary tract or sphincter of Oddi), postprandial dumping syndrome
XX and hyperglycaemia (particularly associated with type 2 diabetes),
XX type 1 diabetes, impaired glucose tolerance, toxin ingestion (an
XX extendin agonist is administered to prevent stomach contents passing
XX into the intestines, then the stomach pumped) and obesity. It can
XX also be administered to subjects undergoing gastrointestinal
XX diagnostic investigation, particularly radiological or by magnetic
XX resonance imaging.
XX Extendins, components of Gila monster venom, have some sequence
XX similarity to glucagon-like peptides (GLP). They are GLP agonists
XX and have been suggested (US5424286) for treatment of diabetes and
XX prevention of hyperglycaemia.
XX Sequence 18 AA;
XX
XX Query Match 33.3%; Score 5; DB 19; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 FPPPP 10
XX Db 13 FPPPP 17
XX
XX RESULT 69
XX AAY03721
XX ID AAY03721 standard; peptide; 18 AA.
XX AC AAY03721;
XX
XX DT 08-JUN-1999 (first entry)
XX DE Extendin agonist compound 1.
XX
XX KW Extendin; agonist; diabetes; disorder; plasma glucose; gastric;
XX diagnostic; gastro-intestinal; radiological.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 18
XX FT /note= "C-terminal amide"
XX
XX PN WO9907404-A1.
XX
XX PD 18-FEB-1999.
XX
XX PF 06-AUG-1998; 98WO-US16387.
XX
XX PR 08-AUG-1997; 97US-0055404.
XX
XX PA (AMYL-) AMYLIN PHARM INC.
XX
XX PI Beeley NRA, Prickett KS;
XX
XX DR WPI; 1999-180403/15.
XX
XX PT New extendin agonists - useful in the treatment of Type I and II
XX diabetes
XX
XX PS Claim 17; Fig 1A-B; 70pp; English.
XX
XX CC The invention relates to extendin agonists which slow gastric emptying
XX and lower plasma glucose levels. The extendin agonists are used to treat
XX Type I and II diabetes, disorders which would be benefited by agents
XX which lower plasma glucose levels, and disorders which would be benefited
XX by agents useful in delaying and/or slowing gastric emptying. Delayed
XX gastric emptying is a useful diagnostic aid in gastro-intestinal
XX radiological examinations. Sequences AAY03721-51 represent specifically
XX claimed examples of the extendin agonist compounds of the invention.
XX (Also see AAY03720 for extendin generic peptide formula and description).
XX

```

```

SQ Sequence 18 AA;
Query Match 33.3%; Score 5; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 13 FPPPP 17

RESULT 70
AAY03723
ID AAY03723 standard; peptide; 18 AA.
XX
AC AAY03723;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extensin agonist compound 3.
XX
KW Extensin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 18 /note= "C-terminal amide"
XX
PN WO9907404-A1.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-US16387.
XX
PR 08-AUG-1997; 97US-0055404.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-180403/15.
XX
PT New extensin agonists - useful in the treatment of Type I and II
PT diabetes
XX
PS Claim 17; Fig 1A-B; 70pp; English.
XX
CC The invention relates to extensin agonists which slow gastric emptying
CC and lower plasma glucose levels. The extensin agonists are used to treat
CC Type I and II diabetes, disorders which would be benefited by agents
CC which lower plasma glucose levels, and disorders which would be benefited
CC by agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the extensin agonist compounds of the invention.
XX (Also see AAY03720 for extensin generic peptide formula and description).
XX
SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 13 FPPPP 17

RESULT 71
AAY03733
ID AAY03733 standard; peptide; 18 AA.

```

```

XX AAY03733;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extensin agonist compound 13.
XX
KW Extensin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 8 /note= "pentylglycine"
FT Modified-site 18 /note= "C-terminal amide"
XX
PN WO9907404-A1.
XX
PD 18-FEB-1999.
XX
PF 06-AUG-1998; 98WO-US16387.
XX
PR 08-AUG-1997; 97US-0055404.
XX
PA (AMYL-) AMYLIN PHARM INC.
XX
PI Beeley NRA, Prickett KS;
XX
DR WPI; 1999-180403/15.
XX
PT New extensin agonists - useful in the treatment of Type I and II
PT diabetes
XX
PS Claim 17; Fig 1A-B; 70pp; English.
XX
CC The invention relates to extensin agonists which slow gastric emptying
CC and lower plasma glucose levels. The extensin agonists are used to treat
CC Type I and II diabetes, disorders which would be benefited by agents
CC which lower plasma glucose levels, and disorders which would be benefited
CC by agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the extensin agonist compounds of the invention.
XX (Also see AAY03720 for extensin generic peptide formula and description).
XX
SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 13 FPPPP 17

RESULT 72
AAY03735
ID AAY03735 standard; peptide; 18 AA.
XX
AC AAY03735;
XX
DT 08-JUN-1999 (first entry)
XX
DE Extensin agonist compound 15.
XX
KW Extensin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.
XX

```


CC and lower plasma glucose levels. The exendin agonists are used to treat
CC Type I and II diabetes, disorders which would be benefited by agents
CC which lower plasma glucose levels, and disorders which would be benefited
CC by agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the exendin agonist compounds of the invention.
CC (Also see AAY03720 for exendin generic peptide formula and description).
XX
SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
|
|
|
|
|
Db 13 FPPPP 17

RESULT 75
AAY03742
ID AAY03742 standard; peptide; 18 AA.
XX
AC AAY03742;
XX
DT 08-JUN-1999 (first entry)
XX
DE Exendin agonist compound 22.
XX
KW Exendin; agonist; diabetes; disorder; plasma glucose; gastric;
KW diagnostic; gastro-intestinal; radiological.
XX
OS Synthetic.

XX
XX Key Location/Qualifiers
PH 18
FT Modified-site /note= "C-terminal amide"
FT

XX WO9907404-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16387.

XX 08-AUG-1997; 97US-0055404.

XX (AMYL-) AMYLIN PHARM INC.

XX Beeley NRA, Prickett KS;

XX WPI; 1999-180403/15.

XX New exendin agonists - useful in the treatment of Type I and II
XX diabetes

XX Claim 17; Fig 1D-E; 70pp; English.

XX The invention relates to exendin agonists which slow gastric emptying
CC and lower plasma glucose levels. The exendin agonists are used to treat
CC Type I and II diabetes, disorders which would be benefited by agents
CC which lower plasma glucose levels, and disorders which would be benefited
CC by agents useful in delaying and/or slowing gastric emptying. Delayed
CC gastric emptying is a useful diagnostic aid in gastro-intestinal
CC radiological examinations. Sequences AAY03721-51 represent specifically
CC claimed examples of the exendin agonist compounds of the invention.
CC (Also see AAY03720 for exendin generic peptide formula and description).
XX

SQ Sequence 18 AA;

Query Match 33.3%; Score 5; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
|
|
|
|
|
Db 13 FPPPP 17

Search completed: November 25, 2003, 18:15:48
Job time : 49.5904 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 29.8404 Seconds
(without alignments)
92.715 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKFPPTPOETVT 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/1/pubpaa/PCT05_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	15	US-10-281-652-7
2	5	33.3	5	9	US-09-825-144-15
3	5	33.3	5	9	US-09-823-240-3
4	5	33.3	5	12	US-10-192-381-47
5	5	33.3	7	15	US-10-281-652-14
6	5	33.3	9	9	US-09-825-144-10
7	5	33.3	9	9	US-09-823-240-7
8	5	33.3	10	9	US-09-823-240-1
9	5	33.3	14	9	US-09-825-144-12
10	5	33.3	15	9	US-09-825-144-1
11	5	33.3	15	12	US-10-161-791-339
12	5	33.3	15	12	US-10-161-791-349
13	5	33.3	15	12	US-10-161-791-367
14	5	33.3	15	12	US-10-161-791-373
15	5	33.3	15	12	US-10-161-791-405
16	16	33.3	5	15	US-10-161-791-439
17	17	33.3	5	12	US-10-331-907-403
18	18	33.3	5	9	US-09-879-957-165
19	19	33.3	18	11	US-09-949-510-4
20	5	33.3	18	12	US-10-161-791-305
21	5	33.3	18	15	US-10-185-050-109
22	5	33.3	20	9	US-09-735-450-4
23	5	33.3	20	12	US-10-161-791-368
24	4	26.7	4	12	US-10-352-704-21
25	4	26.7	4	12	US-10-376-121A-134
26	4	26.7	4	12	US-10-376-121A-135
27	4	26.7	4	15	US-10-222-455-33
28	4	26.7	5	8	US-08-424-550B-716
29	4	26.7	5	9	US-09-823-240-4
30	4	26.7	5	9	US-09-785-921A-15
31	4	26.7	5	12	US-10-315-964A-422
32	4	26.7	5	12	US-10-317-251A-422
33	4	26.7	5	12	US-10-317-252A-422
34	4	26.7	5	12	US-10-352-704-23
35	4	26.7	5	12	US-10-376-121A-120
36	4	26.7	5	14	US-10-014-485A-72
37	4	26.7	5	15	US-10-174-105A-72
38	4	26.7	5	15	US-10-185-050-3
39	4	26.7	5	15	US-10-096-986-9
40	4	26.7	5	15	US-10-281-652-12
41	4	26.7	6	9	US-09-803-136-21
42	4	26.7	6	12	US-10-352-704-25
43	4	26.7	6	14	US-10-078-547-3
44	4	26.7	6	14	US-10-078-547-13
45	4	26.7	6	14	US-10-078-547-14
46	4	26.7	6	14	US-10-078-547-19
47	4	26.7	6	14	US-10-078-547-21
48	4	26.7	6	15	US-10-192-257-5
49	4	26.7	7	9	US-09-825-144-8
50	4	26.7	7	11	US-09-281-495-17
51	4	26.7	7	12	US-10-032-214-312
52	4	26.7	7	12	US-09-261-894-91
53	4	26.7	7	15	US-10-192-257-6
54	4	26.7	7	15	US-10-314-057-8
55	4	26.7	7	15	US-10-235-236-3
56	4	26.7	7	15	US-10-104-607B-3
57	4	26.7	8	10	US-09-843-245-1
58	4	26.7	8	12	US-10-022-066-378
59	4	26.7	8	12	US-10-376-121A-96
60	4	26.7	8	12	US-10-376-121A-99
61	4	26.7	8	12	US-10-376-121A-196
62	4	26.7	8	12	US-10-376-121A-197
63	4	26.7	8	12	US-10-376-121A-198
64	4	26.7	8	12	US-10-376-121A-199
65	4	26.7	8	12	US-10-376-121A-210
66	4	26.7	8	12	US-10-376-121A-211
67	4	26.7	8	12	US-10-376-121A-213
68	4	26.7	8	12	US-10-376-121A-215
69	4	26.7	8	12	US-10-376-121A-216
70	4	26.7	8	12	US-10-376-121A-217
71	4	26.7	8	15	US-10-226-007-452
72	4	26.7	8	15	US-10-226-007-465
73	4	26.7	8	15	US-10-226-007-478
74	4	26.7	8	15	US-10-226-007-491
75	4	26.7	8	15	US-10-226-007-738
76	4	26.7	8	15	US-10-226-007-751
77	4	26.7	8	15	US-10-226-007-764
78	4	26.7	8	15	US-10-226-007-777
79	4	26.7	8	15	US-10-226-007-881
80	4	26.7	8	15	US-10-226-007-894
81	4	26.7	8	15	US-10-226-007-907
82	4	26.7	8	15	US-10-226-007-920
83	4	26.7	8	15	US-10-226-007-1024
84	4	26.7	8	15	US-10-226-007-1037
85	4	26.7	8	15	US-10-226-007-1050
86	4	26.7	8	15	US-10-226-007-1063
87	4	26.7	8	15	US-10-226-007-1167
88	4	26.7	8	15	US-10-226-007-1180

Sequence 439, App
Sequence 403, App
Sequence 165, App
Sequence 4, Appli
Sequence 305, App
Sequence 109, App
Sequence 4, Appli
Sequence 368, App
Sequence 21, Appl
Sequence 134, App
Sequence 135, App
Sequence 33, Appl
Sequence 716, App
Sequence 4, Appli
Sequence 15, Appl
Sequence 422, App
Sequence 422, App
Sequence 422, App
Sequence 23, Appl
Sequence 120, App
Sequence 72, Appl
Sequence 72, Appl
Sequence 3, Appli
Sequence 9, Appli
Sequence 12, Appl
Sequence 21, Appl
Sequence 25, Appl
Sequence 3, Appli
Sequence 13, Appl
Sequence 14, Appl
Sequence 19, Appl
Sequence 21, Appl
Sequence 5, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 378, App
Sequence 96, Appl
Sequence 99, Appl
Sequence 196, App
Sequence 197, App
Sequence 198, App
Sequence 199, App
Sequence 210, App
Sequence 211, App
Sequence 213, App
Sequence 215, App
Sequence 216, App
Sequence 217, App
Sequence 452, App
Sequence 465, App
Sequence 468, App
Sequence 491, App
Sequence 738, App
Sequence 751, App
Sequence 764, App
Sequence 777, App
Sequence 881, App
Sequence 894, App
Sequence 907, App
Sequence 920, App
Sequence 1024, App
Sequence 1037, App
Sequence 1050, App
Sequence 1063, App
Sequence 1167, App
Sequence 1180, App

Sequence 1193, Ap
Sequence 1206, Ap
Sequence 1492, Ap
Sequence 1493, Ap
Sequence 1495, Ap
Sequence 8, Appli
Sequence 11, Appl
Sequence 76, Appl
Sequence 96, Appl
Sequence 97, Appl
Sequence 156, App
Sequence 157, App

89	4	26.7	8	15	US-10-226-007-1193
90	4	26.7	8	15	US-10-226-007-1206
91	4	26.7	8	15	US-10-226-007-1492
92	4	26.7	8	15	US-10-226-007-1493
93	4	26.7	8	15	US-10-226-007-1495
94	4	26.7	9	9	US-09-823-240-8
95	4	26.7	9	9	US-09-835-232-11
96	4	26.7	9	11	US-09-938-864-76
97	4	26.7	9	11	US-09-938-864-96
98	4	26.7	9	11	US-09-938-864-97
99	4	26.7	9	11	US-09-938-864-156
100	4	26.7	9	11	US-09-938-864-157

ALIGNMENTS

RESULT 1
US-10-281-652-7
; Sequence 7, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265,00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-7

Query Match 100.0%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VLEMKFPPPPQQTVT	15
Db	1	VLEMKFPPPPQQTVT	15

RESULT 2
US-09-825-144-15
; Sequence 15, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 5.

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-15

Query Match 33.3%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy	6	FPFPP 10
Db	1	FPFPP 5

RESULT 3

US-09-823-240-3
; Sequence 3, Application US/09823240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jorgen Wehland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-823-240-3

Query Match 33.3%; Score 5; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy	6	FPFPP 10
Db	1	FPFPP 5

RESULT 4

US-10-192-381-47
; Sequence 47, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
; TITLE OF INVENTION: AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18

```
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: optimal ligand
US-10-192-381-47

Query Match      33.3%; Score 5; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FPPPP 10
        |||||
Db       1 FPPPP 5

RESULT 5
US-10-281-652-14
; Sequence 14, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1993-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-14

Query Match      33.3%; Score 5; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPPQ 11
        |||||
Db       2 PPPPQ 6

RESULT 6
US-09-825-144-10
; Sequence 10, Application US/09825144
; Patent No. US20020037286A1
; GENERAL INFORMATION:
; APPLICANT: Matthias Krause
; APPLICANT: Antonio S. Sechi
; APPLICANT: Frank B. Gertler
; APPLICANT: Jorgen Wehland
; TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
; FILE REFERENCE: M0656/7065
; CURRENT APPLICATION NUMBER: US/09/825,144
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/194,215
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT

; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-144-10

Query Match      33.3%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FPPPP 10
        |||||
Db       1 FPPPP 5

RESULT 7
US-09-823-240-7
; Sequence 7, Application US/09823240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jorgen Wehland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (9)...(9)
; OTHER INFORMATION: Xaa is any amino acid
US-09-823-240-7

Query Match      33.3%; Score 5; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FPPPP 10
        |||||
Db       1 FPPPP 5

RESULT 8
US-09-823-240-1
; Sequence 1, Application US/09823240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jorgen Wehland
; APPLICANT: Joseph Loureiro
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
```

ORGANISM: Listeria monocytogenes

FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa is Asp or Glu
NAME/KEY: UNSURE
LOCATION: (7)...(7)
OTHER INFORMATION: Xaa is any amino acid
US-09-823-240-1

Query Match 33.3%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 73; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 2 FPPPP 6

RESULT 9

US-09-825-144-12
Sequence 12, Application US/09825144
Patent No. US20020037286A1
GENERAL INFORMATION:
APPLICANT: Matthias Krause
APPLICANT: Antonio S. Sechi
APPLICANT: Frank B. Gertler
APPLICANT: Jorgen Wehland
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
FILE REFERENCE: M0656/7065
CURRENT APPLICATION NUMBER: US/09/825,144
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,215
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 14
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-09-825-144-12

Query Match 33.3%; Score 5; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 98; 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 3 FPPPP 7

RESULT 10

US-09-825-144-1
Sequence 1, Application US/09825144
Patent No. US20020037286A1
GENERAL INFORMATION:
APPLICANT: Matthias Krause
APPLICANT: Antonio S. Sechi
APPLICANT: Frank B. Gertler
APPLICANT: Jorgen Wehland
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
FILE REFERENCE: M0656/7065
CURRENT APPLICATION NUMBER: US/09/825,144
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,215
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 15
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-09-825-144-1

Query Match 33.3%; Score 5; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
Db 4 FPPPP 8

RESULT 11

US-10-161-791-339
Sequence 339, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-339

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPP 11
Db 6 PPPPP 10

RESULT 12

US-10-161-791-349
Sequence 349, Application US/10161791
Publication No. US20030186863A1

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 349:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-349

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 13
US-10-161-791-367
Sequence 367, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 367:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-367

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 9 PPPPQ 13

RESULT 14
US-10-161-791-373
Sequence 373, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 373:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-373

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 15

US-10-161-791-405
Sequence 405, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 405:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-405

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 16

US-10-161-791-439
Sequence 439, Application US/10161791
Publication No. US20030186863A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 439:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-439

Query Match 33.3%; Score 5; DB 12; Length 15;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 17

```

US-10-331-907-403
; Sequence 403, Application US/10331907
; Publication No. US20030181660A1
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; Hess, John W
; Caskey, Charles T
; Cox, Roger D
; Gerhold, David
; Hammond, Holly
; Hey, Patricia
; Kawaguchi, Yoshiniko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. US20030181660A1e Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 403:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 403:
US-10-331-907-403
Query Match 33.3%; Score 5; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
Db 6 FPPPP 10

RESULT 18
US-09-879-957-165
; Sequence 165, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; HOFFMAN, No. US20020034755A1h
; KAY, Brian K.
; FOWLKES, Dana M.
;
; Query Match 33.3%; Score 5; DB 11; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
;
; US-09-949-510-4
; Sequence 4, Application US/09949510
; Publication No. US20030077840A1
; GENERAL INFORMATION:
; APPLICANT: Chait et al.
; TITLE OF INVENTION: METHOD FOR THE COMPARATIVE QUANTITATIVE ANALYSIS OF
; TITLE OF INVENTION: PROTEINS AND OTHER BIOLOGICAL MATERIAL BY ISOTOPIC
; TITLE OF INVENTION: LABELING AND MASS SPECTROSCOPY
; FILE REFERENCE: Seq. List 1-6
; CURRENT APPLICATION NUMBER: US/09/949,510
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-949-510-4
;
; Query Match 33.3%; Score 5; DB 11; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
;
; US-09-879-957-165
; Sequence 165, Application US/08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-09-879-957-165
Query Match 33.3%; Score 5; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
Db 10 FPPPP 14

RESULT 19
US-09-949-510-4
; Sequence 4, Application US/09949510
; Publication No. US20030077840A1
; GENERAL INFORMATION:
; APPLICANT: Chait et al.
; TITLE OF INVENTION: METHOD FOR THE COMPARATIVE QUANTITATIVE ANALYSIS OF
; TITLE OF INVENTION: PROTEINS AND OTHER BIOLOGICAL MATERIAL BY ISOTOPIC
; TITLE OF INVENTION: LABELING AND MASS SPECTROSCOPY
; FILE REFERENCE: Seq. List 1-6
; CURRENT APPLICATION NUMBER: US/09/949,510
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-949-510-4
;
; Query Match 33.3%; Score 5; DB 11; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
;
; US-09-641-801-7-oligo.rapb
; Title of Invention: POLYPEPTIDES HAVING A FUNCTIONAL
; DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/879,957
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,915
; FILING DATE: 03-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 165:
US-09-879-957-165
Query Match 33.3%; Score 5; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
Db 10 FPPPP 14

RESULT 19
US-09-949-510-4
; Sequence 4, Application US/09949510
; Publication No. US20030077840A1
; GENERAL INFORMATION:
; APPLICANT: Chait et al.
; TITLE OF INVENTION: METHOD FOR THE COMPARATIVE QUANTITATIVE ANALYSIS OF
; TITLE OF INVENTION: PROTEINS AND OTHER BIOLOGICAL MATERIAL BY ISOTOPIC
; TITLE OF INVENTION: LABELING AND MASS SPECTROSCOPY
; FILE REFERENCE: Seq. List 1-6
; CURRENT APPLICATION NUMBER: US/09/949,510
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-949-510-4
;
; Query Match 33.3%; Score 5; DB 11; Length 18;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
;

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QETVT 15
|||||
Db 4 QETVT 8

RESULT 20

US-10-161-791-305
; Sequence 305, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-305

Query Match 33.3%; Score 5; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
|||||
Db 7 FPPPP 11

RESULT 21

US-10-185-050-109
; Sequence 109, Application US/10185050
; Publication No. US2003007577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.

Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING MW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-185-050-109

Query Match 33.3%; Score 5; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FPPPP 10
|||||
Db 10 FPPPP 14

RESULT 22

US-09-735-450-4
; Sequence 4, Application US/09735450
; Patent No. US2002025323A1
; GENERAL INFORMATION:
; APPLICANT: Paterson, Yvonne R
; APPLICANT: Gunn III, George R
; APPLICANT: Peters, Christian
; TITLE OF INVENTION: Compositions and Methods for Enhancing Immunogenicity
; TITLE OF INVENTION: of Antigens
; FILE REFERENCE: PENN-0741
; CURRENT APPLICATION NUMBER: US/09/735,450
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 09/537,642
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-735-450-4

Query Match 33.3%; Score 5; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPPP 10
|
|
|
|
|
Db 10 PPPP 14

RESULT 23
US-10-161-791-368
; Sequence 368, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 368:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-368

Query Match 33.3%; Score 5; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
|
|
|
|
|
Db 13 PPPPQ 17

RESULT 24
US-10-352-704-21
; Sequence 21, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:

APPLICANT: Chatelain, Francois
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; STATE: D.C
; COUNTRY: U.S.A.
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/352,704
FILING DATE: 28-Jan-2003
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/358,556A
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: FR 9315164
FILING DATE: 16-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10577/P58418

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-352-704-21

Query Match 26.7%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
|
|
|
|
|
Db 1 PPPP 4

RESULT 25
US-10-376-121A-134
; Sequence 134, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRFl14CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-10-376-121A-134
Query Match 26.7%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PPPP 10
DB 1 PPPP 4
RESULT 26
US-10-376-121A-135
Sequence 135, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRFl14CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 135:
US-10-376-121A-135
Query Match 26.7%; Score 4; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PPPP 10
DB 1 PPPP 4
RESULT 27
US-10-222-455-33
Sequence 33, Application US/10222455
Publication No. US2003009983A1
GENERAL INFORMATION:
APPLICANT: Holmes, Christopher P.
TITLE OF INVENTION: Cyclic and Substituted Immobilized
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/222,455
FILING DATE: 16-Aug-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/647,618
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: US 07/972,007
FILING DATE: 05-NOV-1992
APPLICATION NUMBER: US 07/796,727
FILING DATE: 22-NOV-1991
APPLICATION NUMBER: US 07/805,727
FILING DATE: 06-DEC-1991
APPLICATION NUMBER: US 07/624,120
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: US 07/492,462
FILING DATE: 07-MAR-1990
APPLICATION NUMBER: US 07/362,901
FILING DATE: 07-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 16528J-000141US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-222-455-33

Query Match      26.7%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      1 PPPP 4

RESULT 28
US-08-424-550B-716
; Sequence 716, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-716

Query Match      26.7%; Score 4; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLEM 4
Db      1 VLEM 4

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-10-222-455-33

Query Match      26.7%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      1 PPPP 4

RESULT 29
US-09-823-240-4
; Sequence 4, Application US/09823240
; Patent No. US20020048813A1
; GENERAL INFORMATION:
; APPLICANT: Frank B. Gertler
; APPLICANT: James E. Bear
; APPLICANT: Jurgen Wehland
; APPLICANT: Joseph Loureio
; TITLE OF INVENTION: Methods and Products for Regulating Cell
; TITLE OF INVENTION: Motility
; FILE REFERENCE: M0656/7064 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,240
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/194,564
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-09-823-240-4

Query Match      26.7%; Score 4; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      2 PPPP 5

RESULT 30
US-09-785-921A-15
; Sequence 15, Application US/09785921A
; Patent No. US20020094334A1
; GENERAL INFORMATION:
; APPLICANT: Keener, William K.
; APPLICANT: Ward, Thomas E.
; TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
; TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: LIT-PI-529
; CURRENT APPLICATION NUMBER: US/09/785,921A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-09-785-921A-15

Query Match      26.7%; Score 4; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      1 PPPP 4

RESULT 31
US-10-315-964A-422
; Sequence 422, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M3
; CURRENT APPLICATION NUMBER: US/10/315,964A
```

; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 422
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-317-251A-422

Query Match 26.7%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4
|||
Db 2 VLEM 5

RESULT 32
US-10-317-251A-422
; Sequence 422, Application US/10317251A
; Publication No. US20030148957A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M2
; CURRENT APPLICATION NUMBER: US/10/317,251A
; CURRENT FILING DATE: 2002-12-11
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 422
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-317-251A-422

Query Match 26.7%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4
|||
Db 2 VLEM 5

RESULT 33
US-10-317-252A-422
; Sequence 422, Application US/10317252A
; Publication No. US20030148958A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company

; APPLICANT: Isfort, Robert J
; APPLICANT: Mazur, Wieslaw A
; TITLE OF INVENTION: Corticotropin Releasing Factor 2 Receptor Agonists
; FILE REFERENCE: 8847M
; CURRENT APPLICATION NUMBER: US/10/317,252A
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/349,117
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/376,337
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/388,895
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/411,988
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 530
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 422
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-317-252A-422

Query Match 26.7%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4
|||
Db 2 VLEM 5

RESULT 34
US-10-352-704-23
; Sequence 23, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Rumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; STATE: D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/352,704
; APPLICATION NUMBER: US/10/352,704
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR

; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-352-704-23

Query Match 26.7%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 35
US-10-376-121A-120
; Sequence 120, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 120:
US-10-376-121A-120

Query Match 26.7%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

Db 1 PPPP 4

RESULT 36
US-10-014-485A-72
; Sequence 72, Application US/10014485A
; Publication No. US20020168684A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: COMB, Michael J.
; APPLICANT: ZHANG, Hui
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES
; FILE REFERENCE: CST-138 CIP2
; CURRENT APPLICATION NUMBER: US/10/014,485A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 4 is phosphorylated
US-10-014-485A-72

Query Match 26.7%; Score 4; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QETV 14
Db 2 QETV 5

RESULT 37
US-10-174-105A-72
; Sequence 72, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 4 is phosphorylated
US-10-174-105A-72

Query Match 26.7%; Score 4; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QETV 14
DB 2 QETV 5

RESULT 38

US-10-185-050-3
; Sequence 3, Application US/10185050
; Publication No. US2003007757A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.

TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL

; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 233

CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/185,050

; FILING DATE: 28-Jun-2002

; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/826,516

; FILING DATE: 03-Apr-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: MISROCK, S. LESLIE

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-208-999

TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 896-8864/9741

; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-185-050-3

Query Match 26.7%; Score 4; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
DB 1 PPPP 4

RESULT 39

US-10-096-986-9

; Sequence 9, Application US/10096986

; Publication No. US2003008346A1

; GENERAL INFORMATION:

; APPLICANT: Ferrari, Franco A.

; Richardson, Charles
; Chambers, James
; Causey, Stuart
; Pollock, Thomas J.
; Cappello, Joseph
; Crissman, John W.

; TITLE OF INVENTION: No. US2003008346A1 Peptides Comprising Repetitive
; Units of Amino Acids and DNA Sequences Encoding the Sam

NUMBER OF SEQUENCES: 117

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/096,986

; FILING DATE: 12-Mar-2002

; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/444,791

; FILING DATE: 22-No. US2003008346A1-1999

; APPLICATION NUMBER: US 08/482,085

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/175,155

; FILING DATE: 29-DEC-1993

; APPLICATION NUMBER: US 08/053,049

; FILING DATE: 22-APR-1993

; APPLICATION NUMBER: US 07/114,618

; FILING DATE: 29-OCT-1987

; APPLICATION NUMBER: US 06/927,258

; FILING DATE: 04-NOV-1986

ATTORNEY/AGENT INFORMATION:

; NAME: Trecartin, Richard F.

; REGISTRATION NUMBER: 31,801

; REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-096-986-9

Query Match 26.7%; Score 4; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
DB 2 PPPP 5

RESULT 40

US-10-281-652-12

; Sequence 12, Application US/10281652

; Publication No. US20030091606A1

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND

```
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-12

Query Match          26.7%; Score 4; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FPPP 9
      |||||
Db      1 FPPP 4

RESULT 41
US-09-803-126-21
; Sequence 21, Application US/09803126
; Patent No. US20020099190A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Alan R.
; APPLICANT: Deng, Gary G.
; APPLICANT: Rubanya, Gabor M.
; TITLE OF INVENTION: Estrogen-Regulated Unconventional Myosin-Related
; FILE REFERENCE: 015303-00031005
; CURRENT APPLICATION NUMBER: US/09/803,126
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/188,488
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: Peptide
US-09-803-126-21

Query Match          26.7%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      |||||
Db      1 PPPP 4

RESULT 42
US-10-352-704-25
; Sequence 25, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
```

```
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,704
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-352-704-25

Query Match          26.7%; Score 4; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      |||||
Db      1 PPPP 4

RESULT 43
US-10-078-547-3
; Sequence 3, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
```

```
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: profilin motif
US-10-078-547-3

Query Match          26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 44
US-10-078-547-13
; Sequence 13, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: PPPPPP domain of WASP
US-10-078-547-13

Query Match          26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 1 PPPP 4

RESULT 45
US-10-078-547-14
; Sequence 14, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
```

```
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: ABM-2 motif
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: Xaa = Any Amino Acid
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-078-547-14

Query Match          26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 46
US-10-078-547-19
; Sequence 19, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
; APPLICANT: Narayanaswamy Ramesh
; APPLICANT: Miguel A. de la Fuente
; APPLICANT: Ines M. Anton
; APPLICANT: Raif S. Geha
; TITLE OF INVENTION: WIP, A WASP-Associated Protein
; FILE REFERENCE: 1242.1022-005
; CURRENT APPLICATION NUMBER: US/10/078,547
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/599,287
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: PCT/US98/27501
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/101,457
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/068,533
; PRIOR FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: APPPPP motif, WIP
US-10-078-547-19

Query Match          26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 47
US-10-078-547-21
; Sequence 21, Application US/10078547
; Publication No. US20020199211A1
; GENERAL INFORMATION:
```

APPLICANT: Narayanaswamy Ramesh
APPLICANT: Miguel A. de la Fuente
APPLICANT: Ines M. Anton
APPLICANT: Raif S. Geha
TITLE OF INVENTION: WIP, A WASP-Associated Protein
FILE REFERENCE: 1242.1022-005
CURRENT APPLICATION NUMBER: US/10/078,547
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/599,287
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: PCT/US98/27501
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/101,457
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/068,533
PRIOR FILING DATE: 1997-12-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 6
TYPE: PRT
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: profilin-binding consensus sequence
NAME/KEY: VARIANT
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa = A, G, L or S
NAME/KEY: VARIANT
LOCATION: 1
OTHER INFORMATION: Xaa = Any Amino Acid
US-10-078-547-21

Query Match 26.7%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 2 PPPP 5

RESULT 48
US-10-192-257-5
Sequence 5, Application US/10192257
Publication No. US20030021786A1
GENERAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condition
FILE REFERENCE: 1102865-0057
CURRENT APPLICATION NUMBER: US/10/192,257
CURRENT FILING DATE: 2002-07-09
PRIOR APPLICATION NUMBER: US 60/303,868
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hypothetical spacer peptide
US-10-192-257-5

Query Match 26.7%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 2 PPPP 5

RESULT 49
US-09-825-144-8
Sequence 8, Application US/09825144
Patent No. US20020037286A1
GENERAL INFORMATION:
APPLICANT: Matthias Krause
APPLICANT: Antonio S. Sechi
APPLICANT: Frank B. Gertler
APPLICANT: Jorgen Wehland
TITLE OF INVENTION: Methods for Altering T-Cell and Macrophage Activation
FILE REFERENCE: M0656/7065
CURRENT APPLICATION NUMBER: US/09/825,144
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/194,215
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 7
TYPE: PRT
ORGANISM: Listeria monocytogenes
FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa is Phe, Leu, or Trp
US-09-825-144-8

Query Match 26.7%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 4 PPPP 7

RESULT 50
US-09-281-495-17
Sequence 17, Application US/09281495
Publication No. US20030059765A1
GENERAL INFORMATION:
APPLICANT: Pomerantz, Roger J
APPLICANT: Bouhmandan, Mohamad
APPLICANT: Duan, Ling-Xun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROVIDING A PROTEIN TO A
FILE REFERENCE: 9855-25U1
CURRENT APPLICATION NUMBER: US/09/281,495
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: US 60/079,822
EARLIER FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Vpr-Specific
OTHER INFORMATION: Polypeptide Binding Region
US-09-281-495-17

Query Match 26.7%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPP 9
Db 4 FPPP 7

RESULT 51
US-10-032-214-312

; Sequence 312, Application US/10032214
; Publication No. US2003013881A1
; GENERAL INFORMATION:
; APPLICANT: PUNNONEN, JUHA
; APPLICANT: LAZETIC, ALEXANDRA
; APPLICANT: LEONG, STEVEN R.
; APPLICANT: CHANG, CHIA-CHUN
; APPLICANT: APT, DORIS
; APPLICANT: GUSTAFSSON, CLAES
; TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
; FILE REFERENCE: 02-106730US
; CURRENT APPLICATION NUMBER: US/10/032,214
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 09/888,324
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: PCT/US01/19973
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,946
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/241,245
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 312
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-10-032-214-312

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 52

US-09-261-894-91
; Sequence 91, Application US/09261894
; Publication No. US20030207324A1
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,894
; FILING DATE: March 3, 1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558

; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-261-894-91

Query Match 26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFP 7
Db 3 MKFP 6

RESULT 53

US-10-192-257-6
; Sequence 6, Application US/10192257
; Publication No. US20030021786A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Treatment and Prevention of Cancerous and Pre-Cancerous Condit
; TITLE OF INVENTION: Liver, Lung and Esophagus
; FILE REFERENCE: 1102865-0057
; CURRENT APPLICATION NUMBER: US/10/192,257
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US 60/303,868
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical spacer peptide
US-10-192-257-6

Query Match 26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 54

US-10-314-057-8
; Sequence 8, Application US/10314057
; Publication No. US20030068326A1
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip
; APPLICANT: Stephen, Grimes
; APPLICANT: Karr, Stephen
; APPLICANT: Michaeli, Dov
; TITLE OF INVENTION: Method for the Treatment of Gastroesophageal Reflux Disease
; FILE REFERENCE: ACGIUSA
; CURRENT APPLICATION NUMBER: US/10/314,057
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/09/700,378
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: PCT/US99/10734
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/085,610
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8

```
; LENGTH: 7
; TYPE: PRT
; ORGANISM: human or synthetic peptide
US-10-314-057-8

Query Match          26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 55
US-10-235-236-3
; Sequence 3, Application US/10235236
; Publication No. US20030086941A1
; GENERAL INFORMATION:
; APPLICANT: Michaeli, Dov
; Caplin, Martyn E.
; Watson, Susan A.
; Grimes, Stephen
; TITLE OF INVENTION: Immunogenic Compositions
; to the CCK-B/Gastrin Receptor and Methods for
; the Treatment of Tumors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White & Case LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/235,236
; FILING DATE: 04-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,201
; FILING DATE: 12-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-0032
; TELEPHONE: (212) 819-8200
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-235-236-3          26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 56
Query Match          26.7%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 3 PPPP 6

RESULT 57
US-09-843-245-1
; Sequence 1, Application US/09843245
; Patent No. US20020164672A1
; GENERAL INFORMATION:
; APPLICANT: McPherson, Peter S.
; APPLICANT: Ramjaun, Antoine Rachid
; TITLE OF INVENTION: REGULATION OF JNK ACTIVITY BY MODULATION OF THE
; TITLE OF INVENTION: INTERACTION BETWEEN THE ENDOCYTIC PROTEIN ENDOPHILIN
; TITLE OF INVENTION: AND THE GERMINAL CENTER KINASE-LIKE KINASE
; FILE REFERENCE: 9555.116US01
; CURRENT APPLICATION NUMBER: US/09/843,245
; CURRENT FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-843-245-1

Query Match          26.7%; Score 4; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 4 PPPP 7

RESULT 58
US-10-022-066-378
; Sequence 378, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
```

```
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 378
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-022-066-378

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      5 PPPP 8

RESULT 59
US-10-376-121A-96
; Sequence 96, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR/114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1..8
; SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-10-022-066-378

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      5 PPPP 8

RESULT 60
US-10-376-121A-99
; Sequence 99, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMR/114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1..8
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-376-121A-99

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      1 PPPP 4
```



```
Db          1 PPPP 4

RESULT 61
US-10-376-121A-196
; Sequence 196, Application US/10376121A
; Publication No. US2003021654A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 196:
US-10-376-121A-196

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 PPPP 10
           ||||
Db          5 PPPP 8

RESULT 62
US-10-376-121A-197
; Sequence 197, Application US/10376121A
; Publication No. US2003021654A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 197:
US-10-376-121A-197

Query Match          26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 PPPP 10
           ||||
Db          4 PPPP 7

RESULT 63
US-10-376-121A-198
; Sequence 198, Application US/10376121A
; Publication No. US2003021654A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
```

/ FILING DATE: April 13, 1992
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ APPLICATION NUMBER: 07/472,947
/ FILING DATE: January 31, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-817-8473
/ TELEFAX: (404)-817-8588
/ INFORMATION FOR SEQ ID NO: 198:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 198:
US-10-376-121A-198

Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 3 PPPP 6

RESULT 64
US-10-376-121A-199
/ Sequence 199, Application US/10376121A
/ Publication No. US20030216544A1
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
/ AUTOANTIBODIES
/ NUMBER OF SEQUENCES: 218
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L. Pabst
/ STREET: Suite 2000, 1201 West Peachtree Street, N.E.
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30309-3400
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/376,121A
/ FILING DATE: 27-Mar-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/867,819
/ FILING DATE: April 13, 1992
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ APPLICATION NUMBER: 07/472,947
/ FILING DATE: January 31, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-817-8473
/ TELEFAX: (404)-817-8588
/ INFORMATION FOR SEQ ID NO: 199:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids

/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 199:
US-10-376-121A-199
Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PPPP 10
Db 1 PPPP 4

RESULT 65
US-10-376-121A-210
/ Sequence 210, Application US/10376121A
/ Publication No. US20030216544A1
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
/ AUTOANTIBODIES
/ NUMBER OF SEQUENCES: 218
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L. Pabst
/ STREET: Suite 2000, 1201 West Peachtree Street, N.E.
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30309-3400
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/376,121A
/ FILING DATE: 27-Mar-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/867,819
/ FILING DATE: April 13, 1992
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ APPLICATION NUMBER: 07/472,947
/ FILING DATE: January 31, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patrea L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-817-8473
/ TELEFAX: (404)-817-8588
/ INFORMATION FOR SEQ ID NO: 210:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 210:
US-10-376-121A-210

Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 3 PPPP 6

RESULT 66
US-10-376-121A-211
; Sequence 211, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 211:
US-10-376-121A-211
Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PPPP 10
Db 2 PPPP 5
RESULT 67
US-10-376-121A-213
; Sequence 213, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA

COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 213:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 213:
US-10-376-121A-213
Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PPPP 10
Db 1 PPPP 4
RESULT 68
US-10-376-121A-215
; Sequence 215, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205

```
;
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRFl14CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-10-376-121A-215
Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 3 PPPP 6

RESULT 69
US-10-376-121A-216
; Sequence 216, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOCANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 27-Mar-2003
; APPLICATION NUMBER: US/10/376,121A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRFl14CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-10-376-121A-216
Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 70
US-10-376-121A-217
; Sequence 217, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOCANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 27-Mar-2003
; APPLICATION NUMBER: US/10/376,121A
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRFl14CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 217:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-10-376-121A-217
Query Match 26.7%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 1 PPPP 4

RESULT 71
```

```

US-10-226-007-452
; Sequence 452, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 452
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-10-226-007-452

Query Match      26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      1 PPPP 4

RESULT 72
US-10-226-007-465
; Sequence 465, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 465
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-10-226-007-465

Query Match      26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      2 PPPP 5

RESULT 73
US-10-226-007-478
; Sequence 478, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection

```

```

; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 478
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-10-226-007-478

Query Match      26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      3 PPPP 6

RESULT 74
US-10-226-007-491
; Sequence 491, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 491
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rous sarcoma virus
US-10-226-007-491

Query Match      26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 PPPP 10
Db      4 PPPP 7

RESULT 75
US-10-226-007-738
; Sequence 738, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005.01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738
; LENGTH: 8

```

```
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-226-007-738
Query Match      26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPP 10
      ||||
Db      1 PPPP 4

Search completed: November 25, 2003, 20:25:33
Job time : 30.8404 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 16.3564 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-7

Perfect score: 15

Sequence: 1 VLEMKFPPTQETVT 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5A COMB pep.*

2: /cgn2_6/prodata/1/iaa/5B COMB pep.*

3: /cgn2_6/prodata/1/iaa/6A COMB pep.*

4: /cgn2_6/prodata/1/iaa/6B COMB pep.*

5: /cgn2_6/prodata/1/iaa/PCITUS COMB pep.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	4	US-09-641-803-7
2	5	33.3	5	2	US-08-867-941-26
3	5	33.3	5	3	US-09-074-658-26
4	5	33.3	6	2	US-08-867-941-47
5	5	33.3	6	3	US-09-074-658-47
6	5	33.3	7	4	US-09-641-803-14
7	5	33.3	9	3	US-09-188-579-88
8	5	33.3	9	3	US-09-315-444-88
9	5	33.3	9	4	US-09-721-362-88
10	5	33.3	15	1	US-08-302-771-1
11	5	33.3	15	3	US-08-602-999A-339
12	5	33.3	15	3	US-08-602-999A-349
13	5	33.3	15	3	US-08-602-999A-367
14	5	33.3	15	3	US-08-602-999A-373
15	5	33.3	15	3	US-08-602-999A-405
16	5	33.3	15	3	US-08-602-999A-439
17	5	33.3	15	4	US-09-500-124-339
18	5	33.3	15	4	US-09-500-124-349
19	5	33.3	15	4	US-09-500-124-367
20	5	33.3	15	4	US-09-500-124-373
21	5	33.3	15	4	US-09-500-124-405
22	5	33.3	15	4	US-09-500-124-439
23	5	33.3	17	4	US-09-060-299-403
24	5	33.3	17	4	US-09-402-923A-403
25	5	33.3	18	3	US-08-630-316A-109
26	5	33.3	18	3	US-08-602-999A-305
27	5	33.3	18	4	US-08-630-915A-165

28	5	33.3	18	4	US-09-304-799-4	Sequence 4, Appli
29	5	33.3	18	4	US-09-500-124-305	Sequence 305, App
30	5	33.3	20	3	US-08-602-999A-368	Sequence 368, App
31	5	33.3	20	4	US-09-500-124-368	Sequence 368, App
32	4	26.7	4	1	US-07-972-007-33	Sequence 33, Appl
33	4	26.7	4	1	US-08-351-058A-1	Sequence 1, Appli
34	4	26.7	4	1	US-08-647-618-33	Sequence 33, Appl
35	4	26.7	4	2	US-08-358-556A-21	Sequence 21, Appl
36	4	26.7	4	4	US-09-295-996B-6	Sequence 6, Appli
37	4	26.7	4	4	US-09-057-162-33	Sequence 33, Appl
38	4	26.7	4	4	US-09-295-846B-9	Sequence 9, Appli
39	4	26.7	4	4	US-09-551-737C-9	Sequence 9, Appli
40	4	26.7	4	5	PCT-US92-09964-1	Sequence 1, Appli
41	4	26.7	5	1	US-08-351-058A-5	Sequence 5, Appli
42	4	26.7	5	1	US-08-477-509B-9	Sequence 9, Appli
43	4	26.7	5	2	US-08-358-556A-23	Sequence 23, Appl
44	4	26.7	5	3	US-08-630-916A-3	Sequence 3, Appli
45	4	26.7	5	3	US-08-482-085B-9	Sequence 9, Appli
46	4	26.7	5	3	US-08-476-509B-38	Sequence 38, Appl
47	4	26.7	5	4	US-09-444-791A-9	Sequence 9, Appli
48	4	26.7	5	4	US-09-295-996B-7	Sequence 7, Appli
49	4	26.7	5	4	US-08-469-260A-716	Sequence 716, App
50	4	26.7	5	4	US-09-641-803-12	Sequence 12, Appl
51	4	26.7	5	4	US-09-119-507B-3	Sequence 3, Appli
52	4	26.7	5	4	US-08-488-446-716	Sequence 716, App
53	4	26.7	5	4	US-09-295-846B-10	Sequence 10, Appl
54	4	26.7	5	4	US-09-551-737C-10	Sequence 10, Appl
55	4	26.7	5	4	US-08-897-556A-3	Sequence 3, Appli
56	4	26.7	5	4	US-08-897-556A-105	Sequence 105, App
57	4	26.7	5	4	US-08-467-344A-716	Sequence 716, App
58	4	26.7	5	5	PCT-US92-09964-5	Sequence 5, Appli
59	4	26.7	6	1	US-08-151-219-5	Sequence 5, Appli
60	4	26.7	6	1	US-08-188-223-4	Sequence 4, Appli
61	4	26.7	6	1	US-08-188-223-11	Sequence 11, Appl
62	4	26.7	6	2	US-08-358-556A-25	Sequence 25, Appl
63	4	26.7	6	3	US-08-968-466-4	Sequence 4, Appli
64	4	26.7	6	3	US-08-968-466-11	Sequence 11, Appl
65	4	26.7	6	3	US-09-001-984C-35	Sequence 35, Appl
66	4	26.7	6	4	US-08-478-546B-4	Sequence 4, Appli
67	4	26.7	6	4	US-08-478-546B-11	Sequence 11, Appl
68	4	26.7	6	4	US-09-396-347E-35	Sequence 35, Appl
69	4	26.7	6	4	US-09-119-507B-117	Sequence 117, App
70	4	26.7	6	5	PCT-US94-13205-5	Sequence 5, Appli
71	4	26.7	7	1	US-08-151-219-3	Sequence 3, Appli
72	4	26.7	7	1	US-08-188-223-9	Sequence 9, Appli
73	4	26.7	7	1	US-08-188-223-10	Sequence 10, Appl
74	4	26.7	7	2	US-08-968-676-91	Sequence 91, Appl
75	4	26.7	7	2	US-08-680-326-73	Sequence 73, Appl
76	4	26.7	7	3	US-08-968-466-9	Sequence 9, Appli
77	4	26.7	7	3	US-08-968-466-10	Sequence 10, Appl
78	4	26.7	7	4	US-09-343-011B-8	Sequence 8, Appli
79	4	26.7	7	4	US-08-478-546B-9	Sequence 9, Appli
80	4	26.7	7	4	US-08-478-546B-10	Sequence 10, Appl
81	4	26.7	7	4	US-09-281-495-17	Sequence 17, Appl
82	4	26.7	7	4	US-09-076-372-3	Sequence 3, Appli
83	4	26.7	7	5	PCT-US94-13205-3	Sequence 3, Appli
84	4	26.7	8	1	US-07-989-290-4	Sequence 4, Appli
85	4	26.7	8	1	US-08-271-698-4	Sequence 4, Appli
86	4	26.7	8	2	US-08-468-596-4	Sequence 4, Appli
87	4	26.7	8	2	US-08-769-745-22	Sequence 22, Appl
88	4	26.7	8	4	US-09-343-011B-9	Sequence 9, Appli
89	4	26.7	8	4	US-09-295-996B-10	Sequence 10, Appl
90	4	26.7	8	4	US-09-295-996B-14	Sequence 14, Appl
91	4	26.7	8	4	US-09-295-846B-13	Sequence 13, Appl
92	4	26.7	8	4	US-09-295-846B-17	Sequence 17, Appl
93	4	26.7	8	4	US-09-551-737C-13	Sequence 13, Appl
94	4	26.7	8	4	US-09-551-737C-17	Sequence 17, Appl
95	4	26.7	9	2	US-08-340-283-125	Sequence 125, App
96	4	26.7	9	3	US-09-188-579-106	Sequence 106, App
97	4	26.7	9	3	US-09-315-444-106	Sequence 106, App
98	4	26.7	9	3	US-09-001-984C-17	Sequence 17, Appl
99	4	26.7	9	4	US-09-343-011B-6	Sequence 6, Appli
100	4	26.7	9	4	US-09-295-996B-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-641-803-7
; Sequence 7, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-7

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLENKFPPTPTVT 15
Db 1 VLENKFPPTPTVT 15

RESULT 2
US-08-867-941-26
; Sequence 26, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-867-941-26

Query Match 33.3%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEMKF 6
Db 1 LEMKF 5

RESULT 3
US-09-074-658-26
; Sequence 26, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: Quijun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-074-658-26

Query Match 33.3%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEMKF 6
Db 1 LEMKF 5

RESULT 4
US-08-867-941-47


```
; Sequence 47, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-867-941-47

Query Match 33.3%; Score 5; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMKF 6
Db 2 LEMKF 6

RESULT 5
US-09-074-658-47
; Sequence 47, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: Quijun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-074-658-47

Query Match 33.3%; Score 5; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMKF 6
Db 2 LEMKF 6

RESULT 6
US-09-641-803-14
; Sequence 14, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-09-641-803-14

Query Match 33.3%; Score 5; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 2 PPPPQ 6

RESULT 7
US-09-188-579-88
; Sequence 88, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
```

; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Motif A of RNA triphosphatase.
US-09-188-579-88

Query Match 33.3%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMKF 6
| | | | |
Db 5 LEMKF 9

RESULT 8
US-09-315-444-88
; Sequence 88, Application US/09315444A
; Patent No. 6232070
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP
; CURRENT APPLICATION NUMBER: US/09/315,444A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/188,579
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Motif A of RNA triphosphatase.
US-09-315-444-88

Query Match 33.3%; Score 5; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMKF 6
| | | | |
Db 5 LEMKF 9

RESULT 9
US-09-721-362-88
; Sequence 88, Application US/09721362
; Patent No. 6420163
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP/D
; CURRENT APPLICATION NUMBER: US/09/721,362
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/315,444
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Motif A of RNA triphosphatase.
US-09-721-362-88

Query Match 33.3%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEMKF 6
| | | | |
Db 5 LEMKF 9

RESULT 10
US-08-302-771-1
; Sequence 1, Application US/08302771
; Patent No. 559541
; GENERAL INFORMATION:
; APPLICANT: MARCHAL, GILLES
; APPLICANT: ROMAIN, FELIX
; TITLE OF INVENTION: PEPTIDE SEQUENCE CAPABLE OF INDUCING
; TITLE OF INVENTION: A
; TITLE OF INVENTION: DELAYED-TYPE HYPERSENSITIVITY REACTION IN THE PRESENCE
; TITLE OF INVENTION: OF
; TITLE OF INVENTION: LIVING BACTERIA OF THE MYCOBACTERIUM TUBERCULOSIS
; TITLE OF INVENTION: COMPLEX
; TITLE OF INVENTION: AND ITS APPLICATIONS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,771
; FILING DATE: OCTOBER 17, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92 03 286
; FILING DATE: 19-MAR-1992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
US-08-302-771-1

Query Match 33.3%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
| | | | |
Db 7 PPPPQ 11

```
RESULT 11
US-08-602-999A-339
; Sequence 339, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-339

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 12
US-08-602-999A-349
; Sequence 349, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 349:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-349

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 13
US-08-602-999A-367
; Sequence 367, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
```

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 367:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-367

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
Db 9 PPPPQ 13

RESULT 14
US-08-602-999A-373
; Sequence 373, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 373:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-373

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 15
US-08-602-999A-405
; Sequence 405, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-405

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 16
US-08-602-999A-439
; Sequence 439, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.

Wed Nov 26 09:08:40 2003

```
;
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 439:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-439

Query Match 33.3%; Score 5; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 17
US-09-500-124-339
; Sequence 339, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
```

```
;
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-339

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 18
US-09-500-124-349
; Sequence 349, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
```

INFORMATION FOR SEQ ID NO: 349:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-349

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPPQ 11
 |||||
Db 6 PPPPQ 10

RESULT 19

US-09-500-124-367
Sequence 367, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/500,124
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 367:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-367

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPPQ 11
 |||||

Db 9 PPPPQ 13

RESULT 20

US-09-500-124-373
Sequence 373, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.

TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 373:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-373

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 7 PPPPQ 11
 |||||
Db 6 PPPPQ 10

RESULT 21

US-09-500-124-405
Sequence 405, Application US/09500124
Patent No. 6432920

GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.

```

; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 405:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-439

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 22
US-09-500-124-439
; Sequence 439, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: OULLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 439:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-439

Query Match 33.3%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 7 PPPPQ 11
Db 6 PPPPQ 10

RESULT 23
US-09-060-299-403
; Sequence 403, Application US/09060299
; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. 6545137el Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vandertye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,299
; FILING DATE: 15-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:

```



```

; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-305

Query Match 33.3%; Score 5; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
Db 7 FPPPP 11

RESULT 27
US-08-630-915A-165
; Sequence 165, Application US/08630915A
; Patent No. 6309820
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820H
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-915A-165

Query Match 33.3%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FPPPP 10
Db 10 FPPPP 14

RESULT 28
US-09-304-799-4
; Sequence 4, Application US/09304799
; Patent No. 6391649
; GENERAL INFORMATION:
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: METHOD FOR THE COMPARATIVE ANALYSIS OF PROTEINS AND OTHER BIOLOGICAL
; FILE REFERENCE: 1119-0002
; CURRENT APPLICATION NUMBER: US/09/304,799
; CURRENT FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-304-799-4

Query Match 33.3%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QETVT 15
Db 4 QETVT 8

RESULT 29
US-09-500-124-305
; Sequence 305, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467

```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-305

Query Match          33.3%; Score 5; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 FPPPP 10
DB      7 FPPPP 11
|||||
;
; RESULT 30
; US-08-602-999A-368
; Sequence 368, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
```

```
;
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-602-999A-368

Query Match          33.3%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 PPPPQ 11
DB      13 PPPPQ 17
|||||
;
; RESULT 31
; US-500-124-368
; Sequence 368, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
```

TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-368

Query Match 33.3%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 11
Db 13 PPPP 17

RESULT 32

US-07-972-007-33
; Sequence 33, Application US/07972007
; Patent No. 5527681
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Cyclic and Substituted Immobilized
; TITLE OF INVENTION: Molecular Synthesis
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,007
FILING DATE: 19921105

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5527681v1el, Vernon A.

REGISTRATION NUMBER: 32,483

REFERENCE/DOCKET NUMBER: 11509-57-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-972-007-33

Query Match 26.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 33

US-08-351-058A-1
; Sequence 1, Application US/08351058A
; Patent No. 5550215
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,058A
FILING DATE: 28-NOV-1994
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/978,940

FILING DATE: 19-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/796,727

FILING DATE: 22-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: Swiss, Gerald F.

REGISTRATION NUMBER: 30,113

REFERENCE/DOCKET NUMBER: 000324-015

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-854-7400

TELEFAX: 415-854-8275

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-351-058A-1

Query Match

26.7%; Score 4; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10

Db 1 PPPP 4

RESULT 34

US-08-647-618-33

; Sequence 33, Application US/08647618

; Patent No. 5770456

; GENERAL INFORMATION:

; APPLICANT: Holmes, Christopher P.

; TITLE OF INVENTION: Cyclic and Substituted Immobilized

; TITLE OF INVENTION: Molecular Synthesis

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/647,618

; FILING DATE: 13-MAY-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/972,007

; FILING DATE: 05-NOV-1992

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,727
; FILING DATE: 22-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,727
; FILING DATE: 06-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/624,120
; FILING DATE: 06-DEC-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/492,462
; FILING DATE: 07-MAR-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/362,901
; FILING DATE: 07-JUN-1989
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-000141US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-647-618-33

Query Match 26.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 35
US-08-358-556A-21
; Sequence 21, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-556A-21

Query Match 26.7%; Score 4; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 36
US-09-295-996B-6
; Sequence 6, Application US/09295996B
; Patent No. 6413530
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: JP-230
; CURRENT APPLICATION NUMBER: US/09/295,996B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking region
; US-09-295-996B-6

Query Match 26.7%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 1 PPPP 4

RESULT 37
US-09-057-162-33
; Sequence 33, Application US/09057162
; Patent No. 6468740
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Cyclic and Substituted Immobilized
; MOLECULAR SYNTHESIS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.125
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,162
FILING DATE: 08-Apr-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/647,618
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: US 07/972,007
FILING DATE: 05-NOV-1992
APPLICATION NUMBER: US 07/796,727
FILING DATE: 22-NOV-1991
APPLICATION NUMBER: US 07/805,727
FILING DATE: 06-DEC-1991
APPLICATION NUMBER: US 07/624,120
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: US 07/492,462
FILING DATE: 07-MAR-1990
APPLICATION NUMBER: US 07/362,901
FILING DATE: 07-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 16528J-000141US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-057-162-33

Query Match 26.7%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
|
|
|
|
Db 1 PPPP 4

RESULT 38
US-09-295-846B-9
; Sequence 9, Application US/09295846B
; Patent No. 6562590
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223
; CURRENT APPLICATION NUMBER: US/09/295,846B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: flanking
; OTHER INFORMATION: region
US-09-295-846B-9

Query Match 26.7%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
|
|
|
|
Db 1 PPPP 4

RESULT 39
US-09-551-737C-9
; Sequence 9, Application US/09551737C
; Patent No. 6566129
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Schlesinger, Yaagov
; APPLICANT: Nauwelaers, Sabine M. I.
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223C1
; CURRENT APPLICATION NUMBER: US/09/551,737C
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/295,846
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking region
US-09-551-737C-9

Query Match 26.7%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
|
|
|
|
Db 1 PPPP 4

RESULT 40
PCT-US92-09964-1
; Sequence 1, Application PC/TUS9209964
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09964
; FILING DATE: 19921119
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,727
; FILING DATE: 22-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-51-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09964-1

Query Match 26.7%; Score 4; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 1 PPPP 4

RESULT 41

US-08-351-058A-5
; Sequence 5, Application US/08351058A
; Patent No. 5550215
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/351,058A
; FILING DATE: 28-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,940
; FILING DATE: 19-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,727
; FILING DATE: 22-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-351-058A-5

Query Match 26.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 1 PPPP 4

RESULT 42

US-08-477-509B-9
; Sequence 9, Application US/08477509B
; Patent No. 5770697
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Cappello, Joseph
; APPLICANT: Crissman, John W.
; APPLICANT: Dorman, Mary A.
; TITLE OF INVENTION: No. 5770697el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,509B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-7/RPT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-477-509B-9

Query Match 26.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 43

US-08-358-556A-23
; Sequence 23, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelein, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its

```
; TITLE OF INVENTION: Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-556A-23
```

Query Match 26.7%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 7 PPPP 10
Db 1 PPPP 4
```

```
RESULT 44
US-08-630-916A-3
; Sequence 3, Application US/08630916A
; Patent No. 6011137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-630-916A-3
```

Query Match 26.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 7 PPPP 10
Db 1 PPPP 4
```

```
RESULT 45
US-08-482-085B-9
; Sequence 9, Application US/08482085B
; Patent No. 6018030
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Richardson, Charles
; APPLICANT: Chambers, James
; APPLICANT: Causey, Stuart
; APPLICANT: Pollock, Thomas J.
; APPLICANT: Cappello, Joseph W.
; APPLICANT: Crissman, John W.
; TITLE OF INVENTION: No. 6018030el Peptides Comprising Repetitive
; TITLE OF INVENTION: Units of Amino Acids and DNA Sequences Encoding the Same
; NUMBER OF SEQUENCES: 112
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,085B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-6/RFT/MTK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
```

TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-085B-9

Query Match 26.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 46
US-08-476-509B-38
Sequence 38, Application US/08476509B
Patent No. 6034212
GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-476-509B-38

Query Match 26.7%; Score 4; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 1 PPPP 4

RESULT 47
US-09-444-791A-9
Sequence 9, Application US/09444791A
Patent No. 6355776
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
Richardson, Charles
Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
TITLE OF INVENTION: No. 6355776el Peptides Comprising Repetitive
Units of Amino Acids and DNA Sequences Encoding the Same
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/444,791A
FILING DATE: 22-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,085
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-444-791A-9

Query Match 26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 48
US-09-295-996B-7
Sequence 7, Application US/09295996B


```
; Patent No. 6413530
; GENERAL INFORMATION:
; APPLICANT: BOROVSKY, Dov
; TITLE OF INVENTION: PESTICIDAL PEPTIDES
; FILE REFERENCE: UF-230
; CURRENT APPLICATION NUMBER: US/09/295,996B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking region
US-09-295-996B-7

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
   ||||
Db 1 PPPP 4

RESULT 49
US-08-469-260A-716
; Sequence 716, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATTIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. WUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-260A-716

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEM 4
   ||||
Db 1 VLEM 4

RESULT 50
US-09-641-803-12
; Sequence 12, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-12

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 PPPP 9
   ||||
Db 1 PPPP 4

RESULT 51
US-09-119-507B-3
; Sequence 3, Application US/09119507B
; Patent No. 6548642
; GENERAL INFORMATION:
; APPLICANT: Kieliszewski, Marcia J.
; TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
; FILE REFERENCE: OHU-03417
; CURRENT APPLICATION NUMBER: US/09/119,507B
; CURRENT FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: SITE
; LOCATION: (2)..(5)
; OTHER INFORMATION: The Proline at these positions is a
; OTHER INFORMATION: hydroxyproline.
US-09-119-507B-3
```

```
Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
DB 2 PPPP 5

RESULT 52
US-08-488-446-716
; Sequence 716, Application US/08488446
; Patent No. 6558898
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,446
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, FRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-446-716

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4
DB 1 VLEM 4

RESULT 53
US-09-295-846B-10
; Sequence 10, Application US/09295846B
; Patent No. 6562590
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223
; CURRENT APPLICATION NUMBER: US/09/295,846B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: flanking
; OTHER INFORMATION: region
US-09-295-846B-10

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
DB 1 PPPP 4

RESULT 54
US-09-551-737C-10
; Sequence 10, Application US/09551737C
; Patent No. 6566129
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Schlesinger, Yaagov
; APPLICANT: Nauwelaers, Sabine M. I.
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223C1
; CURRENT APPLICATION NUMBER: US/09/551,737C
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/295,846
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking region
US-09-551-737C-10

Query Match          26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
DB 1 PPPP 4

RESULT 55
US-08-897-556A-3
; Sequence 3, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSZEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
```

CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,556A
FILING DATE: 21-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OHU-02908
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2..5
OTHER INFORMATION: /note= "The proline at these positions is a hydroxyproline."
US-08-897-556A-3

Query Match 26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 2 PPPP 5

RESULT 56
US-08-897-556A-105
; Sequence 105, Application US/08897556A
; Patent No. 6570062
; GENERAL INFORMATION:
; APPLICANT: KIELSEWSKI, MARCIA J.
; TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
; TITLE OF INVENTION: HYDROXYPROLINE-RICH GLYCOPROTEINS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,556A
; FILING DATE: 21-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: OHU-02908
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2..5
; OTHER INFORMATION: /note= "The proline at positions 2,
; OTHER INFORMATION: 3, 4, and 5 is a hydroxyproline."
; US-08-897-556A-105

Query Match 26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PPPP 10
Db 2 PPPP 5

RESULT 57
US-08-467-344A-716
; Sequence 716, Application US/08467344A
; Patent No. 6586568
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; TAMI J. PILOT-MATIAS
; GEORGE J. DAWSON
; GEORGE G. SCHLAUDER
; SURESH M. DESAI
; THOMAS P. LEARY
; ANTHONY SCOTT MUERHOFF
; JAMES C. ERKER
; SHERI L. BUIJK
; ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,344A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,550
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 716:
US-08-467-344A-716

Query Match      26.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEM 4
Db 1 VLEM 4

RESULT 58
PCT-US92-09964-5
; Sequence 5, Application PC/TUS9209964
; GENERAL INFORMATION:
; APPLICANT: Holmes, Christopher P.
; TITLE OF INVENTION: Polymer Reversal on Solid Surfaces
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09964
; FILING DATE: 19921119
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,727
; FILING DATE: 22-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-51-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: both
; MOLECULE TYPE: peptide
PCT-US92-09964-5

Query Match      26.7%; Score 4; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 59
US-08-151-219-5
; Sequence 5, Application US/08151219
; Patent No. 5468494
; GENERAL INFORMATION:
; APPLICANT: Gevas, Philip C.
; APPLICANT: Grimes, Stephen
; APPLICANT: Karr, Stephen
```

```
;
; APPLICANT: Michaeli, Dov
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
; TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, White and Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,219
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas, Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 819-8286
; TELEFAX: (212) 354-8113
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-151-219-5

Query Match      26.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 60
US-08-188-223-4
; Sequence 4, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
```

```
;
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
US-08-188-223-4
Query Match 26.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PPPP 10
Db 2 PPPP 5
;
; RESULT 61
; US-08-188-223-11
; Sequence 11, Application US/08188223
; Patent No. 5688506
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,223
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
;
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
US-08-188-223-11
Query Match 26.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PPPP 10
Db 2 PPPP 5
;
; RESULT 62
; US-08-358-556A-25
; Sequence 25, Application US/08358556A
; Patent No. 5869643
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELETYPE: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-358-556A-25
Query Match 26.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PPPP 10
Db 1 PPPP 4
;
; RESULT 63
; US-08-968-466-4
; Sequence 4, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
```

```
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: C-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
;
; US-08-968-466-4
;
; Query Match 26.7%; Score 4; DB 3; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 7 PPPP 10
; Db 2 PPPP 5
;
; RESULT 64
; US-08-968-466-11
; Sequence 11, Application US/08968466
; Patent No. 6132720
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Immunogens Against Gonadotropin
; TITLE OF INVENTION: Releasing Hormone
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dimitrios T. Drivas, Esq.
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,466
; FILING DATE: 27-JAN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Drivas Esq., Dimitrios T.
; REGISTRATION NUMBER: 32,218
; REFERENCE/DOCKET NUMBER: 1102865-300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8286
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "spacer"
;
; US-08-968-466-11
;
; Query Match 26.7%; Score 4; DB 3; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 7 PPPP 10
; Db 2 PPPP 5
;
; RESULT 65
; US-09-001-984C-35
; Sequence 35, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Leal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
;
; US-09-001-984C-35
;
; Query Match 26.7%; Score 4; DB 3; Length 6;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 11 QETV 14
; Db 1 QETV 4
;
; RESULT 66
; US-08-478-546B-4
; Sequence 4, Application US/08478546B
; Patent No. 6303123
; GENERAL INFORMATION:
; APPLICANT: Grimes, Stephen
; APPLICANT: Scibienski, Robert
; TITLE OF INVENTION: Methods for the Treatment of Hormone-Dependent
```


APPLICANT: Kieliszewski, Marcia J.
TITLE OF INVENTION: No. 6548642e1 Synthetic Genes for Plant Gums
FILE REFERENCE: OHU-03417
CURRENT APPLICATION NUMBER: US/09/119,507B
CURRENT FILING DATE: 1998-07-20
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 117
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
NAME/KEY: SITE
LOCATION: (2), (5)
OTHER INFORMATION: The Proline at these positions is a
OTHER INFORMATION: hydroxyproline.
US-09-119-507B-117
Query Match 26.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PPPP 10
Db 2 PPPP 5
RESULT 70
PCT-US94-13205-5
Sequence 5, Application PC/TUS9413205
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,219
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-119-507B-117
Query Match 26.7%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PPPP 10
Db 2 PPPP 5
RESULT 71
US-08-151-219-3
Sequence 3, Application US/08151219
Patent No. 5468494
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,219
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-151-219-3
Query Match 26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 PPPP 10
Db 3 PPPP 6
RESULT 72
US-08-188-223-9
Sequence 9, Application US/08188223
Patent No. 5688506
GENERAL INFORMATION:
APPLICANT: Grimes, Stephen

PCT-US94-13205-5

Query Match 26.7%; Score 4; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 2 PPPP 5

RESULT 71

US-08-151-219-3
Sequence 3, Application US/08151219
Patent No. 5468494
GENERAL INFORMATION:
APPLICANT: Gevas, Philip C.
APPLICANT: Grimes, Stephen
APPLICANT: Karr, Stephen
APPLICANT: Michaeli, Dov
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS
TITLE OF INVENTION: AGAINST HUMAN GASTRIN 17
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, White and Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 100036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,219
FILING DATE: 12-NOV-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Drivas, Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-028
TELEPHONE: (212) 819-8286
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-151-219-3

Query Match 26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PPPP 10
Db 3 PPPP 6

RESULT 72

US-08-188-223-9
Sequence 9, Application US/08188223
Patent No. 5688506
GENERAL INFORMATION:
APPLICANT: Grimes, Stephen

APPLICANT: Scibienski, Robert
TITLE OF INVENTION: Immunogens Against Gonadotropin
TITLE OF INVENTION: Releasing Hormone
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, Esq.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,223
FILING DATE: 27-JAN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Drivas Esq., Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..7
OTHER INFORMATION: /note= "spacer"
US-08-188-223-9
Query Match 26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PPPP 10
Db 2 PPPP 5
RESULT 73
US-08-188-223-10
Sequence 10, Application US/08188223
Patent No. 568566
GENERAL INFORMATION:
APPLICANT: Grimes, Stephen
APPLICANT: Scibienski, Robert
TITLE OF INVENTION: Immunogens Against Gonadotropin
TITLE OF INVENTION: Releasing Hormone
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dimitrios T. Drivas, Esq.
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/188,223
FILING DATE: 27-JAN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Drivas Esq., Dimitrios T.
REGISTRATION NUMBER: 32,218
REFERENCE/DOCKET NUMBER: 1102865-300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8286
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: C-terminal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..7
OTHER INFORMATION: /note= "spacer"
US-08-188-223-10
Query Match 26.7%; Score 4; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 PPPP 10
Db 3 PPPP 6
RESULT 74
US-08-968-676-91
Sequence 91, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-968-676-91

Query Match 26.7%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MKFP 7
|||
Db 3 MKFP 6

RESULT 75

US-08-680-326-73
; Sequence 73, Application US/08680326
; Patent No. 5925733
; GENERAL INFORMATION:
; APPLICANT: ROSE, TIMOTHY M.
; APPLICANT: BOSCH, MARINX
; APPLICANT: STRAND, KURT
; APPLICANT: TODARO, GEORGE J.
; TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
; TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
; TITLE OF INVENTION: FIBROMATOSIS
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/680,326
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 29938-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-680-326-73

Query Match 26.7%; Score 4; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No.2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ETVT 15
|||
Db 3 ETVT 6

Search completed: November 25, 2003, 20:16:03
Job time : 17.3564 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 13.8032 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKPPFKLVKVEVFPFP 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	4	26.7	11	2 S33519	probable secreted
2	3	20.0	5	2 C41225	copper resistance
3	3	20.0	6	2 A61049	halo-toxin - Pseud
4	3	20.0	8	2 A42689	major postsynaptic
5	3	20.0	9	2 A60356	118K stomach cance
6	3	20.0	9	2 I54379	Gene NF2 protein -
7	3	20.0	9	2 S66635	alpha-2-macroglobu
8	3	20.0	9	2 PC7073	ubiquinol-cytochro
9	3	20.0	10	2 GXHU1	gastric juice pept
10	3	20.0	10	2 B33143	pneumadin - human
11	3	20.0	10	2 A33443	pneumadin - rat
12	3	20.0	10	2 S65728	hemoglobin, extrac
13	3	20.0	10	2 S43625	cytochrome-c oxida
14	3	20.0	11	2 S66606	quinoline 2-oxidor
15	3	20.0	11	2 PA0028	protein QA300042 -
16	3	20.0	12	2 S26559	T-cell receptor be
17	3	20.0	12	2 A20907	Ig kappa chain J1
18	3	20.0	12	2 PH1466	T-cell receptor be
19	3	20.0	13	2 S21152	tryptophyllin-rela
20	3	20.0	13	2 H64124	hypothetical prote
21	3	20.0	13	2 B44957	protein L7 - commo
22	3	20.0	13	2 A26999	carboxylesterase (
23	3	20.0	13	2 S23638	Ig kappa chain J s
24	3	20.0	13	2 S65612	tubulin alpha-chain
25	3	20.0	13	2 S01904	H+-transporting tw
26	3	20.0	14	2 S14336	mastoparan B - hor
27	3	20.0	14	2 PC7075	guanylate cyclase
28	3	20.0	14	2 PH0753	T-cell receptor be
29	3	20.0	14	2 PH0762	T-cell receptor be

30	3	20.0	15	2 S10891	ubiquitin thiolest
31	3	20.0	15	2 PA0027	protein QA100006 -
32	3	20.0	15	2 PA0026	protein QA300027 -
33	3	20.0	15	2 PA0024	protein QA300050 -
34	3	20.0	15	2 PT0082	protein QA600023 -
35	3	20.0	15	2 S13973	chlorophyll a/b-bi
36	3	20.0	15	2 S43321	RNA-binding protei
37	3	20.0	15	2 PS0452	32K protein 3306 -
38	3	20.0	15	2 PS0452	milk band B protei
39	3	20.0	15	2 S03955	acidic fibroblast
40	3	20.0	15	2 PQ0074	T-cell receptor be
41	3	20.0	15	2 PH0752	T-cell receptor be
42	3	20.0	15	2 PH0760	ubiquitin thiolest
43	3	20.0	15	2 PT0093	shikimate 5-dehydr
44	3	20.0	16	2 I40065	regulatory protein
45	3	20.0	16	2 AS3337	blaz protein - Sta
46	3	20.0	16	2 S34444	zinc finger protei
47	3	20.0	16	2 D45193	T-cell receptor be
48	3	20.0	16	2 PH0758	T-cell receptor be
49	3	20.0	16	2 PH0759	T-cell receptor be
50	3	20.0	16	2 S33590	beta-crystallin A3
51	3	20.0	17	2 I54269	vitamin D binding
52	3	20.0	17	2 S50901	chlorophyll a/b-bi
53	3	20.0	17	2 S15064	hypothetical prote
54	3	20.0	17	2 A35550	adrenocortical cel
55	3	20.0	17	2 A60889	olfactory glycopro
56	3	20.0	17	2 G85956	hypothetical prote
57	3	20.0	17	4 I76673	hypothetical COL1
58	3	20.0	18	2 G02018	proteasome chain L
59	3	20.0	18	2 S09731	photosystem I prot
60	3	20.0	18	2 A29558	pigment-dispersing
61	3	20.0	18	2 S54272	CTC 75 protein - h
62	3	20.0	18	4 I54078	hypothetical BML/R
63	3	20.0	19	2 B56613	virion morphogenes
64	3	20.0	19	2 T02624	hypothetical prote
65	3	20.0	19	2 S19532	globin - polychaet
66	3	20.0	19	2 S19613	globin - polychaet
67	3	20.0	19	2 S43624	cytochrome-c oxida
68	3	20.0	19	2 S02808	nucleolin - bovine
69	3	20.0	20	2 S77981	cytochrome-c oxida
70	3	20.0	20	2 B53875	creatine kinase IE
71	3	20.0	20	2 A53875	creatine kinase IE
72	3	20.0	20	2 A45806	T-cell receptor be
73	3	20.0	20	2 A54538	39k major outer me
74	3	20.0	20	2 S57286	translation elonga
75	3	20.0	20	2 S09720	2S albumin small c
76	3	20.0	20	2 B30208	hypothetical prote
77	3	20.0	20	2 A34859	heliothermine - Mex
78	3	20.0	20	2 A25335	myosin-light-chain
79	3	20.0	20	2 S58382	hypothetical prote
80	3	20.0	20	2 S03954	acidic fibroblast
81	3	20.0	20	2 A41439	acid ribonuclease
82	3	20.0	20	2 S03508	T-cell receptor al
83	3	20.0	20	2 S68341	procathepsin L - g
84	3	20.0	20	2 A61526	major milk gland p
85	2	13.3	4	2 A02147	phagocytosis-stimu
86	2	13.3	4	2 T46627	hypothetical prote
87	2	13.3	4	2 S53508	starvation-induced
88	2	13.3	5	2 T14908	hypothetical prote
89	2	13.3	5	2 JS0319	subesophageal gang
90	2	13.3	6	2 S02617	alcohol dehydrogen
91	2	13.3	6	2 A35890	RNA-directed DNA p
92	2	13.3	6	2 B34835	dnaa protein - Pse
93	2	13.3	6	2 A60986	N-formyl oligopept
94	2	13.3	6	2 B60110	repetitive protein
95	2	13.3	6	2 A61140	sperm acrosomal pr
96	2	13.3	6	2 I51317	bHLH transcription
97	2	13.3	6	2 H48394	glycoprotein compo
98	2	13.3	6	2 S78764	ribosomal protein
99	2	13.3	6	2 A20186	fatty-acid synthas
100	2	13.3	6	2 I48126	alpha-tubulin - Ch

ALIGNMENTS

RESULT 1

probable secreted protein - Acholeplasma laidlawii (fragment)
C;Species: Acholeplasma laidlawii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999
C;Accession: S33519
R;Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.
submitted to the EMBL Data Library, June 1993
A;Description: Sequence regions from Acholeplasma laidlawii which restore export of beta
A;Reference number: S33518
A;Accession: S33519
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <BOY>
A;Cross-references: EMBL:Z22875; NID:g311706; PIDN:CAA60495.1; PID:g311708

Query Match 26.7%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVV 9
|||
Db 3 KLVV 6

RESULT 2

Copper resistance protein - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: C41225
R;Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer mem
A;Reference number: A41225; MUID:92020961; PMID:1924351
A;Accession: C41225
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <CHA>

Query Match 20.0%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKL 7
|||
Db 2 PKL 4

RESULT 3

halo-toxin - Pseudomonas syringae pv. mori
C;Species: Pseudomonas syringae pv. mori
A;Note: host mulberry tree
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C;Accession: A61049
R;Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.;
Chem. Lett. 00, 679-680, 1989
A;Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri
A;Reference number: A61049
A;Accession: A61049
A;Molecule type: protein
A;Residues: 1-6 <KAJ>
A;Note: sequence confirmed by synthesis
C;Comment: This toxin is one of the etiological agents of halo bright disease in mulber
C;Keywords: toxin

Query Match 20.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPP 5
|||
Db 1 PPP 3

RESULT 4

major postsynaptic density protein - rat (fragment)
A42689
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 26-May-1994
C;Accession: A42689
R;Wu, K.; Huang, Y.; Adler, J.; Black, I.B.
Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992
A;Title: On the identity of the major postsynaptic density protein.
A;Reference number: A42689; MUID:92212958; PMID:1313576
A;Accession: A42689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <WUA>

Query Match 20.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9
|||
Db 2 LKV 4

RESULT 5

118K stomach cancer antigen - human (fragment)
A60356
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60356
R;Shiraishi, Y.
Int. J. Cancer 45, 783-787, 1990
A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens
A;Reference number: A60356; MUID:90216080; PMID:2333853
A;Accession: A60356
A;Molecule type: protein
A;Residues: 1-9 <SHI>
C;Keywords: glycoprotein

Query Match 20.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3
|||
Db 3 LKP 5

RESULT 6

gene NF2 protein - human (fragment)
I54379
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C;Accession: I54379
R;Arai, E.; Ikeuchi, T.; Nakamura, Y.
Hum. Mol. Genet. 3, 937-939, 1994
A;Title: Characterization of the translocation breakpoint on chromosome 22q12.2 in a
A;Reference number: I54379; MUID:95038750; PMID:77951241
A;Accession: I54379
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-9 <RES>
A;Cross-references: GB:S75841; NID:g861532; PIDN:AAD14190.1; PID:g4261890
C;Genetics:

A;Gene: GDB:NF2
A;Cross-references: GDB:120232; OMIM:101000
A;Map position: 22q12.2-22q12.2

A:Molecule type: protein
A:Residues: 1-10 <FUS>

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKV 9
|||
Db 8 LKV 10

RESULT 13

S43625
cytochrome-c oxidase (EC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C:Accession: S43625
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase
A:Reference number: S43624; MUID:94237150; PMID:8181469

A:Accession: S43625
A:Molecule type: protein
A:Residues: 1-10 <FRE>
A:Note: the source is designated as Salmo gairdneri
C:Genetics:

A:Genome: nuclear
A:Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||
Db 4 KVE 6

RESULT 14

S66606
quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S66606
R:Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.
Eur. J. Biochem. 232, 536-544, 1995
A:Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from *Comamonas testosteroni*
A:Reference number: S66606; MUID:96035889; PMID:7556204

A:Accession: S66606
A:Molecule type: protein
A:Residues: 1-11 <SCH>
A:Experimental source: strain 53

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3
|||
Db 8 LKP 10

RESULT 15

PA0028
protein QA300042 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0028
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
A:Reference number: PA0001

A:Accession: PA0028
A:Molecule type: protein
A:Residues: 1-11 <KAM>
A:Experimental source: seed
C:Keywords: seed

Query Match 20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5
|||
Db 6 PPP 8

RESULT 16

S26559
T-cell receptor beta chain (clone Cw3/Cas15) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26559
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Virelizier, A.
Exp. Med. 176, 439-447, 1992

A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061

A:Accession: S26559
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>

A:Cross-references: EMBL:X68009
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas15
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 8 EVF 10

RESULT 17

A20907
IG kappa chain J1 region - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Jul-2000
C:Accession: A20907; A53275
R:Emorine, L.; Max, E.E.
Nucleic Acids Res. 11, 8877-8890, 1983

A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple rearrangements
A:Reference number: A20907; MUID:84169523; PMID:6324107

A:Accession: A20907
A:Molecule type: DNA
A:Residues: 1-12 <EMO>

A:Cross-references: GB:X00232; NID:gl582; PIDN:CAA25052.1; PID:gl364236
R:Ayadi, R.; Marche, P.N.; Cazenave, P.A.

Immunogenetics 34, 201-207, 1991

A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A:Reference number: A53275; MUID:91372868; PMID:1909995

A:Accession: A53275
A:Molecule type: DNA
A:Residues: 1-12 <AYA>

A:Note: sequence extracted from NCBI backbone (NCBI:56069, NCBI:56161)
C:Comment: This J1 segment may not be functional because of a short space between the C and J1 segments
C:Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||

Db 8 KVE 10

RESULT 18

PH1466
 1-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C:Accession: PH1466
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K...
 J. Exp. Med. 177, 811-820, 1993
 A>Title: T cell receptor selection by and recognition of two class I major histocompatib...
 A:Reference number: PH1430; MUID:93171821; PMID:8436911
 A:Accession: PH1466
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 20.0%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
 ||||
 Db 8 EVF 10

RESULT 19

S21152
 tryptophyllin-related peptide - two-colored leaf frog
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
 C:Accession: S21152
 R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G...
 FEBS Lett. 302, 151-154, 1992
 A>Title: Identification and characterization of two dermorphins from skin extracts of th...
 A:Reference number: S21152; MUID:92339502; PMID:1633846
 A:Accession: S21152
 A:Molecule type: protein
 A:Residues: 1-13 <MG>
 A:Experimental source: skin
 C:Superfamily: unassigned animal peptides

Query Match 20.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPF 4
 ||||
 Db 3 KPF 5

RESULT 20

H64124
 hypothetical protein H11460 - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 31-Oct-1997
 C:Accession: H64124
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A...
 i; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J...
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.I.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter...
 A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: H64124
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <TIGR>

A:Cross-references: GB:U32824; GB:I42023; NID:gl574299; PID:gl574306; TIGR:H11460

Query Match 20.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
 ||||
 Db 4 KLK 6

RESULT 21

B44957
 protein L7 - common tobacco (cv. Samsun NN) (fragment)
 C:Species: Nicotiana tabacum (common tobacco)
 C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 30-Sep-1993
 C:Accession: B44957
 R:Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.
 Plant Cell Physiol. 31, 215-221, 1990
 A>Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacu...
 A:Reference number: A44957
 A:Accession: B44957
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <TAK>

Query Match 20.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPF 4
 ||||
 Db 9 KPF 11

RESULT 22

A26999
 carboxylesterase (EC 3.1.1.1), intestinal - Caenorhabditis elegans (fragment)
 C:Species: Caenorhabditis elegans
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 07-Feb-1997
 C:Accession: A26999
 R:McGhee, J.D.
 Biochemistry 26, 4101-4107, 1987
 A>Title: Purification and characterization of a carboxylesterase from the intestine of...
 A:Reference number: A26999; MUID:88000636; PMID:3651439
 A:Accession: A26999
 A:Molecule type: protein
 A:Residues: 1-13 <MCG>

C:Keywords: carboxylic ester hydrolase; intestine

Query Match 20.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
 ||||
 Db 10 KVE 12

RESULT 23

S23638
 IG kappa chain J segment (J-kappa-1) - human
 C:Species: Homo sapiens (man)
 C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C:Accession: S23638
 R:Huber, C.; Klobeck, H.G.; Zachau, H.G.
 Eur. J. Immunol. 22, 1561-1565, 1992
 A>Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kap...
 A:Reference number: S23637; MUID:92289816; PMID:1601042
 A:Accession: S23638
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-13 <HUB>

A:Cross-references: EMBL:X63370

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991

C;Keywords: heterotetramer; immunoglobulin

Query Match 20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||
Db 8 KVE 10

RESULT 24
S65612
tubulin alpha-chain - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S65612
R;Ruediger, M.; Plessmann, U.; Ruediger, A.H.; Weber, K.
FEBS Lett. 364, 147-151, 1995
A;Title: Beta tubulin of bull sperm is polyglycylated.
A;Reference number: S65611; MUID:95269788; PMID:7750559
A;Accession: S65612
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <RUE>

Query Match 20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
|||
Db 5 VEV 7

RESULT 25
S01904
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloro
C;Species: chloroplast Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 03-Jun-2002
C;Accession: S01904
R;Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.T.N.
Nucleic Acids Res. 16, 10372, 1988
A;Title: Nucleotide sequence of chloroplast CF1-ATPase epsilon-subunit and elongator TRN
A;Reference number: S01903; MUID:89057486; PMID:2904134
A;Accession: S01904
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-13 <CHE>
C;Genetics:
A;Gene: atpB
A;Genome: chloroplast
C;Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 20.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
|||
Db 10 KLK 12

RESULT 26
S14336
mastoparan B - hornet (Vespa basalis)
C;Species: Vespa basalis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Apr-1999
C;Accession: S14336
R;Ho, C.L.; Hwang, L.L.
Biochem. J. 274, 453-456, 1991
A;Title: Structure and biological activities of a new mastoparan isolated from the venom

A;Reference number: S14336; MUID:91174755; PMID:2006909
A;Accession: S14336
A;Molecule type: protein
A;Residues: 1-14 <HOC>
A;Experimental source: venom
C;Function:
A;Description: possesses a potent hemolytic activity which acts in synergy with the lei
C;Keywords: amidated carboxyl end; mast cell; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
|||
Db 2 KLK 4

RESULT 27
PC7075
guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: PC7075
R;Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y
Electrophoresis 21, 1853-1871, 2000
A;Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles o
A;Reference number: PC7072
A;Accession: PC7075
A;Molecule type: protein
A;Residues: 1-14 <TSU>
A;Experimental source: strain C57BL/6Cr Slc, male; brain, striatum
C;Keywords: brain; phosphorus-oxygen lyase

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 12 EVF 14

RESULT 28
PH0753
T-cell receptor beta chain (H3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0753
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility compl
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0753
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60846; NID:g51199; PIDN:CAA43237.1; PID:g51200
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 10 EVF 12

RESULT 29
PH0762

T-cell receptor beta chain (K1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0762
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-related allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0762
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60856; NID:g52768; PIDN:CAA43246.1; PID:g52769
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12
|||
Db 10 EVF 12

RESULT 30
S10891
ubiquitin thiolesterase (EC 3.1.2.15) PGP9.5 - human (fragment)
N;Alternate names: ubiquitin carboxyl-terminal hydrolase, neuron-specific
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C;Accession: S10891
R;Day, I.N.M.; Hinks, L.J.; Thompson, R.J.
Biochem. J. 268, 521-524, 1990
A;Title: The structure of the human gene encoding protein gene product 9.5 (PGP9.5), a nuclear protein.
A;Reference number: S10891; MUID:90303237; PMID:2163617
A;Accession: S10891
A;Molecule type: DNA
A;Residues: 1-15 <DAY>
A;Cross-references: EMBL:X17377; NID:g35441; PIDN:CAA35249.1; PID:g296799
C;Genetics:
A;Introns: 11/3
C;Superfamily: human ubiquitin thiolesterase
C;Keywords: thiolester hydrolase

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3
|||
Db 3 LKP 5

RESULT 31
PA0027
protein QA10006 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0027
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of plant proteins and standardization of
A;Reference number: PA0001
A;Accession: PA0027
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: callus

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9
|||
Db 2 LKV 4

RESULT 32
PA0026
protein QA300027 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0026
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of plant proteins and standardization of
A;Reference number: PA0001
A;Accession: PA0026
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: leaf

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9
|||
Db 2 LKV 4

RESULT 33
PA0024
protein QA300050 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0024
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis of plant proteins and standardization of
A;Reference number: PA0001
A;Accession: PA0024
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: seed

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
|||
Db 6 PFP 8

RESULT 34
PT0082
protein QA600023 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 06-Jun-1997
C;Accession: PT0082
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A;Description: Two dimensional electrophoresis of plant proteins and standardization of
A;Reference number: PN0173
A;Accession: PT0082
A;Molecule type: protein
A;Residues: 1-15 <TSU>
A;Experimental source: leaf

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKL 7

```

Db          |||
           5 PKL 7

RESULT 35
SI3973
Chlorophyll a/b-binding protein type II - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: SI3973
R:Jains, P.; Junge, W.
Eur. J. Biochem. 193, 731-736, 1990
A:Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of the P
A:Reference number: SI3973; MUID:91065379; PMID:2174365
A:Accession: SI3973
A:Molecule type: protein
A:Residues: 1-15 <UAH>
C:Genetics:
A:Genome: nuclear
C:Keywords: chlorophyll; chloroplast; light-harvesting complex; thylakoid; transmembrane

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
   |||
Db 4 EVF 6

RESULT 36
S43321
RNA-binding protein - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 01-Feb-1999
C:Accession: S43321
R:Lakhani, S.; Khanna, N.C.; Tewari, K.K.
Plant Mol. Biol. 23, 963-979, 1993
A:Title: Nascent transcript-binding protein of the pea chloroplast transcriptionally act
A:Reference number: S43321; MUID:94083566; PMID:8260634
A:Accession: S43321
A:Molecule type: protein
A:Residues: 1-15 <LAK>
C:Function:
A:Description: probably involved in the transcription of chloroplast genes
C:Keywords: RNA binding

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
   |||
Db 10 KVE 12

RESULT 37
PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0452
R:Tsuigita, A.; Miyatake, N.
submitted to JIPID, April 1993
A:Reference number: PS0208
A:Accession: PS0452
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: bran, strain Nihonbare
C:Comment: molecular weight 32K, pi 5.3.

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;

```

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
   |||
Db 6 PFP 8

RESULT 38
C61511
milk band B protein - Australian echidna (fragment)
C:Species: Tachyglossus aculeatus (Australian echidna)
C:Date: 09-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 11-May-2000
C:Accession: C61511
R:Teahan, C.G.; McKenzie, H.A.; Griffiths, M.
Comp. Biochem. Physiol. B 99, 99-118, 1991
A:Title: Some monotreme milk "whey" and blood proteins.
A:Reference number: A61511; MUID:92070088; PMID:1959333
A:Accession: C61511
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <GRI>
C:Keywords: glycoprotein

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PFP 14
   |||
Db 13 PFP 15

RESULT 39
S03955
acidic fibroblast growth factor - dog (fragment)
N:Alternate names: alpha-endothelial cell growth factor
C:Species: Canis lupus familiaris (dog)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S03955
R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Scha
Eur. J. Biochem. 181, 67-73, 1989
A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine f
A:Reference number: S03953; MUID:89231704; PMID:2714282
A:Accession: S03955
A:Molecule type: protein
A:Residues: 1-15 <QUI>
C:Keywords: growth factor

Query Match          20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
   |||
Db 5 PKL 7

RESULT 40
PQ0074
T-cell receptor beta chain (BTB82) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: PQ0074
R:Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A:Reference number: JQ0472
A:Accession: PQ0074
A:Molecule type: mRNA
A:Residues: 1-15 <TAN>
A:Experimental source: T cell
C:Genetics:
A:Gene: BTB82

```

C;Keywords: receptor

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 3 EVF 5

RESULT 41

PH0752
T-cell receptor beta chain (C1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0752
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0752
A;Molecule type: mRNA
A;Residues: 1-15 <CAS>
A;Cross-references: EMBL:X60845; NID:g50230; PIDN:CAA43236.1; PID:g50231
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 11 EVF 13

RESULT 42

PH0760
T-cell receptor beta chain (H2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0760
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0760
A;Molecule type: mRNA
A;Residues: 1-15 <CAS>
A;Cross-references: EMBL:X60855; NID:g51194; PIDN:CAA43245.1; PID:g51195
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 11 EVF 13

RESULT 43

PT0093
ubiquitin thiolesterase (EC 3.1.2.15) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 18-Sep-1998
C;Accession: PT0093; PNO045
R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, July 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PT0091
A;Accession: PT0093
A;Molecule type: Protein
A;Residues: 1-15 <KAW>
A;Experimental source: brain, striatum
R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neu
A;Reference number: PNO041
A;Accession: PNO045
A;Molecule type: Protein
A;Residues: 1-15 <KAT>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 28,000 and the pI is 5.0.
C;Keywords: brain; thiolester hydrolase

Query Match 20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3
|||
Db 3 LKP 5

RESULT 44

I40065
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)
C;Species: Buchnera aphidicola
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 08-Oct-1999
C;Accession: I40065
R;Rounbakhsh, D.; Baumann, P.
Gene 155, 107-112, 1995
A;Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (enc
A;Reference number: I40061; MUID:95212914; PMID:7535281
A;Accession: I40065
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-16 <RES>
A;Cross-references: EMBL:U10499; NID:g854717; PIDN:AAA79128.1; PID:g854718
C;Genetics:
A;Gene: aroE
C;Keywords: oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPK 6
|||
Db 9 FPK 11

RESULT 45

A53337
regulatory protein tyrR - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 07-May-1999
C;Accession: A53337
R;Argaet, V.P.; Wilson, T.J.; Davidson, B.E.
J. Biol. Chem. 269, 5171-5178, 1994
A;Title: Purification of the Escherichia coli regulatory protein TyrR and analysis of
A;Reference number: A53337; MUID:94148980; PMID:8106498
A;Accession: A53337
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <ARG>

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 4 EVF 6

RESULT 46

S34444
bla2 protein - Staphylococcus aureus plasmid p1258 (fragment)
C:Species: Staphylococcus aureus
C:Date: 22-Nov-1993 #sequence_revision 09-Mar-1996 #text_change 07-May-1999
C:Accession: S34444
R;Wang, P.Z.; Projan, S.J.; Novick, R.P.
Nucleic Acids Res. 19, 4000, 1991
A:Title: Nucleotide sequence of beta-lactamase regulatory genes from staphylococcal plasmid p1258
A:Reference number: S34444; MUID:91319567; PMID:1861992
A:Accession: S34444
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-16 <WAN>
A:Cross-references: EMBL:M62650
A:Experimental source: strain RN11
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: bla2
A:Genome: plasmid p1258

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
|||
Db 4 KLK 6

RESULT 47

D45193
zinc finger protein ZNF60 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: D45193
R;Lichter, P.; Bray, P.; Ried, T.; Dawid, I.B.; Ward, D.C.
Genomics 13, 999-1007, 1992
A:Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile sites
A:Reference number: A43284; MUID:92372070; PMID:1505991
A:Accession: D45193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <LIC>
A:Cross-references: GB:M88369; NID:g340475; PIDN:AAA61327.1; PID:g340476
A:Note: sequence extracted from NCBI backbone (NCBIN:111662, NCBIP:111664)

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPF 4
|||
Db 6 KPF 8

RESULT 48

PH0758
T-cell receptor beta chain (E22) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0758
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-1 allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0758

A:Molecule type: mRNA
A:Residues: 1-16 <CAS>

A:Cross-references: EMBL:X60853; NID:g50743; PIDN:CAA43243.1; PID:g50744
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 12 EVF 14

RESULT 49

PH0759
T-cell receptor beta chain (QB7.3.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0759
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-1 allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0759
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Cross-references: EMBL:X60854; NID:g53878; PIDN:CAA43244.1; PID:g53879
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
|||
Db 12 EVF 14

RESULT 50

S33590
beta-crystallin A3 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S33590
R;David, L.L.; Shearer, T.R.
FEBS Lett. 324, 265-270, 1993
A:Title: beta-crystallins insolubilized by calpain II in vitro contain cleavage sites
A:Reference number: S33586; MUID:94009594; PMID:8405363
A:Accession: S33590
A:Molecule type: protein
A:Residues: 1-16 <DAV>

Query Match 20.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||
Db 6 KVE 8

RESULT 51

I54269
vitamin D binding protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C:Accession: I54269
R;Braun, A.; Bichlmaier, R.; Muller, B.; Cleve, H.
Hum. Genet. 90, 526-532, 1993

A;Title: Molecular evaluation of an Alu repeat including a polymorphic variable poly(da)
A;Reference number: I54269; MUID:93154720; PMID:8381387
A;Accession: I54269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-17 <RES>
A;Cross-references: GB:SS4074; NID:9264876; PIDN:AD13872.1; PID:g4261572
C;Superfamily: serum albumin; serum albumin repeat homology

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred.No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12
|||
Db 13 EVF 15

RESULT 52
S50901
Chlorophyll a/b-binding protein Lhcb4 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIa protein
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50901
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1063-1069, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclohexylphosphoribosyl pyrophosphate (DCCPP)
A;Reference number: S50900; MUID:95112835; PMID:7813461
A;Accession: S50901
A;Molecule type: protein
A;Residues: 1-17 <WAL>
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosynthesis

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred.No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12
|||
Db 9 EVF 11

RESULT 53
S15064
Hypothetical protein A - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1997
C;Accession: S15064; S12677
R;Clayton, C.E.
Submitted to the EMBL Data Library, April 1990
A;Reference number: S15063
A;Accession: S15064
A;Molecule type: DNA
A;Residues: 1-17 <CLA>
A;Cross-references: EMBL:X52586; NID:gl0397; PID:g10402
R;Vijayarath, S.; Ernest, I.; Itzhaki, J.E.; Sherman, D.; Mowatt, M.R.; Michels, P.A.
Nucleic Acids Res. 18, 2967-2975, 1990
A;Title: The genes encoding fructose biphosphate aldolase in Trypanosoma brucei are interrupted
A;Reference number: S12673; MUID:90272402; PMID:2349093
A;Accession: S12677
A;Molecule type: DNA
A;Residues: 1-9 <VIJ>
A;Cross-references: EMBL:X52586

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred.No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEV 11
|||
Db 5 VEV 7

RESULT 54
A35550
Adrenocortical cell major secreted protein - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
C;Accession: A35550
R;Shi, D.L.; Savona, C.; Gagnon, J.; Cochet, C.; Chambaz, E.M.; Feige, J.J.
J. Biol. Chem. 265, 2881-2887, 1990
A;Title: Transforming growth factor-beta stimulates the expression of alpha-2-macroglobulin
A;Reference number: A35550; MUID:90153919; PMID:1689294
A;Accession: A35550
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <SHI>

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred.No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3
|||
Db 4 LKP 6

RESULT 55
A60889
Olfactory glycoprotein RB-8 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60889
R;Schwob, J.E.; Gottlieb, D.I.
J. Neurosci. 8, 3470-3480, 1988
A;Title: Purification and characterization of an antigen that is spatially segregated
A;Reference number: A60889; MUID:89010968; PMID:3171685
A;Accession: A60889
A;Molecule type: protein
A;Residues: 1-17 <SCH>
A;Note: this protein was purified from whole brain
C;Comment: The monoclonal antibody RB-8 binds this integral membrane glycoprotein on t
C;Keywords: glycoprotein; membrane protein; olfaction

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred.No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
|||
Db 10 KVE 12

RESULT 56
G85956
Hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDI
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: G85956
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimailanta, E.; Potamou, K.; Apodac
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85956
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-17 <STO>
A;Cross-references: GB:AE005174; NID:gl2517539; PIDN:AGS8115.1; GSPDB:GN00145; UWGP:Z
C;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4331

Query Match 20.0%; Score 3; DB 2; Length 17;
Best Local Similarity 100.0%; Pred.No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5
|||
Db 6 PFP 8

RESULT 57

176673
hypothetical COII/ND5 mutant fusion protein - mouse mitochondrion (fragment)
N:Alternate names: COII/ND5 protein
C:Species: mitochondrion Mus musculus (house mouse)
C>Date: 12-Aug-1996 #sequence_revision 16-Jul-1998 #text_change 20-Apr-2000
C:Accession: I76673; I76674
R:Nelson, I.; Gerasimov, S.; Marsac, C.; Lestienne, P.; Boursot, P.
Mamm. Genome 4, 680-683, 1993
A:Title: Sequence analysis of a deleted mitochondrial DNA molecule in heteroplasmic mice
A:Reference number: I57011; MUID:94108239; PMID:8281018

A:Accession: I76673
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-17 <NEL1>
A:Cross-references: GB:S68119; NID:g544777
A:Accession: I76674
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 8-17 <NEL2>

A:Cross-references: GB:S68119; NID:g544777
A:Comment: This is the hypothetical translation of a sequence believed to result from a
C:Genetics:

A:Gene: COII/ND5
A:Genome: mitochondrion
A:Genetic code: SGC1
C:Keywords: fusion protein; mitochondrion
F:1-7/Region: cytochrome-c oxidase chain II
F:8-17/Region: NADH dehydrogenase (ubiquinone) chain 5

Query Match 20.0%; Score 3; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
|||
Db 4 KLK 6

RESULT 58

G02018
proteasome chain LMP7 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 22-Jun-1999
C:Accession: G02018
R:Kim, T.

submitted to the EMBL Data Library, July 1995
A:Reference number: G09054
A:Accession: G02018

A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-18 <KIM>

A:Cross-references: EMBL:U32862; NID:g1045468; PIDN:AAA80234.1; PID:g1045469
C:Genetics:

A:Gene: LMP7
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||
Db 10 KVE 12

RESULT 59

S09731
photosystem I protein psal - spinach chloroplast (fragment)
C:Species: chloroplast Spinacia oleracea (spinach)

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 19-Jan-1996
C:Accession: S09731
R:Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.

FEBS Lett. 263, 274-278, 1990
A:Title: Polypeptide composition of higher plant photosystem I complex. Identification

A:Reference number: S09730; MUID:90242987; PMID:2185953
A:Accession: S09731

A:Molecule type: protein
A:Residues: 1-18 <IKB>
C:Genetics:

A:Gene: psal
A:Genome: chloroplast
A:Superfamily: photosystem I protein psal
C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem I; t

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFP 13
|||
Db 14 VFP 16

RESULT 60

A29558
pigment-dispersing hormone - eastern lubber grasshopper
C:Species: Romalea guttata (eastern lubber grasshopper)

C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 03-Mar-1994
C:Accession: A29558
R:Rao, K.R.; Mohrher, C.J.; Riehm, J.P.; Zahn, C.A.; Norton, S.; Johnson, L.; Tarr,

J. Biol. Chem. 262, 2672-2675, 1987
A:Title: Primary structure of an analog of crustacean pigment-dispersing hormone from

A:Reference number: A29558; MUID:87137516; PMID:3818616
A:Accession: A29558

A:Molecule type: protein
A:Residues: 1-18 <RAO>

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
|||
Db 12 PKL 14

RESULT 61

S54272
CTC 75 protein - human

C:Species: Homo sapiens (man)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999

C:Accession: S54272

R:Gensch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.
EMBO J. 14, 791-800, 1995

A:Title: Purification of the sequence-specific transcription factor CTCBF, involved in

A:Reference number: S54272; MUID:95188883; PMID:7882982

A:Accession: S54272
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <GEN>

Query Match 20.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||

Db 9 KVE 11

RESULT 62

I54078

hypothetical PML/RARA mutant fusion protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Feb-1997

C;Accession: I54078

R;Yoshida, H.; Naoe, T.; Fukutani, H.; Kiyoi, H.; Kubo, K.; Ohno, R.

Genes Chromosomes Cancer 12, 37-44, 1995

A;Title: Analysis of the joining sequences of the t(15;17) translocation in human acute

rt stretches

A;Reference number: I54078; MUID:95194921; PMID:7534109

A;Accession: I54078

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-18 <RES>

A;Cross-references: GB:S76369; NID:G913695

C;Comment: This sequence is the chimeric product of a translocation mutation.

C;Genetics:

A;Gene: PML/RARA

A;Map position: 15q22/17q12

C;Keywords: fusion protein; leukemia

Query Match 20.0%; Score 3; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 4.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12

Db 2 EVF 4

RESULT 63

B56613

viron morphogenesis late F alternate orf - phage Mu (fragment)

C;Species: phage Mu

C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995

C;Accession: B56613

R;Baxa, C.A.; Chiang, L.; Howe, M.M.

DNA Seq. 2, 329-333, 1992

A;Title: DNA sequence characterization of the G gene region of bacteriophage Mu.

A;Reference number: A56613; MUID:92338399; PMID:1385991

A;Accession: B56613

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-19 <BAX>

A;Note: sequence extracted from NCBI backbone (NCBIN:109379, NCBIIP:109381)

Query Match

20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3

Db 4 LKP 6

RESULT 64

T02624

hypothetical protein At2g25990 [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein T19L18.20

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001

C;Accession: T02624; B84655

R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, August 1998

A;Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.

A;Reference number: Z14681

A;Accession: T02624

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-19 <ROU>

A;Cross-references: EMBL:AC004747; NID:G3413696; PID:G3413713

A;Experimental source: Cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: B84655

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-19 <STO>

A;Cross-references: GB:AE002093; NID:G3413713; PIDN:AAC31236.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g25990; T19L18.20

A;Map position: 2

Query Match

20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLK 8

Db 8 KLK 10

RESULT 65

S19532

globin - polychaete (Eudistylia vancouveri) (fragment)

N;Alternate names: chlorocruorin

C;Species: Eudistylia vancouveri

C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998

C;Accession: S19532

R;Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O

J. Mol. Biol. 222, 1109-1129, 1991

A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular

A;Reference number: S19532; MUID:92106333; PMID:1762147

A;Accession: S19532

A;Molecule type: protein

A;Residues: 1-19 <QAB>

A;Experimental source: plume

C;Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dode

C;Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match

20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9

Db 8 LKV 10

RESULT 66

S19613

globin - polychaete (Eudistylia vancouveri) (fragment)

C;Species: Eudistylia vancouveri

C;Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998

C;Accession: S19613

R;Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O

J. Mol. Biol. 222, 1109-1129, 1991

A;Title: Hierarchy of globin complexes. The quaternary structure of the extracellular

A;Reference number: S19613; MUID:92106333; PMID:1762147

A;Accession: S19613

A;Molecule type: protein

A;Residues: 1-19 <QAB>

A;Experimental source: plume

C;Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dode

C;Keywords: calcium; dodecamer; heme; homotetramer; oxygen carrier

Query Match

20.0%; Score 3; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKV 9
|||
Db 8 LKV 10

RESULT 67
S43624
cytochrome-c oxidase (EC 1.9.3.1) chain IV, cardiac - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C:Accession: S43624
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase from rainbow trout
A:Reference number: S43624; MUID:94237150; PMID:8181469
A:Accession: S43624
A:Molecule type: protein
A:Residues: 1-19 <PRE>
A>Note: the source is designated as Salmo gairdneri
C:Genetics:
A:Genome: nuclear
C:Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
|||
Db 6 VEV 8

RESULT 68
S02808
nucleolin - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S02808
R:Sapp, M.; Richter, A.; Weisshart, K.; Caizergues-Ferrer, M.; Amalric, F.; Wallace, M.C.
Eur. J. Biochem. 179, 541-548, 1989
A:Title: Characterization of a 48-kDa nucleic-acid-binding fragment of nucleolin.
A:Reference number: S02808; MUID:89153087; PMID:2920725
A:Accession: S02808
A:Molecule type: protein
A:Residues: 1-19 <SAP>

Query Match 20.0%; Score 3; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||
Db 16 KVE 18

RESULT 69
S77981
cytochrome-c oxidase (EC 1.9.3.1) chain Va.1 - bigeye tuna (fragment)
C:Species: Thunnus obesus (bigeye tuna)
C>Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 26-Feb-1998
C:Accession: S77981
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77981
A:Molecule type: protein
A:Residues: 1-20 <ARN>
A:Experimental source: heart; liver
C:Genetics:
A:Genome: nuclear
C:Function:

A:Pathway: oxidative phosphorylation; respiratory chain
A:Superfamily: mammalian cytochrome-c oxidase chain Va
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||
Db 4 KVE 6

RESULT 70
B53875
creatine kinase (EC 2.7.3.2) CK-I - coho salmon (fragment)
C:Species: Oncorhynchus kisutch (coho salmon)
C>Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997
C:Accession: B53875
R:White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.
J. Protein Chem. 11, 489-494, 1992
A:Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB
A:Reference number: A53875; MUID:93080727; PMID:1449598
A:Accession: B53875
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-20 <WHI>
A:Experimental source: Brockmann body, principal islet
A>Note: sequence extracted from NCBI backbone (NCBIP:120600)
C:Superfamily: creatine kinase; creatine kinase repeat homology
C:Keywords: phosphotransferase

Query Match 20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
|||
Db 8 KLK 10

RESULT 71
A53875
creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)
C:Species: Oncorhynchus kisutch (coho salmon)
C>Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997
C:Accession: A53875
R:White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.
J. Protein Chem. 11, 489-494, 1992
A:Title: The principal islet of the Coho salmon (Oncorhynchus kisutch) contains the BB
A:Reference number: A53875; MUID:93080727; PMID:1449598
A:Accession: A53875
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-20 <WHI>
A:Experimental source: Brockmann body, principal islet
A>Note: sequence extracted from NCBI backbone (NCBIP:120599)
C:Superfamily: creatine kinase; creatine kinase repeat homology
C:Keywords: phosphotransferase

Query Match 20.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|||
Db 14 KVE 16

RESULT 72
A45806
T-cell receptor beta chain C region type 1 - human (fragment)
C:Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Jul-1999
 C;Accession: A45806
 R;Dent, A.L.; Fink, P.J.; Hedrick, S.M.
 J. Immunol. 143, 322-328, 1989
 A;Title: Characterization of an alternative exon of the murine T cell receptor beta chain
 A;Reference number: A45806; MUID:89278666; PMID:2525149
 A;Accession: A45806
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-20 <DEN>
 A;Cross-references: GB:M27225; NID:G339373; PIDN:AA61099.1; PID:G553781
 A;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 20.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFP 13
 |||
 Db 5 VFP 7

RESULT 73

A54538
 39k major outer membrane protein - Actinobacillus actinomycetemcomitans (strain 14) (EPR)
 C;Species: Actinobacillus actinomycetemcomitans
 C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
 C;Accession: A54538
 R;Koikeguchi, S.; Kato, K.; Nishimura, F.; Kurihara, H.; Murayama, Y.
 FEBS Microbiol. Lett. 77, 85-90, 1991
 A;Title: Isolation and partial characterization of a 39 kDa major outer membrane protein
 A;Reference number: A54538
 A;Accession: A54538
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <XOK>

Query Match 20.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
 |||
 Db 10 KVE 12

RESULT 74

S57286
 translation elongation factor aEF-1 beta - Sulfolobus solfataricus (fragments)
 C;Species: Sulfolobus solfataricus
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
 C;Accession: S57286
 R;Arcari, P.; Raimo, G.; Ianniciello, G.; Gallo, M.; Bocchini, V.
 Biochim. Biophys. Acta 1263, 86-88, 1995
 A;Title: The first nucleotide sequence of an archaeal elongation factor 1-beta gene.
 A;Reference number: S57286; MUID:95359209; PMID:7632739
 A;Accession: S57286
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <ARC>

Query Match 20.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKV 9
 |||
 Db 7 LKV 9

RESULT 75

S09720

2S albumin small chain nII - rape (fragments)
 C;Species: Brassica napus (rape)
 C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
 C;Accession: S09720
 R;Monsalve, R.L.; Menéndez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
 FEBS Lett. 263, 27-32, 1990
 A;Title: beta-turns as structural motifs for the proteolytic processing of seed protein
 A;Reference number: S 720; MUID:90542974; PMID:2185951
 A;Accession: S09720
 A;Molecule type: protein
 A;Residues: 1-9; 13-20 <KN>
 A;Experimental source: Seed
 A;Note: 1-Sei was also found

Query Match 20.0%; Score 3; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKL 7
 |||
 Db 8 PKL 10

Search completed: November 25, 2003, 18:28:19
 Job time: 14.803.868

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 7.26064 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKPPPKLKVEVFPPF 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	20.0	10	1 COXA_ONCMY	P80328 oncorhynchu
2	3	20.0	10	1 GATU_HUMAN	P21038 homo sapien
3	3	20.0	10	1 PNEU_HUMAN	P22103 homo sapien
4	3	20.0	10	1 PNEU_RAT	P21996 rattus norv
5	3	20.0	11	1 CSIS_BACSU	P81095 bacillus su
6	3	20.0	11	1 Q2OA_COMTE	P80464 comamonas t
7	3	20.0	13	1 IDHP_RAT	P56574 rattus norv
8	3	20.0	14	1 MAST_VESBA	P21654 vespa basal
9	3	20.0	15	1 FGPI_CANFA	P18651 canis famil
10	3	20.0	15	1 RMI2_YEAST	P36522 saccharomyc
11	3	20.0	15	1 UBL1_MONDO	P50103 monodelphis
12	3	20.0	15	1 VORA_METTM	P80907 methanobact
13	3	20.0	17	1 YALA_TRYBB	P17961 trypanosoma
14	3	20.0	19	1 COXA_ONCMY	P80327 oncorhynchu
15	3	20.0	20	1 COXA_THUOB	P80972 thunnus obe
16	3	20.0	20	1 JHBP_BOMMO	P81627 bombyx mori
17	3	20.0	20	1 MI17_BOVIN	P35451 bos taurus
18	3	20.0	20	1 OM4V_VIBAL	P83149 vibrio algi
19	3	20.0	20	1 OMP1_ACTAC	P20242 actinobacil
20	3	20.0	20	1 TRYL-STREX	P80420 streptomyce
21	2	13.3	4	1 TUFT_HUMAN	P01858 homo sapien
22	2	13.3	5	1 PAP2_PARMA	P81864 pardachirus
23	2	13.3	5	1 SUGA_ACHDO	P19991 acheta dome
24	2	13.3	6	1 UC22_WAIZE	P80628 zea mays (m
25	2	13.3	6	1 OVM_LBPDE	P42985 leptinotars
26	2	13.3	7	1 CCF1_ENTFA	P20104 enterococcu
27	2	13.3	7	1 FAR1_HELTI	P41871 helisoma tr
28	2	13.3	7	1 FAR4_PANRE	P41875 panagrellus
29	2	13.3	7	1 TPFY_PACDA	P83455 pachymedusa
30	2	13.3	7	1 UF04_MOUSE	P38642 mus musculu
31	2	13.3	7	1 UN06_PINPS	P81675 pinus pinas
32	2	13.3	8	1 ANG2_BOTJA	Q10582 bothrops ja
33	2	13.3	8	1 LPMS_STAEP	P23211 staphylococ

34	2	13.3	8	1 PPK2_PERAM	P82692 periplaneta
35	2	13.3	8	1 PPK3_PERAM	P82618 periplaneta
36	2	13.3	8	1 RS7_MYCIT	P33564 mycobacteri
37	2	13.3	9	1 BUK_CLOPA	P81337 clostridium
38	2	13.3	9	1 CCAE_CARMA	P38556 carcinus ma
39	2	13.3	9	1 CONO_CONGE	P05486 conus geogr
40	2	13.3	9	1 COW_CONVE	P83047 conus ventr
41	2	13.3	9	1 FAR4_CALVO	P41859 calliphora
42	2	13.3	9	1 FAR5_ASCSU	P43170 ascaris suu
43	2	13.3	9	1 FIBB_ERYPA	P19346 erythrocebu
44	2	13.3	9	1 KNL3_BOMVA	P83058 bombina var
45	2	13.3	9	1 LMT3_LOCMI	P41489 locusta mig
46	2	13.3	9	1 SAMP_MUSCA	P19095 mustelus ca
47	2	13.3	9	1 ULAK_MOUSE	P39031 mus musculu
48	2	13.3	9	1 UP43_HUMAN	P30089 homo sapien
49	2	13.3	10	1 ANGL1_BOTJA	Q10581 bothrops ja
50	2	13.3	10	1 ANGT_BOVIN	P01017 bos taurus
51	2	13.3	10	1 ANGT_CHICK	P01018 gallus gall
52	2	13.3	10	1 BPP_VIPAS	P31351 vipera aspi
53	2	13.3	10	1 COXK_ONCMY	P80332 oncorhynchu
54	2	13.3	10	1 COXQ_RABIT	P80336 oryctolagus
55	2	13.3	10	1 COXQ_SHEEP	P80337 ovis aries
56	2	13.3	10	1 FARP_PANRE	P82660 panagrellus
57	2	13.3	10	1 FARP_LOCMI	P38553 locusta mig
58	2	13.3	10	1 GON1_CHEPR	P80677 chelyosoma
59	2	13.3	10	1 GON1_PETMA	P04378 petromyzon
60	2	13.3	10	1 GON3_PETMA	P30948 petromyzon
61	2	13.3	10	1 LCMS_LEUMA	P21144 leucophaea
62	2	13.3	10	1 MALE_KLEPN	Q05564 klebsiella
63	2	13.3	10	1 ODP2_BOVIN	P11180 bos taurus
64	2	13.3	10	1 PVK_LOCMI	P83382 locusta mig
65	2	13.3	10	1 Q2O8_COMTE	P80465 comamonas t
66	2	13.3	10	1 RCA_PINPS	P81084 pinus pinas
67	2	13.3	10	1 RL16_ACHLA	P29221 acholeplasm
68	2	13.3	10	1 SLAP_BACTG	P49325 bacillus th
69	2	13.3	10	1 SPI_HALRO	Q10997 halocynthia
70	2	13.3	10	1 SVK_CAMUP	Q46464 campylobact
71	2	13.3	10	1 TEMK_RANTE	P56923 rana tempor
72	2	13.3	10	1 TKNB_RANR1	P29135 rana ridibu
73	2	13.3	10	1 UHA3_HUMAN	P40930 homo sapien
74	2	13.3	10	1 UPA5_HUMAN	P30091 homo sapien
75	2	13.3	10	1 URE3_MORMO	P17339 morganelia
76	2	13.3	10	1 XYNB_DICB4	P80717 dictyoglomu
77	2	13.3	11	1 ANGT_CRIGE	P09037 crinia geor
78	2	13.3	11	1 BPPB_AGRHA	P01021 agkistrodon
79	2	13.3	11	1 BRK_MEGFL	P12797 megascolia
80	2	13.3	11	1 CX5A_CONAL	P58848 conus aulic
81	2	13.3	11	1 CXL1_CONNR	P58807 conus maruo
82	2	13.3	11	1 HS70_PINPS	P81672 pinus pinas
83	2	13.3	11	1 MHB1_KLEPN	P80580 klebsiella
84	2	13.3	11	1 MORN_HUMAN	P01163 homo sapien
85	2	13.3	11	1 RS30_ONCMY	P83328 oncorhynchu
86	2	13.3	11	1 TKN2_UPERU	P08616 uperoleia r
87	2	13.3	11	1 TKNA_GADMO	P28498 gadus morhu
88	2	13.3	11	1 TKNA_HORSE	P01290 equus cabal
89	2	13.3	11	1 TKNA_ONCMY	P28439 oncorhynchu
90	2	13.3	11	1 TKNA_RANCA	P22688 rana catesb
91	2	13.3	11	1 TKNA_RANR1	P29207 rana ridibu
92	2	13.3	11	1 TKNA_SCYCA	P41333 scylliorhinu
93	2	13.3	11	1 TKND_RANCA	P22691 rana catesb
94	2	13.3	11	1 UXB2_YEAST	P93013 saccharomyc
95	2	13.3	12	1 FAR7_PENMO	P83322 penaeus mon
96	2	13.3	12	1 NO40_SESMO	Q24369 sesbania ro
97	2	13.3	12	1 PSP3_PHPVA	P80662 physcomitre
98	2	13.3	12	1 RF1_CONSP	P58805 conus spuri
99	2	13.3	12	1 RR16_GINBI	P36207 glankgo bilo
100	2	13.3	12	1 RS19_ELYFP	Q47881 elm yellows

ALIGNMENTS

RESULT 1

```

COXA_ONCMY
ID COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncochrychus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund B., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 4 KVE 6

RESULT 2
GAJU_HUMAN
ID GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01358;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Gastric juice peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RX MEDLINE=75150968; PubMed=5539385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXHU1.
DR MM; L37220; -.
DR GO; GO:0007586; P:digestion; NAS.
FT PEPTIDE 1 10
FT PEPTIDE 2 10
SQ SEQUENCE 10 AA; 1004 MW; CFERC6AB02C3387D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 5 KVE 7

COXA_ONCMY
ID COXA_ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncochrychus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund B., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR; S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535C5B1AB02C33D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 4 KVE 6

RESULT 2
GAJU_HUMAN
ID GAJU_HUMAN STANDARD; PRT; 10 AA.
AC P01358;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Gastric juice peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RX MEDLINE=75150968; PubMed=5539385;
RA Heathcote J.G., Washington R.J.;
RT "Peptides of normal human gastric juice.";
RL Int. J. Protein Res. 2:117-126(1970).
DR PIR; A01628; GXHU1.
DR MM; L37220; -.
DR GO; GO:0007586; P:digestion; NAS.
FT PEPTIDE 1 10
FT PEPTIDE 2 10
SQ SEQUENCE 10 AA; 1004 MW; CFERC6AB02C3387D CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 5 KVE 7

PNEU_HUMAN
ID PNEU_HUMAN STANDARD; PRT; 10 AA.
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.
DR PIR; B33143; B33143.
DR GO; GO:0030103; P:vasopressin secretion; NAS.
KW Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
DB 4 PKL 6

PNEU_RAT
ID PNEU_RAT STANDARD; PRT; 10 AA.
AC P21956;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE, AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RT "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
DR PIR; A33143; A33143.
KW Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 20.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
DB 4 PKL 6

CSIS_BACSU
ID CSIS_BACSU STANDARD; PRT; 11 AA.

```

AC P81095;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
 OS Bacillus subtilis.
 OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=168 / JH642;
 RA Graumann P.L., Schmid R., Marahiel M.A.;
 RL Submitted (OCT-1997) to the SWISS-PROT data bank.
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=168 / JH642;
 RX MEDLINE=96345629; PubMed=8755892;
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
 RT "Cold shock stress-induced proteins in *Bacillus subtilis*.";
 RL J. Bacteriol. 178:4611-4619(1996).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- INDUCTION: In response to low temperature.
 CC -!- CAUTION: Could not be found in the genome of *B. subtilis* 168.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1360 MW; 15F6E6CE6322C330 CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KPF 4
 DB |||
 7 KPF 9
 RESULT 6
 Q20A COMTE STANDARD; PRT; 11 AA.
 ID _Q20A_COMTE
 AC P80464;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Quinolone 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Comamonas.
 OX NCBI_TaxID=285;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=63;
 RX MEDLINE=96035889; PubMed=7556204;
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
 RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from *Comamonas testosteroni* 63. The first two enzymes in quinoline and 3-methylquinoline degradation.";
 RL Eur. J. Biochem. 222:536-544(1995).
 CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-1,2-DIHYDROQUINOLINE.
 CC -!- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-1(2H)-one + reduced acceptor.
 CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first step.
 CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND TWO GAMMA CHAINS (PROBABLE).
 CC PIR: S66606; S66606.
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3
 DB |||
 8 LKP 10
 RESULT 7
 IDHP RAT STANDARD; PRT; 13 AA.
 AC P56574;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)
 DE [Oxalosuccinate decarboxylase] (IDH) (NADP+-specific IDH) (IDP) (ICD-M) (Fragment).
 GN IDH2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.
 CC -!- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2) + NADPH.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN (SPOT P8) IS: 9.0. ITS MW IS: 42 kDa.
 CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE DEHYDROGENASES FAMILY.
 DR InterPro; IPR001804; Isoch.
 DR PROSITE; PS00470; IDH_IMDH; PARTIAL.
 KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle; Mitochondrion.
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;
 Query Match 20.0%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KVE 10
 DB |||
 6 KVE 8
 RESULT 8
 MAST_VESBA STANDARD; PRT; 14 AA.
 ID _MAST_VESBA
 AC P21654;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mastoparan B.
 OS Vespa basalis (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7444;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=91174755; PubMed=2006909;
 RA Lo C.-L., Hwang L.-L.;
 RT "Structure and biological activities of a new mastoparan isolated

```

RT from the venom of the hornet Vespa basalis." ;
RL Biochem. J. 274:453-456(1991).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR; S14336; S14336
KW Mast cell degranulation; Amidation.
FT MOD_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
DB 2 KLK 4

RESULT 9
FGF1_CANFA STANDARD; PRT; 15 AA.
AC P18651;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heparin-binding growth factor 1 (HBGF-1) (Acidic fibroblast growth
DE factor) (AFGF) (Alpha-endothelial cell growth factor) (Fragment).
GN FGF1 OR FGF-1.
OS Canis familiaris (Dog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
[1]
RN SEQUENCE.
RX MEDLINE=89231704; PubMed=2714282;
RA Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethke N.,
RA Sharma H.S., Schaper W.;
RT "Isolation of heparin-binding growth factors from bovine, porcine and
RT canine hearts." ;
RL Eur. J. Biochem. 181:67-73(1989).
CC -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
CC IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
CC VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CC CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC -!- SUBUNIT: Monomer.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
CC THAN DOES BFGF.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
DR PIR; S03955; S03955. IL1 HBGF.
DR InterPro; IPR002348; IL1 HBGF.
DR PROSITE; PS00247; HBGF_FGF; PARTIAL.
KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDDDAA1 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
DB 5 PKL 7

RESULT 10
RM12_YEAST STANDARD; PRT; 15 AA.
AC P36522;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L12 (YmL12) (Fragment).
GN MRPL12.

```

```

OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
[1]
RN SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria." ;
RL FEBS Lett. 284:51-56(1991).
DR SGD; L0002687; MRPL12.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1851 MW; 74BCD9FEDDB3900 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
DB 7 VEV 9

RESULT 11
UBL1_MONDO STANDARD; PRT; 15 AA.
AC P50103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
GN UCHL1.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowen A.R., Lavender F.L., Whittaker P.A.,
RA Thompson R.J.;
RT "Identification of evolutionary conserved regulatory sequences in the
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
RT hydrolase (PGP9.5) gene." ;
RL J. Neurochem. 66:35-46(1996).
CC -!- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U32208; AAA89059.1; -.
DR InterPro; IPR001578; UCH 1.
DR PROSITE; PS00140; UCH 1; PARTIAL.
KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.
FT NON_TER 15 15

```

```
SQ SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79 CRC64;
Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKP 3
Db 3 LKP 5

RESULT 12
VORA_METTM STANDARD; PRT; 15 AA.
AC P80907;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ketoisovalerate oxidoreductase subunit vora (EC 1.-.-.-) (VOR) (2-oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-ferredoxin oxidoreductase alpha subunit) (Fragment).
GN VORA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Testeegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- SUBUNIT: HETEROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.
CC -!- MISCELLANEOUS: As a pH optimum of 9.7 and an optimal temperature of 75 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1779 MW; 31320B6531CA528F CRC64;

Query Match 20.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EVF 12
Db 13 EVF 15

RESULT 13
YALA_TRYBB STANDARD; PRT; 17 AA.
AC P17961;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 1.9 kDa protein in aldolase locus (ORFA).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=427;
RX MEDLINE=90272402; PubMed=2349093;
RA Vijayasarathy S., Ernest I., Itzhaki J., Sherman D., Mowatt M.R.,
RA Michels P.A.M., Clayton C.E.;
RT "The genes encoding fructose biphosphate aldolase in Trypanosoma brucei are interspersed with unrelated genes.";
RL Nucleic Acids Res. 18:2967-2975(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
```

```
CC use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52586; CAA36821.1; -
DR PIR; S15064; S15064.
KW Hypothetical protein.
SQ SEQUENCE 17 AA; 1939 MW; 5FC2B9AF44AEF420 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEV 11
Db 5 VEV 7

RESULT 14
COX4_ONCMY STANDARD; PRT; 19 AA.
AC P80327;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) (Fragments).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE IV FAMILY.
DR PIR; S43624; S43624.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 9
FT NON_TER 10
FT NON_TER 19
SQ SEQUENCE 19 AA; 1963 MW; 9280E1D8EC77987E CRC64;

Query Match 20.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEV 11
Db 6 VEV 8

RESULT 15
COXA_THUOB STANDARD; PRT; 20 AA.
AC P80972;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va-1 (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
```

```

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RT Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver.";
RL Eur. J. Biochem. 248:99-103(1997).
CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR; S77981; S77981.
DR InterPro; IPR003204; Cyt_c_ox5A.
DR Pfam; PF02284; COX5A; 1.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2404 MW; 7E82E43B7157355E CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 4 KVE 6

RESULT 16
JHBP_BOMMO
ID JHBP_BOMMO STANDARD; PRT; 20 AA.
AC P81627;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Juvenile hormone-binding protein (Fragment).
GN JHBP.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=Backokjam; TISSUE=Hemolymph;
RA Park C.-H., Kim H.R.;
RT "Characterization of high affinity juvenile hormone binding protein in
RT the hemolymph of Bombyx mori L.";
RL Tongmul Hakhoe Chi 37:495-503(1994).
RN [2]
RP IDENTIFICATION OF CYS-9.
RA Park C.-H.;
RL Submitted (DEC-1998) to the SWISS-PROT data bank.
CC -1- FUNCTION: PREVENTS JUVENILE HORMONE FROM BEING HYDROLYZED BY
CC GENERAL ESTERASES BY COMBINING WITH IT SPECIFICALLY.
CC -1- SUBCELLULAR LOCATION: Secreted.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2090 MW; B336332F08AE2FB8 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3
DB 6 LKP 8

```

```

RESULT 17
MI17_BOVIN
ID MI17_BOVIN STANDARD; PRT; 20 AA.
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 kDa milk glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
RX MEDLINE=93308294; PubMed=8320368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
RT the proteose peptone fraction of bovine milk.";
RL J. Dairy Res. 60:189-197(1993).
CC -1- PTM: N-GLYCOSYLATED.
CC -1- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON TER 1 1
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
DB 10 PKL 12

RESULT 18
OM4V_VIBAL
ID OM4V_VIBAL STANDARD; PRT; 20 AA.
AC P83149;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Outer membrane protein 40Va (Omp40Va) (Fragment).
OS Vibrio alginolyticus
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIMB 1903T;
RA Onji M., Hirabayashi J., Suzuki S.;
RT "Characterization of major outer membrane proteins of Vibrio
RT alginolyticus and the stability against proteases.";
RL Microbes Environ. 0:0-0(2002).
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- SIMILARITY: BELONGS TO THE OMP/PHO FAMILY OF PORINS.
KW Transmembrane; Porin; Outer membrane.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2229 MW; 4FA95CB24FEC3CDE CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
DB 2 EVF 4

RESULT 19

```

```

OMPI_ACTAC
ID _OMPI_ACTAC STANDARD; PRT; 20 AA.
AC P20242;
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE 39 kDa major outer membrane protein (Fragment)
OS Actinobacillus actinomycetemcomitans (Haemophilus
actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE.
RC STRAIN=Y4;
RA MEDLINE=91169244; PubMed=2004699;
RA Koeguchi S., Kato K., Nishimura F., Kurihara H., Murayama Y.;
RT "Isolation and partial characterization of a 39 kDa major outer
RT membrane protein of Actinobacillus actinomycetemcomitans Y4.";
RL FEMS Microbiol. Lett. 61:85-89(1991).
DR PIR: A54538; A54538.
KW Outer membrane; Transmembrane; Porin.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2316 MW; A837A8C4764F527E CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 10 KVE 12

RESULT 20
TRYL_STREX
ID _TRYL_STREX STANDARD; PRT; 20 AA.
AC P80420;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trypsin-like protease (EC 3.4.21.-) (Fragment)
OS Streptomyces exfoliatus (Streptomyces hydrogenans).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1905;
RN [1]
RP SEQUENCE.
RC STRAIN=SMF13;
RA MEDLINE=95291424; PubMed=7773379;
RA Kim I.S., Lee K.J.;
RT "Physiological roles of leupeptin and extracellular proteases in
RT mycelium development of Streptomyces exfoliatus SMF13.";
RL Microbiology 141:1017-1025(1995).
CC -1- FUNCTION: INVOLVED IN MYCELIUM DIFFERENTIATION.
CC -1- SIMILARITY: BELONGS TO PETIDASE FAMILY S2A.
DR MOPRS; S01.101; -.
DR InterPro; IPR001254; Ser. protease Try.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2129 MW; 4568F56D0E7393AF CRC64;

Query Match 20.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 PFF 14
Db 12 PFF 14

```

```

RESULT 21
TUFT_HUMAN
ID _TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
RT stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RC MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -1- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
CC ACTIVITY OF NEUTROPHILS.
DR PIR: A02147; A02147.
DR MIM; 191150; -.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006909; P:phagocytosis; NAS.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KP 3
Db 2 KP 3

RESULT 22
PAP2_PARMA
ID _PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -1- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.

```


CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C9C8100000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PP 5
Db 4 PP 5

RESULT 23
SUGA_ACHDO STANDARD; PRT; 5 AA.
AC P1991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 34, Last annotation update)
DE Subesophageal ganglion pentapeptide.
OS Acheta domesticus (House cricket).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
CC Acheta.
OX NCBI_TaxID=6997;
RN [1]_TaxID=6997;
RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT subesophageal ganglion of Acheta domesticus (orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC -!- GANGLIA.
CC PIR; JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PP 4
Db 4 PP 5

RESULT 24
UC22_MAIZE STANDARD; PRT; 5 AA.
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Fernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.1, ITS MW IS: 30.4 kDa.

DR Maize-2DPAGE; P80628; COLEOPTILE.
DR MaizedB; 123954; -.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EV 11
Db 4 EV 5

RESULT 25
OVM_LEPDE STANDARD; PRT; 6 AA.
AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (Leb-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
CC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
CC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RX MEDLINE=91271080; PubMed=2052497;
RA Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de Loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
RT decemlineata.";
RL Peptides 12:31-36(1991).
CC -!- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KP 3
Db 4 KP 5

RESULT 26
CCF1_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008113; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline
RT resistance plasmid, pCF10.";

```
RL J. Biol. Chem. 263:14574-14578 (1988).
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR: A30812; A30812.
KW Phormone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VF 12
   ||
Db 5 VF 6

RESULT 27
FAR1_HELTI STANDARD; PRT; 7 AA.
ID FAR1_HELTI
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GDPFLRF-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis".
RL Peptides 15:31-36 (1994).
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76A810 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
   ||
Db 3 PF 4

RESULT 28
FAR4_PANRE STANDARD; PRT; 7 AA.
ID FAR4_PANRE
AC P41875;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimidae; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95232026; PubMed=7716079;
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
RA Thim L., Kubiak T.M., Martin R.A., Geary T.G.;
RT "Isolation and preliminary biological characterization of
RT KPNFIRFamide, a novel FMRFamide-related peptide from the free-living
```

```
RT nematode, Panagrellus redivivus.";
RL Peptides 16:87-93 (1995).
CC -!- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
CC MUSCLE TENSION INCREASE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
   ||
Db 1 KP 2

RESULT 29
TPFY_PACDA STANDARD; PRT; 7 AA.
ID TPFY_PACDA
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (Pdt-1).
OS Pachymedusa dactylos (Giant mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxID=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RT "Pachymedusa dactylos tryptophyllin-1 (Pdt-1): structural
RT characterization, pharmacological activity and cloning of precursor
RT CDNA".
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
CC smooth muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD RES 3 3
   3 3
   HYDROXYLATION.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
   ||
Db 1 KP 2

RESULT 30
UF04_MOUSE STANDARD; PRT; 7 AA.
ID UF04_MOUSE
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RC TISSUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907; Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON_TER 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
DB 1 PK 2

RESULT 31
UN06_PINPS STANDARD; PRT; 7 AA.
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle; PubMed=10344291;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Prigiero J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 6 PF 7

RESULT 32
ANG2_BOTJA STANDARD; PRT; 8 AA.
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma; PubMed=8829801;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 7 PF 8

RESULT 33
LPMS_STAEP STANDARD; PRT; 8 AA.
ID LPMS_STAEP STANDARD; PRT; 8 AA.
AC P23211;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Probable msra leader peptide.
OS Staphylococcus epidermidis.
OG Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=966; PubMed=2233255;
RX MEDLINE=91041730; PubMed=2233255;
RA Ross J.I., Eady E.A., Cove J.H., Cunliffe W.J., Baumberg S.,
RA Wootton J.C.;
RT "Inducible erythromycin resistance in staphylococci is encoded by a
member of the ATP-binding transport super-gene family.";
RL Mol. Microbiol. 4:1207-1214(1990).
CC -!- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
CC PROTEIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; X52085; CAA36303.1; -.
DR PIR; S11157; LFSAME.
KW Leader peptide; Plasmid.
SQ SEQUENCE 8 AA; 937 MW; FA37340685BDC1A6 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LK 2
DB 7 LK 8

RESULT 34
PPK2_PERAM STANDARD; PRT; 8 AA.
ID PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;

```

```

CC      (MYOTROPIC ACTIVITY).
CC      -1- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC      -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.
CC      -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
CC      KW Neuropeptide; Amidation; Pyrokinin.
FT      MOD RES      8      8      AMIDATION
SQ      SEQUENCE      8 AA;  997 MW;  OB34177409D772C7 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PF 4
Db      3 PF 4

RESULT 36
RS7_MYCIT
ID_RS7_MYCIT      STANDARD;      PRT;      8 AA.
AC      P33564;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      30S ribosomal protein S7 (Fragment).
GN      RPSG.
OS      Mycobacterium intracellulare.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX      NCBI_TaxID=1767;
RN      [1]
RS      SEQUENCE FROM N.A.
RX      MEDLINE=93197130; PubMed=8451173;
RA      Nair J., Rouse D.A., Morris S.L.;
RT      "Nucleotide sequence analysis of the ribosomal S12 gene of
RT      Mycobacterium intracellulare";
RL      Nucleic Acids Res. 21:1039-1039 (1993).
CC      -1- FUNCTION: One of the primary rRNA binding proteins, it binds
CC      directly to 16S rRNA where it nucleates assembly of the head
CC      domain of the 30S subunit. Is located at the subunit interface
CC      close to the decoding center, probably blocks exit of the E-site
CC      tRNA (By similarity).
CC      -1- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC      and S11 (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; L08171; AAA25376.1; -.
CC      PIR; S35538; S35538.
CC      HAMAP; MF 00480; -. 1.
CC      InterPro; IPR000235; Ribosomal S7.
CC      PROSITE; PS00052; RIBOSOMAL_S7_PARTIAL.
CC      KW Ribosomal protein; rRNA-binding; tRNA-binding; tRNA-binding.
FT      INIT.MET      0      0      BY SIMILARITY.
FT      NON TER      8      8
SQ      SEQUENCE      8 AA;  850 MW;  63276DC768732417 CRC64;

Query Match      13.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PK 6
Db      7 PK 8

```

```

RESULT 37
BUK_CLOPA STANDARD; PRT; 9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (BC 2.7.2.7) (BK) (CP 38) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetate kinase family.
DR HAMAP: MF 00542; -; 1.
DR InterPro: IPR000890; Acetate kin.
DR PROSITE: PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE: PS01076; ACETATE_KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON TER 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KL 7
DB 3 KL 4

RESULT 38
CCAP_CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunodea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangler J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexata;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
hawkmoth, Manduca sexta.";
FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
INTO THE HEMOLYMPH.
DR PIR; A26363; A26363.
DR PIR; S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 1 PF 2

RESULT 39
CONO_CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
DR InterPro: IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6

```

```

Db          |||
            7 PK 8
Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 KP 3
DB          1 KP 2

RESULT 40
COW_CONVE   STANDARD;      PRT;      9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mediterranean cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=117992;
[1]
RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP TISSUE=Venom;
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascenzi P., Politicelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RL Biochem. Biophys. Res. Commun. 288:908-913(2001).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1088.6; METHOD=WALDI.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Amidation; D-amino acid.
FT DISULFID 3 5 5 D-TRYPTOPHAN.
FT MOD_RES 5 5 5
FT MOD_RES 9 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 KP 3
DB          6 KP 7

RESULT 41
FAR4 CALVO
ID FAR4 CALVO STANDARD;      PRT;      9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 4.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
[1]
RN SEQUENCE.
RP TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; D41978;
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 KP 3
DB          3 KP 4

RESULT 42
FAR5 ASCSU
ID FAR5 ASCSU STANDARD;      PRT;      9 AA.
AC P43170;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AFS.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
[1]
RN SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum."
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1052 MW; 340B0059D1B76338 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 KP 3
DB          3 KP 4

RESULT 43
FIBB ERYPA
ID FIBB ERYPA STANDARD;      PRT;      9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID=9538;
[1]
RN SEQUENCE.
RX MEDLINE=85289140; PubMed=1928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons."
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

```

CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR PIR; D24180; D24180. Fibrinogen C.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EV 11
Db 3 EV 4

RESULT 44

KNL3_BOMVA
ID_KNL3_BOMVA STANDARD; PRT; 9 AA.

AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]_

RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RC TISSUE-Skin secretion;
RA Chen T.B., Orr D.F., Bjorson A.J., McClean S., Rao P.P., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (Jul-2001) to the SWISS-PROT data bank.

CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.

KW Amphibian defense peptide; Vasodilator; Bradykinin.

SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
Db 7 PF 8

RESULT 45

LMT3_LOCM1

ID_LMT3_LOCM1 STANDARD; PRT; 9 AA.

AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Locustamytropin 3 (LOM-MT-3).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;

OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI_TaxID=7004;

RN [1]_

RP SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain;

RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,

RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).

CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).

CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.

DR PIR; A61620; A61620.

DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin.

FT MOD RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
Db 4 PF 5

RESULT 46

SAMP_MUSCA

ID_SAMP_MUSCA STANDARD; PRT; 9 AA.

AC P19095;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Serum amyloid P-component (SAP) (Fragment).

OS Mustelus canis (Smooth dogfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Galeomorphii; Galeoidea; Carchariniiformes; Triakidae;

OC Mustelus

OX NCBI_TaxID=7812;

RN [1]_

RP SEQUENCE.

RX MEDLINE=83160932; PubMed=6403520;

RA Robey P.A., Tanaka T., Liu T.-Y.;

RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";

RL J. Biol. Chem. 258:3889-3894(1983).

CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID

CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND

CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.

CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.

DR PIR; B20569; B20569.

DR InterPro; IPR001759; Pentaxin.

DR PROSITE; PS00289; PENTAXIN; PARTIAL.

KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.

FT DOMAIN 1 >9 PENTAXIN.

FT NON TER 9 9

SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match

Best Local Similarity 13.3%; Score 2; DB 1; Length 9;
Matches 2; Conservative 100.0%; Pred. No. 1.3e+05;
Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PF 5
Db 2 PF 3

RESULT 47

ULAK_MOUSE

ID_ULAK_MOUSE STANDARD; PRT; 9 AA.

AC P99031;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 13-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 2D-00141LD)
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Van J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Cowthorne M.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.
 DR SWISS-2DPAGE; P99031; MOUSE.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1106 MW; E1E842C3240B145A CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KV 9
 ||
 Db 6 KV 7

RESULT 48

UPA3_HUMAN
 ID UPA3_HUMAN STANDARD; PRT; 9 AA.
 AC P30089;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RL "Plasma protein map: an update by microsequencing."
 RL Electrophoresis 13:707-714(1992).
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
 DR SWISS-2DPAGE; P30089; HUMAN.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FP 5
 ||
 Db 4 FP 5

RESULT 49

ANG1_BOTJA
 ID ANG1_BOTJA STANDARD; PRT; 10 AA.
 AC Q10581;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide I (Fragment).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Chordata; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borghesei R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RL plasma of the snake Bothrops jararaca."
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PF 4
 ||
 Db 7 PF 8

RESULT 50

ANGT_BOVIN
 ID ANGT_BOVIN STANDARD; PRT; 10 AA.
 AC P01017;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 13-SEP-2003 (Rel. 42, Last annotation update)
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II) (Fragment).
 DE (Fragment).
 GN AGT OR SERPIN8.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA Elliott D.F., Peart W.S.;
 RT "The amino acid sequence in a hypertensin."
 RL Biochem. J. 65:246-254(1957).
 CC -|- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the
 CC plasma.
 CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR; A90345; A90345.
 DR PDB; 3ER5; 15-JUL-92.
 DR InterPro; IPR000215; Serpin.
 DR PROSITE; PS00284; SERPIN; PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT PEPTIDE 1 8 ANGIOTENSIN II.
 FT PEPTIDE 2 8 ANGIOTENSIN III.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1282 MW; CEEFBDD761F2DB42 CRC64;

RESULT 52
BPP VIPAS

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KL 7

Db 9 KL 10

RESULT 54

COXQ_RABIT
ID COXQ_RABIT STANDARD; PRT; 10 AA.
AC P80336;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
GN COX8H.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RL Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferrocycochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1027 MW; 2C325CB40DC76338 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KP 3

Db 4 KP 5

RESULT 55

COXQ_SHEEP
ID COXQ_SHEEP STANDARD; PRT; 10 AA.
AC P80337;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RL Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycochrome c + O(2) = 4 ferrocycochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KP 3

Db 4 KP 5

RESULT 56

FAR6_PANRE
ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of FMRFamide-related
RT peptides (fARPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 10 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PF 4

Db 6 PF 7

RESULT 57

FARP_LOCM1
ID FARP_LOCM1 STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistocerca gregaria (PVDHFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004, 7010;
RN [1]
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelincx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PVDHFLRFamide
RT (Schistocerca gregaria) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct.";
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;

```

RX MEDLINE=89246543; PubMed=2719702;
RA ROBB S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistostylx-amide, a
RT FMRF-amide-like neuropeptide from the locust, Schistocerca
RT gregaria.";
RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A32543; A32543..
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VF 12
   ||
Db 6 VF 7

RESULT 58
GONI CHEPR
ID -GONI CHEPR STANDARD; PRT; 10 AA.
AC P80677;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberein I (Gonadotropin-releasing hormone I) (GnRH-I)
DE (Luliberin I).
OS Chelyosoma productum.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Corellidae; Chelyosoma.
CX NCBI_TaxID=71177;
RN [1]
RP SEQUENCE.
RX MEDLINE=96413669; PubMed=8816823;
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT "Two new forms of gonadotropin-releasing hormone in a protochordate
RT and the evolutionary implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: GnRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
CC THE GONADUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
CC THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC -!- MASS SPECTROMETRY: MW=1246.56; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR InterPro; IPR002012; GnRH.
DR PIR; A32543; A32543..
DR PROSITE; PS00473; GnRH; 1.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1264 MW; 284B3639DB5A5A3 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
   ||
Db 8 KP 9

RESULT 59
GONI PETMA
ID -GONI PETMA STANDARD; PRT; 10 AA.
AC P04378;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberein I (Gonadotropin-releasing hormone I) (GnRH-I)
DE (Luliberin I).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
CX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT "Primary structure of gonadotropin-releasing hormone from lamprey
RT brain.";
RL J. Biol. Chem. 261:4812-4819(1986).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A01412; RHLMSG.
DR InterPro; IPR002012; GnRH.
DR PIR; A01412; RHLMSG.
DR PROSITE; PS00473; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1244 MW; 1B4B36237B1735AB CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KP 3
   ||
Db 8 KP 9

RESULT 60
GONI PETMA
ID -GONI PETMA STANDARD; PRT; 10 AA.
AC P30948;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberein III (Gonadotropin-releasing hormone III) (GnRH-III)
DE (Luliberin III).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
CX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RX MEDLINE=93178316; PubMed=8440174;
RA Sower S.A., Chiang Y.-C., Lovas S., Conlon J.M.;
RT "Primary structure and biological activity of a third gonadotropin-
RT releasing hormone from lamprey brain.";
RL Endocrinology 132:1125-1131(1993).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR InterPro; IPR002012; GnRH.
DR PIR; A01412; RHLMSG.

```

DR PROSITE; PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1277 MW; 284B36237AA1F5A3 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KP 3
 Db 8 KP 9
 RESULT 61
 LCMS LEUMA
 ID LCMS LEUMA STANDARD; PRT; 10 AA.
 AC P21144; P41497;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leucomyosuppressin (LMS) (Lem-MS).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucomyosuppressin, an insect neuropeptide that inhibits spontaneous contractions of the cockroach hindgut."
 RL Comp. Biochem. Physiol. 85C:329-333(1986).
 CC -!- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH PROTODEUM (HINDGUT).
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 VF 12
 Db 6 VF 7
 RESULT 62
 MALE KLEPN
 ID MALE KLEPN STANDARD; PRT; 10 AA.
 AC Q05564;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Maltose-binding periplasmic protein (Maltodextrin-binding protein) (MBP) (Fragment).
 DE (MBP) (Fragment).
 GN MALE.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1033-5PI4 / KAY2026;
 RX MEDLINE=93211295; PubMed=8459773;
 RA Bachellier S., Perrin D., Hofnung M., Gilson E.;
 RT "Bacterial interspersed mosaic elements (BIMES) are present in the genome of Klebsiella.";

RL Mol. Microbiol. 7:537-544(1993).
 CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND CHEMOTAXIS TOWARD MALTOLOGOSACCHARIDES.
 CC -!- SUBCELLULAR LOCATION: Periplasmic.
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING PROTEIN FAMILY 1.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X68329; CAA48406.1; -.
 DR InterPro; IPR006061; SBP dom1.
 DR PROSITE; PS01037; SBP_BACTERIAL_1; PARTIAL.
 KW Transport; Sugar transport; Periplasmic.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1159 MW; 8FD8DC4415A6DDDA CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LK 2
 Db 1 LK 2
 RESULT 63
 ODP2 BOVIN
 ID ODP2 BOVIN STANDARD; PRT; 10 AA.
 AC F11180;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) (E2) (Fragment).
 DE DLAT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88024154; PubMed=3117054;
 RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.;
 RT "Primary structure around the lipate-attachment site on the E2 component of bovine heart pyruvate dehydrogenase complex.";
 RL Biochem. J. 245:919-922(1987).
 CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall conversion of pyruvate to acetyl-CoA and CO(2). It contains multiple copies of three enzymatic components: pyruvate dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and lipoamide dehydrogenase (E3).
 CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-acetyldihydrolipoamide.
 CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPOYL COFACTOR.
 CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL SYMMETRY.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
 CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
 DR InterPro; IPR003016; Lipoyl.
 DR PROSITE; PS00189; LIPOYL; PARTIAL.
 KW Glycolysis; Transferrase; Acyltransferase; Repeat; Mitochondrion;
 KW Lipoyl
 FT NON_TER 1 1

FT BINDING 5 5 LIPOYL.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1066 MW; 889BECDA1ADD33AB1 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 VE 10
 ||
 Db 1 VE 2
 RESULT 64
 PVK_LOCMI STANDARD; PRT; 10 AA.
 AC P83382;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Periviscerokinin (Lom-PVK-1).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Abdominal perisymphathetic organs;
 RX MEDLINE=21896327; PubMed=11897380;
 RA Predel R., Gaede G.;
 RT "Identification of the abundant neuropeptide from abdominal
 perisymphathetic organs of locusts.";
 RL Peptides 23:621-627(2002).
 CC -!- FUNCTION: Myotropic peptide; increases the frequency of
 contraction of the heart and stimulates amplitude and tonus of the
 foregut.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
 DR GO; GO:0005576; C:extracellular; IDA.
 DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FP 5
 ||
 Db 7 FP 8
 RESULT 65
 Q2OB_COMTE STANDARD; PRT; 10 AA.
 AC P80465;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).
 OS Comamonas testosteroni (Pseudomonas testosteroni).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Comamonas.
 OX NCBI_TaxID=285;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=63;
 RX MEDLINE=96035889; PubMed=7556204;
 RA Schach S., Tshisuaka B., Retznar S., Lingens F.;
 RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-

RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
 RT quinoline and 3-methylquinoline degradation.";
 RL Eur. J. Biochem. 232:536-544(1995).
 CC -!- FUNCTION: CONVERTS (3-METHYL-) -QUINOLINE TO (3-METHYL-)2-OXO-
 1,2-DIHYDROQUINOLINE.
 CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
 1(2H)-one + reduced acceptor.
 CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
 CC step.
 CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
 CC TWO GAMMA CHAINS (PROBABLE).
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 FP 5
 ||
 Db 3 FP 4
 RESULT 66
 RCA_PINPS STANDARD; PRT; 10 AA.
 AC P81084;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable ribulose biphosphate carboxylase/oxygenase activase (RuBisCO
 DE activase) (RA) (Water stress responsive protein 4) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=98418576; PubMed=9747804;
 RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
 RT "Water-deficit-responsive proteins in maritime pine.";
 RL Plant Mol. Biol. 38:587-596(1998).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- FUNCTION: ACTIVATION OF RUBISCO (RIBULOSE-1,5-BISPHOSPHATE
 CC CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
 CC CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
 CC CARBAMATE STRUCTURE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
 CC -!- INDUCTION: By water stress.
 CC -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
 KW Chloroplast; ATP-binding.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1171 MW; COA506D2C72B1EA6 CRC64;
 Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 VF 12
 ||
 Db 7 VF 8

```
RESULT 67
RL16_ACHLA
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]_TaxID=29338;
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckeich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
DB 4 PK 5

RESULT 68
SLAP_BACTG
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]_TaxID=29338;
RP SEQUENCE.
RC STRAIN=NRRL 4045;
RX MEDLINE=90078111; PubMed=2592346;
RA Luckeich M.D., Beveridge T.J.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
DB 4 PK 5

RESULT 69
SPI_HALRO
ID SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10397;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE Serine proteinase inhibitor (Fragment).
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]_TaxID=7729;
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=96321313; PubMed=8759295;
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RT "Purification and characterization of a 58,000-Da proteinase
inhibitor from the hemolymph of a solitary ascidian, Halocynthia
roretzi.";
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KV 9
DB 8 KV 9

RESULT 70
SYK_CAMUP
ID SYK_CAMUP STANDARD; PRT; 10 AA.
AC Q46164;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Lysyl-tRNA synthetase (BC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
DE (Fragment).
GN LYSS.
OS Campylobacter upsaliensis.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=28080;
RN [1]_TaxID=28080;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43954;
```

RX MEDLINE=97149302; PubMed=8996110;
RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
RT "Characterization of Campylobacter upsaliensis fur and its
RT localization in a highly conserved region of the Campylobacter
RT genome";
RL Gene 183:219-224(1996).
CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC + L-lysyl-tRNA(Lys).
CC -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L77076; AAB41342.1; --
CC HAVAP: MF_00252; 1
CC InterPro: IPR006195; tRNA_Ligase_II.
CC PROSITE: PS00862; AA_TRNA_LIGASE_II; PARTIAL.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Metal-binding; Magnesium.
CC NON TER 1
CC SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LK 2
Db ||
1 LK 2

RESULT 71

TEMP_RANTE STANDARD; PRT; 10 AA.
ID TEMP_RANTE STANDARD; PRT; 10 AA.
AC P56923;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin K.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria";
RL Eur. J. Biochem. 242:788-792(1996).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 10
FT MOD RES 10 AMIDATION.
SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LK 2
Db ||
6 LK 7

RESULT 72

TKNB_RANRI STANDARD; PRT; 10 AA.
ID TKNB_RANRI STANDARD; PRT; 10 AA.
AC P29135;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurokinin A.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=93075037; PubMed=1332683;
RA Wang Y., Badgery-Parker T., Lovas S., Chartrel N., Vaudry H.,
RA Burcher E., Conlon J.M.;
RT "Primary structure and receptor-binding properties of a neurokinin A-
RT related peptide from frog gut";
RL Biochem. J. 287:827-832(1992).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 10
FT MOD RES 10 AMIDATION.
SQ SEQUENCE 10 AA; 1160 MW; 526B407059D5BAA7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LK 7
Db ||
2 LK 3

RESULT 73

UHA3_HUMAN STANDARD; PRT; 10 AA.
ID UHA3_HUMAN STANDARD; PRT; 10 AA.
AC P40930;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of heart (Spot 7513) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=95203287; PubMed=7895732;
RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
RT "The human myocardial two-dimensional gel protein database: update
RT 1994";
RL Electrophoresis 15:1459-1465(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 47.3 kDa.
CC NON TER 10
CC NON TER 10
SQ SEQUENCE 10 AA; 1049 MW; 6B8CDE41A041B76B CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VE 10
 ||
 Db 2 VE 3

RESULT 74

UPAS_HUMAN STANDARD; PRT; 10 AA.
 ID UPAS_HUMAN STANDARD; PRT; 10 AA.
 AC P30031;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30091; HUMAN.
 FT NON_TER 1 1 G->Y.
 FT VARIANT 9 9 /FTID=VAR_000002.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
 ||
 Db 4 PK 5

RESULT 75

URE3_MORMO STANDARD; PRT; 10 AA.
 ID URE3_MORMO STANDARD; PRT; 10 AA.
 AC P17339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
 DE amidohydrolase) (Fragment).
 GN UREA.
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences."
 RL J. Bacteriol. 172:3073-3080(1990).

CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
 DR PIR; C35389; C35389.
 KW Hydrolase.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 13.3%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EV 11
 ||
 Db 7 EV 8

Search completed: November 25, 2003, 18:17:28
 Job time : 8.26064 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 36.1436 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-8
Perfect score: 15
Sequence: 1 LKFPFKLKEVFFFP 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	26.7	11	2	Q44090 acholeplasm
2	4	26.7	14	11	Q99PB8 mus musculus
3	4	26.7	15	8	Q9T2Q3 chlamydomon
4	4	26.7	16	10	Q94F61 triticum ae
5	3	20.0	7	2	Q8GL00 borrelia bu
6	3	20.0	8	4	Q9BYV5 homo sapien
7	3	20.0	8	4	Q9UJ50 homo sapien
8	3	20.0	8	6	Q9BF93 megaptera n
9	3	20.0	8	6	Q9BFA0 macaca mula
10	3	20.0	8	6	Q9BF99 hylobates c
11	3	20.0	8	8	Q34909 locusta mig
12	3	20.0	9	4	Q16276 homo sapien
13	3	20.0	9	4	Q16605 homo sapien
14	3	20.0	10	2	Q9XBH3 bacillus ce
15	3	20.0	10	6	Q9GKI5 pan troglod
16	3	20.0	10	6	Q9GKI4 macaca arc

Q8SL54	aeonium haw	10	8	Q8SL54
Q9rfz2	mycoplasma	11	2	Q9RFZ2
P82700	leucophaea	11	5	P82700
Q8VLX8	thermus the	12	4	Q8VLX8
Q9BR06	homo sapien	12	4	Q9BR06
Q8SL49	aeonium lan	12	8	Q8SL49
Q9G196	sargassum p	12	8	Q9G196
Q8SL40	aeonium urb	12	8	Q8SL40
Q8SL42	aeonium sim	12	8	Q8SL42
Q8SL28	aeonium hol	12	8	Q8SL28
Q41744	zea mays (m	12	10	Q41744
Q9PVC2	gadus morhu	12	13	Q9PVC2
Q9PVC3	lampiris sp.	12	13	Q9PVC3
Q9PVC0	mugil cepha	12	13	Q9PVC0
Q9PVC1	lophius sp.	12	13	Q9PVC1
Q9PVB9	oryzias lat	12	13	Q9PVB9
Q9PVC6	plecoglossu	12	13	Q9PVC6
Q9PVB8	hemiramphus	12	13	Q9PVB8
Q9PVA8	mullus sp.	12	13	Q9PVA8
Q9PVC7	esox lucius	12	13	Q9PVC7
Q9PVC4	harpadon sp	12	13	Q9PVC4
Q8SL43	aeonium spa	13	8	Q8SL43
Q8SL74	aichryson p	13	8	Q8SL74
Q8S941	beta vulgar	13	10	Q8S941
Q9PVA0	colisa lali	13	13	Q9PVA0
Q9PVB1	dendrochiru	13	13	Q9PVB1
Q9PVB5	mola mola (13	13	Q9PVB5
Q9PVA7	dissostichu	13	13	Q9PVA7
Q9PVB3	hippocampus	13	13	Q9PVB3
Q9PVB8	psittodes s	13	13	Q9PVB8
Q9PVB2	baistetes sp	13	13	Q9PVB2
Q9PVA2	maastacembel	13	13	Q9PVA2
Q9PVB0	thunnus sp.	13	13	Q9PVB0
Q9PVB4	dicentrarch	13	13	Q9PVB4
Q9PVB9	zeus faber	13	13	Q9PVB9
Q9PVA5	channa sp.	13	13	Q9PVA5
Q9PVA3	cryptocentr	13	13	Q9PVA3
Q9PVA9	acanthurus	13	13	Q9PVA9
Q9PVC5	epinephelus	13	13	Q9PVC5
Q9PVA4	galaxias ma	13	13	Q9PVA4
Q9PVA1	siganus sp.	13	13	Q9PVA1
Q9PVB6	stromateus	13	13	Q9PVB6
Q9PVB5	ostracion s	13	13	Q9PVB5
Q9PVB7	sargocentro	13	13	Q9PVB7
Q9PVB6	fundulus he	13	13	Q9PVB6
Q9PVA6	poecilia la	13	13	Q9PVA6
Q9PVA6	salarias sp	14	2	Q9PVA6
Q9PVA6	salarias sp	14	2	Q9PVA6
Q8KSE3	enterococcu	14	2	Q8KSE3
Q52636	escherichia	14	2	Q52636
Q54394	streptomyce	14	2	Q54394
Q16232	homo sapien	14	4	Q16232
Q96062	homo sapien	14	4	Q96062
Q13022	homo sapien	14	4	Q13022
Q55249	bacterioph	14	9	Q55249
Q9QVF3	rattus sp.	14	11	Q9QVF3
Q84072	influenzavi	14	12	Q84072
Q54298	salmonella	15	2	Q54298
Q52304	escherichia	15	2	Q52304
Q9R4U7	acinetobact	15	2	Q9R4U7
Q9S0V1	nitrogen fi	15	2	Q9S0V1
Q9HCX8	homo sapien	15	4	Q9HCX8
Q9T2J9	pisum sativ	15	8	Q9T2J9
Q8SM11	lilium cand	15	8	Q8SM11
Q8SL26	aeonium vis	15	8	Q8SL26
Q8SL36	monanthes i	15	8	Q8SL36
P82430	nicotiana t	15	10	P82430
Q9QV76	mus sp. pre	15	11	Q9QV76
Q44610	buchnera ap	16	2	Q44610
Q9UD41	homo sapien	16	4	Q9UD41
Q9UCI8	homo sapien	16	4	Q9UCI8
Q9BGG8	sorex arane	16	6	Q9BGG8
Q8SL50	aeonium mas	16	8	Q8SL50

90 Q8SL27 aonium leu
 91 Q8SL38 aichryson t
 92 Q9BC18 rosa stella
 93 Q8SL52 aonium kor
 94 Q8SL55 aonium bal
 95 Q8SL53 aonium hie
 96 Q8SL57 aonium gom
 97 O21922 streptococc
 98 P83511 delonix reg
 99 Q8CIS2 mus musculu
 100 O89560 kaposi's sa

ALIGNMENTS

RESULT 1
 Q44090 PRELIMINARY; PRT; 11 AA.
 AC Q44090;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Hypothetical export segment (Fragment).
 OS Acholeplasma laidlawii.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Acholeplasma.
 OX NCBI_TaxID=2148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A-EF22;
 RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
 RT "Sequence regions from Acholeplasma laidlawii which restore export of
 RT beta-lactamase in Escherichia coli."
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 222875; CAA80495.1; --
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1234 MW; 5C9D2AE8A682C337 CRC64;

Query Match 26.7%; Score 4; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKV 9
 DB 3 KLKV 6
 RESULT 2
 Q99PB8 PRELIMINARY; PRT; 14 AA.
 AC Q99PB8;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Adenosine kinase (EC 2.7.1.20) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Singh B., Lin A., Wu Z.-C., Gupta R.S.;
 RT "Gene Structure for Adenosine Kinase in Chinese Hamster and Human:
 RT High Frequency Mutants of CHO cells involve deletions of several
 RT introns and exons."
 RL DNA Cell Biol. 0:0-0(2001).
 DR EMBL; AF318953; AAK07186.1; --
 KW Kinase; Transferase.
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1526 MW; 27863376667D5A27 CRC64;

Query Match 26.7%; Score 4; DB 11; Length 14;

Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 KLKV 9
 DB 11 KLKV 14
 RESULT 3
 Q9T2Q3 PRELIMINARY; PRT; 15 AA.
 AC Q9T2Q3;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE II-65 respiratory protein (Fragment).
 OS Chlamydomonas reinhardtii.
 OC Mitochondrion.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95079249; PubMed=7826432;
 RA Atteia A.;
 RT "Identification of mitochondrial respiratory proteins from the green
 RT alga Chlamydomonas reinhardtii."
 RL C. R. Acad. Sci., III, Sci. Vie 317:11-19(1994).
 SQ SEQUENCE 15 AA; 1584 MW; 6E0B3B843E4379B6 CRC64;

Query Match 26.7%; Score 4; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10
 DB 5 LKVE 8

RESULT 4
 Q94F61 PRELIMINARY; PRT; 16 AA.
 AC Q94F61;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Prolamin-box binding factor (Fragment).
 GN PBF.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Cheyenne;
 RA Chen Z., Fleming J., Zhi Y., Yi M.;
 RT "Sequence of the prolamin-box binding factor (PBF) promoter sequence
 RT from wheat."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF385139; AAK64285.1; --
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1770 MW; B406423B4FFEF76B CRC64;

Query Match 26.7%; Score 4; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVFP 13
 DB 3 EVFP 6

```

RESULT 5
Q8GL00
ID Q8GL00 PRELIMINARY; PRT; 7 AA.
AC Q8GL00;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Bacteroid group cp32-13.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA15;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY142106; AN17857.1; -.
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLV 8
DB 5 KLV 7

RESULT 6
Q9BY5
ID Q9BY5 PRELIMINARY; PRT; 8 AA.
AC Q9BY5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL: AY011664; AAG47575.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EBAB572A CRC64;

Query Match 20.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 6 KVE 8

RESULT 7
Q9UJ50
ID Q9UJ50 PRELIMINARY; PRT; 8 AA.
AC Q9UJ50;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```

```

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE latrophilin-2 (Fragment).
GN LPHH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9153747; PubMed=10030676;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Isolation and characterisation of a human homologue of the
RT latrophilin gene from a region of lp31.1 implicated in breast
RT cancer.";
RL Oncogene 17:3513-3519(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20225451; PubMed=10760572;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Genomic structure and expression profile of LPHH1, a 7TM gene
RT variably expressed in breast cancer cell lines.";
RL Biochim. Biophys. Acta 1491:75-92(2000).
DR EMBL: AJ244509; CAB60204.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1025 MW; 4D59D763344AAB0B CRC64;

Query Match 20.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPF 4
DB 5 KPF 7

RESULT 8
Q9BF93
ID Q9BF93 PRELIMINARY; PRT; 8 AA.
AC Q9BF93;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balenopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL: AY011669; AAG47580.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1025 MW; DF02C3240EAB572A CRC64;

Query Match 20.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 6 KVE 8

RESULT 9
Q9BFA0
ID Q9BFA0 PRELIMINARY; PRT; 8 AA.

```

```

AC Q9BFA0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011661; AAG47572.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;

Query Match 20.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 6 KVE 8

RESULT 10
ID Q9BF99 PRELIMINARY; PRT; 8 AA.
AC Q9BF99;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011662; AAG47573.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;

Query Match 20.0%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVE 10
Db 6 KVE 8

RESULT 11
ID Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome b (Fragment).
OS Locusta migratoria (Migratory locust).

```

```

OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Uhlenbusch I., Geilissen G.;
RT "Structure of the cloned Locusta migratoria mitochondrial genome:
RT restriction mapping and sequence of its ND-1 (URF-1) gene.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1; -.
RN Mitochondrion.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLK 8
Db 5 KLK 7

RESULT 12
ID Q16276 PRELIMINARY; PRT; 9 AA.
AC Q16276;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Neurofibromatosis type 2 (Fragment).
GN NF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95038750; PubMed=7951241;
RA Arai E., Ikeuchi T., Nakamura Y.;
RT "Characterization of the translocation breakpoint on chromosome
RT 22q12.2 in a patient with neurofibromatosis type 2 (NF2).";
RL Hum. Mol. Genet. 3:937-939(1994).
DR EMBL; S75841; AAD14190.2; -.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1044 MW; 1E4CBDD337232404 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLK 8
Db 4 KLK 6

RESULT 13
ID Q16605 PRELIMINARY; PRT; 9 AA.
AC Q16605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutathione S-transferase 2 (Fragment).
GN GSTA2 OR GST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN SEQUENCE FROM N.A.
RP MEDLINE=68330756; PubMed=3138230;
RX "Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
RA "Human glutathione S-transferases. The Ha multigene family encodes
RT products of different but overlapping substrate specificities.";
RL J. Biol. Chem. 263:12797-12800(1988).
DR EMBL; M21867; AAA52617.1; -.
DR EMBL; M21866; AAA52618.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1116 MW; D168E72327633B1D CRC64;

Query Match 20.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKL 7
Db 5 PKL 7

RESULT 14
Q9XEH3 PRELIMINARY; PRT; 10 AA.
ID Q9XBH3
AC Q9XBH3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CelF-like protein (Fragment).
GN CELF.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 10987;
RC MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;
RT "Genome organisation is not conserved between Bacillus cereus and
RL Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL; AJ000394; CAB40625.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1264 MW; D3757BC33339C9D6 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 7 KVE 9

RESULT 15
Q9GKI5 PRELIMINARY; PRT; 10 AA.
ID Q9GKI5
AC Q9GKI5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fragile X mental retardation 1 protein (Fragment).
GN FMR1.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21264938; PubMed=11058604;
RA Kumari D., Usdin K.;
RT "Interaction of the transcription factors USF1, USF2, and alpha-
RT Pal/Nrf-1 with the FMR1 promoter. Implications for fragile x mental
```

```

RT retardation syndrome.";
RL J. Biol. Chem. 276:4357-4364(2001).
DR EMBL; AF251349; AAG44598.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1160 MW; 7C2A2B02D2C72B CRC64;

Query Match 20.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
Db 6 VEV 8

RESULT 16
Q9GKI4 PRELIMINARY; PRT; 10 AA.
ID Q9GKI4
AC Q9GKI4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fragile X mental retardation 1 protein (Fragment).
GN FMR1.
OS Macaca arctoides (Stump-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9540;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21264938; PubMed=11058604;
RA Kumari D., Usdin K.;
RT "Interaction of the transcription factors USF1, USF2, and alpha-
RT Pal/Nrf-1 with the FMR1 promoter. Implications for fragile x mental
RT retardation syndrome.";
RL J. Biol. Chem. 276:4357-4364(2001).
DR EMBL; AF251350; AAG44599.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1160 MW; 7C2A2B02D2C72B CRC64;

Query Match 20.0%; Score 3; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
Db 6 VEV 8

RESULT 17
Q8SL54 PRELIMINARY; PRT; 10 AA.
ID Q8SL54
AC Q8SL54;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PsbA (Fragment).
GN PSBA.
OS Aeonium haworthii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=35950;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
RT Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082203; AM13947.1; -.
KW Chloroplast.
```

```

FT  NON TER      1      1
SQ  SEQUENCE 10 AA; 988 MW;  COED9F45A772CB02 CRC64;

Query Match      20.0%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  9 VEV 11
    |||
Db  3 VEV 5

RESULT 18
Q9RFZ2
AC  Q9RFZ2      PRELIMINARY;      PRT;      11 AA.
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  Fructose biphosphate aldolase (Fragment).
GN  FBA.
OS  Mycoplasma mycoides subsp. capri.
OC  Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC  Entomoplasmataceae.
OX  NCBI_TaxID=40477;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PG3;
RX  MEDLINE=20193983; PubMed=10727835;
RA  Thaucourt F., Lorenzon S., David A., Breard A.;
RT  "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
RT  of a putative membrane protein gene.";
RL  Vet. Microbiol. 72:251-268(2000).
DR  EMBL; AF162998; AAF15255.1; -.
FT  NON TER      11
SQ  SEQUENCE 11 AA; 1371 MW;  50B0881A3331FB57 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5 PKL 7
    |||
Db  2 PKL 4

RESULT 19
P82700
ID  P82700      PRELIMINARY;      PRT;      11 AA.
AC  P82700;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  Periviscerokinin-3 (DEM-PVK-3).
OS  Leucophaea maderae (Madeira cockroach),
OS  Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS  Blaberus craniifer,
OS  Blaptica dubia (Argentinian wood cockroach), and
OS  Gronphadorina portentosa (Cockroach).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC  Blaberidae; Leucophaea.
OX  NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN  [1]
RP  SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC  TISSUE=ABDOMINAL PERISYPHATHETIC ORGANS;
RX  MEDLINE=20307624; PubMed=10849006;
RA  Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT  "Identification of novel periviscerokinin from single neurohaemal
RT  release sites in insects. MS/MS fragmentation complemented by Edman
RT  degradation.";
RL  Eur. J. Biochem. 267:3869-3873(2000).
CC  -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY

```

```

CC  (MYOTROPIC ACTIVITY).
KW  -!- MASS SPECTROMETRY; MW=1146.6; METHOD=MALDI.
KW  Neuropeptide; Amidation.
FT  MOD RES      11
SQ  SEQUENCE 11 AA; 1147 MW;  2F4D9FF2D7605698 CRC64;

Query Match      20.0%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 PFP 5
    |||
Db  7 PFP 9

RESULT 20
Q8VLX8
ID  Q8VLX8      PRELIMINARY;      PRT;      12 AA.
AC  Q8VLX8;
DT  01-MAR-2002 (TrEMBLrel. 20, Created)
DT  01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT  01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE  Lysyl-tRNA synthetase (Fragment).
GN  LYS.
OS  Thermus thermophilus.
OC  Bacteria; Deinococcus-Thermus; Deinococci; Thermaceae;
OC  Thermus.
OX  NCBI_TaxID=274;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=KT8;
RA  Spada S., Pembroke J.T., Wall J.G.;
RT  "Cloning and characterisation of the czrB metal cation efflux protein
RT  from T. thermophilus.";
RL  Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AJ307316; CAC83721.1; -.
KW  Aminoacyl-tRNA synthetase.
FT  NON TER      1
SQ  SEQUENCE 12 AA; 1327 MW;  5D2A33E27ECDD813 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LKP 3
    |||
Db  1 LKP 3

RESULT 21
Q9BR06
ID  Q9BR06      PRELIMINARY;      PRT;      12 AA.
AC  Q9BR06;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  DJ343K2.3 (Novel protein) (Fragment).
GN  DJ621N11.4.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Laird G.;
RL  Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AL031659; CAC34516.1; -.
FT  NON TER      12
SQ  SEQUENCE 12 AA; 1422 MW;  DC7FF1578B2C9D2 CRC64;

Query Match      20.0%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      10 EVF 12
Db      4 EVF 6

RESULT 22
Q8SL49
ID Q8SL49 PRELIMINARY; PRT; 12 AA.
AC Q8SL49;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PsbA (Fragment).
GN PSBA.
OS Aeonium lancelottense.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=111152;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
RT Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082208; AAM13952.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 12 AA; 1291 MW; COEDC9DC3D72CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VEV 11
Db      5 VEV 7

RESULT 23
Q9GI96
ID Q9GI96 PRELIMINARY; PRT; 12 AA.
AC Q9GI96;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit
DE (Fragment).
GN RBCS.
OS Sargassum polycystum.
OG Chloroplast.
OC Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
OC Sargassum.
OX NCBI_TaxID=127578;
RN [1]
RP SEQUENCE FROM N.A.
RA Phillips N.E.;
RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
RT (Fucales, Phaeophyceae).";
RL Thesis (1998), University of Hawaii.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=nepi27;
RA Phillips N.E., Smith C.M., Morden C.W.;
RT "Testing the systematics of the genus Sargassum (Fucales,
RT Phaeophyceae) with the Rubisco operon.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF244344; AAF98114.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 12 AA; 1200 MW; C0FB1B6DF372CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VEV 11
Db      5 VEV 7

RESULT 24
Q8SL40
ID Q8SL40 PRELIMINARY; PRT; 12 AA.
AC Q8SL40;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PsbA (Fragment).
GN PSBA.
OS Aeonium urbicum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=111161;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
RT Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082217; AAM13961.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 12 AA; 1291 MW; COEDC9DC3D72CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VEV 11
Db      5 VEV 7

RESULT 25
Q8SL42
ID Q8SL42 PRELIMINARY; PRT; 12 AA.
AC Q8SL42;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PsbA (Fragment).
GN PSBA.
OS Aeonium simsii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=35955;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
RT Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082215; AAM13959.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 12 AA; 1200 MW; C0FB1B6DF372CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
|
|
|
Db 5 VEV 7

RESULT 26

Q8SL28 ID Q8SL28 PRELIMINARY; PRT; 12 AA.
AC Q8SL28;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PSBA (Fragment).
GN PSBA.
OS Aeonium holochrysum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=35951;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of
RT Crassulaceae inferred from chloroplast and nuclear data."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082283; AAM13973.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1200 MW; C0FB1B6DF372CB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
|
|
|
Db 5 VEV 7

RESULT 27

Q41744 ID Q41744 PRELIMINARY; PRT; 12 AA.
AC Q41744;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alcohol dehydrogenase (Fragment).
GN ADH1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSOM=Mu3;
RX MEDLINE=87277357; PubMed=3038674;
RA Chen C.H., Oishi K.K., Kloeckner-Gruissem B., Freeling M.;
RT "Organ-specific expression of maize Adh1 is altered after a Mu
RT transposon insertion."
RL Genetics 116:469-477(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TRANSPOSOM=Mu3;
RA Freeling M.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U19613; AAC48978.1; -.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1217 MW; 233663790942C338 CRC64;

Query Match 20.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
|
|
|
Db 9 KLK 11

RESULT 28

Q9PVC2 ID Q9PVC2 PRELIMINARY; PRT; 12 AA.
AC Q9PVC2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
OX NCBI_TaxID=8049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aCod;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134603; AAD54088.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31B69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
|
|
|
Db 8 KVE 10

RESULT 29

Q9PVC3 ID Q9PVC3 PRELIMINARY; PRT; 12 AA.
AC Q9PVC3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Lampiris sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Lampridiformes; Lampridae; Lampiris.
OX NCBI_TaxID=94303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aLamp;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134602; AAD54087.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.


```

FT NON_TER      1 1
FT NON_TER      12 12
SQ SEQUENCE     12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10
      |||

RESULT 30
Q9PVC0
ID Q9PVC0 PRELIMINARY; PRT; 12 AA.
AC Q9PVC0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Mugil cephalus (Flathead mullet) (Mugil japonicus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Mugilomorpha; Mugilidae;
OC Mugil.
OX NCBI_TaxID=48193;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aMullet;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134605; AAD54090.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER      1 1
FT NON_TER      12 12
SQ SEQUENCE     12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10
      |||

RESULT 31
Q9PVC1
ID Q9PVC1 PRELIMINARY; PRT; 12 AA.
AC Q9PVC1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Lophius sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
OX NCBI_TaxID=30791;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aAngler;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."

```

```

RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134604; AAD54089.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER      1 1
FT NON_TER      12 12
SQ SEQUENCE     12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10
      |||

RESULT 32
Q9PVB9
ID Q9PVB9 PRELIMINARY; PRT; 12 AA.
AC Q9PVB9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aMedaka;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134606; AAD54091.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER      1 1
FT NON_TER      12 12
SQ SEQUENCE     12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10
      |||

RESULT 33
Q9PVC6
ID Q9PVC6 PRELIMINARY; PRT; 12 AA.
AC Q9PVC6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Plecoglossus altivelis.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Osmeridae; Plecoglossus.
OX NCBI_TaxID=61084;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aAyu;

```

```

RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF134598; AAD54084.1; -.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF001103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 34
Q9PVB8 PRELIMINARY; PRT; 12 AA.
AC Q9PVB8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Hemirhamphus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;
OC Belontiiformes; Hemirhamphidae; Hemiramphus.
OX NCBI_TaxID=94223;
RN [1]_TaxID=94223;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aHalifbeak;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF134607; AAD54092.1; -.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF001103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 35
Q9PVA8 PRELIMINARY; PRT; 12 AA.
AC Q9PVA8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Mullus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciiformes; Percoidae;

```

```

OC Mullidae; Mullus.
OX NCBI_TaxID=94224;
RN [1]_TaxID=94224;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aGoatfish;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF134617; AAD54102.1; -.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF001103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 36
Q9PVC7 PRELIMINARY; PRT; 12 AA.
AC Q9PVC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Esoc lucius (Northern pike).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Esociformes;
OC Esocidae; Esoc.
OX NCBI_TaxID=8010;
RN [1]_TaxID=8010;
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aPike;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL: AF134598; AAD54083.1; -.
DR InterPro: IPR001400; Somatotropin.
DR Pfam: PF001103; hormone; 1.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BE5A8E4C31E69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 37
Q9PVC4 PRELIMINARY; PRT; 12 AA.
AC Q9PVC4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.

```

OS Harpadon sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Aulipiformes; Synodontidae; Harpadontinae; Harpadon.
OX NCBI_TaxID=94310;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aBduck; PubMed=10468597;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134601; AAD54086.1; --
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone.1.
FT NON_TER 1
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 97BESA8E4C31B69A CRC64;

Query Match 20.0%; Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.e+04; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 38
Q8SL43
ID Q8SL43 PRELIMINARY; PRT; 13 AA.
AC Q8SL43
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DE beta-2 polypeptide (HC 3.6.1.1) (Fragment).
DE FsbA (Fragment).
DE PSBA.
GN PSBA.
OS Aeonium spatulatum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aeonium.
OX NCBI_TaxID=35956;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082214; AAM13958.1; --
KW Chloroplast.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA; 1313 MW; C0FB1B6DAD0ECB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+04; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 9 VEV 11
Db 6 VEV 8

RESULT 39
Q8SL74
ID Q8SL74 PRELIMINARY; PRT; 13 AA.
AC Q8SL74;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FsbA (Fragment).
GN PSBA.

OS Aichryson porphyrogenetos.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Crassulaceae; Aichryson.
OX NCBI_TaxID=190205;
RN [1]
RP SEQUENCE FROM N.A.
RA Mort M.E., Soltis D.E., Soltis P.S., Francisco J., Santos A.;
RT "Evolution and diversification of the Macaronesian clade of Crassulaceae.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082183; AAM13927.1; --
KW Chloroplast.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA; 1313 MW; C0FB1B6DAD0ECB02 CRC64;

Query Match 20.0%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+04; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 9 VEV 11
Db 6 VEV 8

RESULT 40
Q9S941
ID Q9S941 PRELIMINARY; PRT; 13 AA.
AC Q9S941;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE H(+)-translocating (pyrophosphate-ENERGIZED) inorganic pyrophosphatase
DE beta-2 polypeptide (HC 3.6.1.1) (Fragment).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Beta.
OX NCBI_TaxID=161934;
RN [1]
RP SEQUENCE.
RX MEDLINE=92179265; PubMed=1311852;
RA Sarafian V., Kim Y., Poole R.J., Rea P.A.;
RT "Molecular cloning and sequence of cDNA encoding the pyrophosphate-energized vacuolar membrane proton pump of Arabidopsis thaliana.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1775-1779(1992).
SQ SEQUENCE 13 AA; 1243 MW; C9DB193C37C22AAD CRC64;

Query Match 20.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.e+04; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 8 KVE 10
Db 11 KVE 13

RESULT 41
Q9PVA0
ID Q9PVA0 PRELIMINARY; PRT; 13 AA.
AC Q9PVA0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Colisa lalia (dwarf gourami).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Anabantoidae; Belontiidae; Colisa.
OX NCBI_TaxID=50373;

```

RN SEQUENCE FROM N.A.
RP STRAIN=Gh4aGouramy;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134625; AAD54110.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31B6 CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 42
Q9PV51 ID Q9PV51 PRELIMINARY; PRT; 13 AA.
AC Q9PV51;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Dendrochirus zebra (zebra turkeyfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Scorpaenoidae; Scorpaenidae; Dendrochirus.
OX NCBI_TaxID=94308;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aGouramy;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134614; AAD54099.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31B6 CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 43
Q9PV95 ID Q9PV95 PRELIMINARY; PRT; 13 AA.
AC Q9PV95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Mola mola (ocean sunfish).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Molidae; Mola.
OX NCBI_TaxID=94237;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4aSunfish;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134630; AAD54115.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 44
Q9PVA7 ID Q9PVA7 PRELIMINARY; PRT; 13 AA.
AC Q9PVA7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Growth hormone (fragment).
GN GH.
OS Dissostichus mawsoni (Antarctic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidae; Nototheniidae; Dissostichus.
OX NCBI_TaxID=36200;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Gh4atooth;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134618; AAD54103.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

  Query Match      20.0%; Score 3; DB 13; Length 13;
  Best Local Similarity 100.0%; Pred. No. 1.1e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db 8 KVE 10

RESULT 45
Q9PVB3 ID Q9PVB3 PRELIMINARY; PRT; 13 AA.
AC Q9PVB3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

```

```

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
DE GH.
OS Hippocampus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
OC Syngnathidae; Hippocampus.
OX NCBI_TaxID=72047;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aSeahorse;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134612; AAD54097.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 8 KVE 10

RESULT 46
Q9PV98
ID Q9PV98 PRELIMINARY; PRT; 13 AA.
AC Q9PV98;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
DE GH.
OS Psettoodes sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Psettoidei; Psettoidae; Psettoodes.
OX NCBI_TaxID=94241;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aFlatfish;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134627; AAD54112.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 8 KVE 10

RESULT 47
Q9PV97
ID Q9PV97 PRELIMINARY; PRT; 13 AA.
AC Q9PV97;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
DE GH.
OS Balistes sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Balistidae; Balistes.
OX NCBI_TaxID=94230;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aTrigger;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134628; AAD54113.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 8 KVE 10

RESULT 48
Q9PV92
ID Q9PV92 PRELIMINARY; PRT; 13 AA.
AC Q9PV92;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
DE GH.
OS Mastacembelus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Synbranchiiformes;
OC Mastacembelidae; Mastacembelus.
OX NCBI_TaxID=94235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aMasta;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
RT evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134613; AAD54098.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 8 KVE 10

```

```

QY      8 KVE 10
Db      8 KVE 10

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 49
Q9PVA2 PRELIMINARY; PRT; 13 AA.
AC Q9PVA2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Thunnus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aTuna;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134623; AAD54100.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 50
Q9PVB0 PRELIMINARY; PRT; 13 AA.
AC Q9PVB0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Dicentrarchus labrax (European sea bass).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;
OC Moronidae; Dicentrarchus.
OX NCBI_TaxID=13489;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aseabass;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134615; AAD54100.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 51
Q9PVB4 PRELIMINARY; PRT; 13 AA.
AC Q9PVB4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Zeus faber (John Dory).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Zeiformes; Zeidae; Zeus.
OX NCBI_TaxID=64108;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aDirties;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134611; AAD54096.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVE 10
Db      8 KVE 10

RESULT 52
Q9PV99 PRELIMINARY; PRT; 13 AA.
AC Q9PV99;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Channa sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Channoidae;
OC Channidae; Channa.
OX NCBI_TaxID=94222;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4amurrel;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134626; AAD54111.1; -.
DR InterPro; IPR001400; Somatotropin.

```

```

DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KVE 10
Db      8 KVE 10

RESULT 53
Q9PVA5 PRELIMINARY; PRT; 13 AA.
AC Q9PVA5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Cryptocentrus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Gobioidae;
OC Gobiidae; Cryptocentrus.
OX NCBI_TaxID=94314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4ablenny; PubMed=10468597;
RX MEDLINE=99398697;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134620; AAD54105.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KVE 10
Db      8 KVE 10

RESULT 54
Q9PVA3 PRELIMINARY; PRT; 13 AA.
AC Q9PVA3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Acanthurus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes;
OC Acanthuroidei; Acanthuridae; Acanthurus.
OX NCBI_TaxID=94220;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4asurgeon; PubMed=10468597;
RX MEDLINE=99398697;
RA Venkatesh B., Ning Y., Brenner S.;

```

```

RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134622; AAD54107.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KVE 10
Db      8 KVE 10

RESULT 55
Q9PVA9 PRELIMINARY; PRT; 13 AA.
AC Q9PVA9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Epinephelus coioides (Orange-spotted grouper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Percioidae;
OC Serranidae; Epinephelus.
OX NCBI_TaxID=94232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4Agrouper;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134616; AAD54101.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KVE 10
Db      8 KVE 10

RESULT 56
Q9PVC5 PRELIMINARY; PRT; 13 AA.
AC Q9PVC5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Galaxias maculatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Profacanthopterygii; Salmoniformes; Galaxiidae; Galaxias.
OX NCBI_TaxID=61620;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aGal;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134620; AAD54085.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db |||
8 KVE 10

RESULT 57
Q9PVA4 PRELIMINARY; PRT; 13 AA.
AC Q9PVA4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Siganus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Acanthuroidei; Siganidae; Siganus.
OX NCBI_TaxID=94227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aRabbitfish;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134621; AAD54106.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db |||
8 KVE 10

RESULT 58
Q9PVA1 PRELIMINARY; PRT; 13 AA.
AC Q9PVA1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Stromateus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Stromateoidei; Stromateidae; Stromateus.
OX NCBI_TaxID=94245;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aPomfret;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134624; AAD54109.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db |||
8 KVE 10

RESULT 59
Q9PV96 PRELIMINARY; PRT; 13 AA.
AC Q9PV96;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Ostracion sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Ostraciidae; Ostracion.
OX NCBI_TaxID=94239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aBoxfish;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate
  evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134629; AAD54114.1; -.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BE5A8E4C31E6 CRC64;

Query Match      20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
Db |||
8 KVE 10

RESULT 60
Q9PVBS PRELIMINARY; PRT; 13 AA.
ID Q9PVBS
AC Q9PVBS;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

```


DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Sargocentron sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Beryciformes; Holocentridae;
OC Sargocentron.
OX NCBI_TaxID=94226;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aFundulus;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134610; AAD54095.1; -;
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BES8A8E4C31E6 CRC64;
Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KVE 10
DB 8 KVE 10
RESULT 61
Q9PVB7 ID Q9PVB7 PRELIMINARY; PRT; 13 AA.
AC Q9PVB7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
OX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aFundulus;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134608; AAD54093.1; -;
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BES8A8E4C31E6 CRC64;
Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KVE 10
DB 8 KVE 10

RESULT 62

Q9PVB6 ID Q9PVB6 PRELIMINARY; PRT; 13 AA.
AC Q9PVB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Poecilia latipinna.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Poecilia.
OX NCBI_TaxID=48699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aMolly;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134609; AAD54094.1; -;
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BES8A8E4C31E6 CRC64;
Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KVE 10
DB 8 KVE 10
RESULT 63
Q9PVA6 ID Q9PVA6 PRELIMINARY; PRT; 13 AA.
AC Q9PVA6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Salarias sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Blennioidei;
OC Blennioidei; Salarias.
OX NCBI_TaxID=94312;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gh4aGoby;
RX MEDLINE=99398697; PubMed=10468597;
RA Venkatesh B., Ning Y., Brenner S.;
RT "Late changes in spliceosomal introns define clades in vertebrate evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 96:10267-10271(1999).
DR EMBL; AF134619; AAD54104.1; -;
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1642 MW; AA37BES8A8E4C31E6 CRC64;
Query Match 20.0%; Score 3; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KVE 10

```
Db      8 KVE 10
RESULT 64
Q9R782  PRELIMINARY;      PRT;      14 AA.
AC Q9R782;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Beta lactamase (fragment).
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3498148;
RX MEDLINE=8731866;
RA Grossmann M.J., Lampen J.O.;
RT "Purification and DNA binding properties of the blaI gene product,
RT repressor for the beta-lactamase gene, blaP, of Bacillus
RT licheniformis."
RL Nucleic Acids Res. 15:6049-6062(1987).
DR EMBL; X05798; CAA29241.1; -.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1665 MW; 9F544EA613DB0E31 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 KLK 8
Db      9 KLK 11
RESULT 65
Q8KSE3  PRELIMINARY;      PRT;      14 AA.
AC Q8KSE3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated protein kinase.
GN VANS.
OS Enterococcus faecium (Streptococcus faecium).
OG Plasmid pUW786.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
CX NCBI_TaxID=1352;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UW786;
RA Werner G., Klare I., Witte W.;
RT "Multi-resistance gene cluster on a plasmid in a clinical isolate of
RT Enterococcus faecium."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516335; AAM77883.1; -.
KW Kinase; Plasmid.
SQ SEQUENCE 14 AA; 1628 MW; 0AAE44BCDE720A34 CRC64;

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 KLK 8
Db      4 KLK 6
RESULT 66
Q52636  PRELIMINARY;      PRT;      14 AA.
ID Q52636
AC Q52636;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 10, Last annotation update)

Db      8 KVE 10
RESULT 67
Q54394  PRELIMINARY;      PRT;      14 AA.
ID Q54394
AC Q54394;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE S-adenosyl-L-homocysteine hydrolase (fragment).
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
CX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK21;
RA Romero N.M., Mellado R.P.;
RT "Activation of the actinorhodin biosynthetic pathway in Streptomyces
RT lividans."
RL FEMS Microbiol. Lett. 121:79-84(1995).
DR EMBL; X79814; CAA56211.1; -.
DR InterPro; IPR000043; Ado_hcyase.
DR Pfam; PF00670; AdoHcyase_1.
KW Hydrolase.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1725 MW; 1303D5023C485D2B CRC64;

Query Match 20.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 KVE 10
Db      2 KVE 4
RESULT 68
Q16232  PRELIMINARY;      PRT;      14 AA.
ID Q16232
AC Q16232;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 10, Last annotation update)
```

```

DE NF2 protein (Fragment).
GN NF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94348501; PubMed=8069299;
RA Arakawa H., Hayashi N., Nagase H., Ogawa M., Nakamura Y.;
RT "Alternative splicing of the NF2 gene and its mutation analysis of
RT breast and colorectal cancers.";
RL Hum. Mol. Genet. 3:565-568(1994).
DR EMBL; S73855; AAD14139.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1513 MW; 82766955653CCB2A CRC64;

Query Match 20.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKP 3
DB 1 LKP 3

RESULT 69
Q96Q62 PRELIMINARY; PRT; 14 AA.
ID Q96Q62 (TrEMBLrel. 19, Created)
AC Q96Q62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Mitochondrial ribosomal protein S11 (Fragment).
GN MRPS11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429115; PubMed=11543634;
RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
RA Watanabe K., Tanaka T.;
RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes
RT to the chromosomes and implications for human disorders.";
RL Genomics 77:65-70(2001).
DR EMBL; AB051349; BAB54939.2; -.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1585 MW; C07121F2234438DD CRC64;

Query Match 20.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVE 10
DB 2 KVE 4

RESULT 70
Q13022 PRELIMINARY; PRT; 14 AA.
ID Q13022 (TrEMBLrel. 01, Created)
AC Q13022;
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Prohibitin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

DE NF2 protein (Fragment).
GN NF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT prohibitin-encoding genes.";
RL Gene 158:291-294(1995).
DR EMBL; U17179; AAA86691.1; -.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1586 MW; EFA1DA48DB1B3BC1 CRC64;

Query Match 20.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEV 11
DB 8 VEV 10

RESULT 71
O55249 PRELIMINARY; PRT; 14 AA.
ID O55249 (TrEMBLrel. 06, Created)
AC O55249;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RegB protein (Fragment).
GN REGB.
OS Bacteriophage T6.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
ON NCBI_TaxID=10656;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=T6;
RX MEDLINE=94357192; PubMed=8076614;
RA Repella F., Tetart F., Bouet J., Krusch H.M.;
RT "Genomic polymorphism in the T-even bacteriophages.";
RL EMBO J. 13:4181-4192(1994).
DR EMBL; Z35074; CAA84449.1; -.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1735 MW; DC726CF8795B60D2 CRC64;

Query Match 20.0%; Score 3; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVF 12
DB 6 EVF 8

RESULT 72
Q9QVF3 PRELIMINARY; PRT; 14 AA.
ID Q9QVF3 (TrEMBLrel. 13, Created)
AC Q9QVF3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TRANSFERRIN-PEPTIDE 35 (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10118;
[1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
```

```

RT  metastasizing tumor cells: identification as transferrin.";
RL  J. Cell. Biochem. 47:261-271(1991).
DR  InterPro; IPR001156; Transferrin.
DR  Pfam; PF00405; transferrin; 1.
FT  NON_TER 1
FT  NON_TER 14 14
SQ  SEQUENCE 14 AA; 1499 MW; 01AE8289E54E3224 CRC64;

Query Match      20.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LKP 3
Db  8 LKP 10

RESULT 73
Q84072          PRELIMINARY; PRT; 14 AA.
ID  Q84072;
AC  Q84072;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  Influenza A/fpv/rostock/34 (H7n1), polymerase 1 (Seg 2), 3' end of
DE  vrna (Initiator region for protein coding) (Fragment).
OS  Influenzavirus A.
OC  Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC  Influenza A viruses.
OX  NCB1_TaxID=197911;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=80034428; PubMed=493121;
RA  Robertson J.S.;
RT  "5' and 3' terminal nucleotide sequences of the rna genome segments of
RL  influenza virus.";
RL  Nucleic Acids Res. 6:3745-3757(1979).
DR  EMBL; J02119; AAA43580.1; -.
DR  InterPro; IPR001407; Flu_Pbl.
DR  Pfam; PF00602; Flu_Pbl; 1.
FT  NON_TER 14 14
SQ  SEQUENCE 14 AA; 1558 MW; 41863E77ED22FE27 CRC64;

Query Match      20.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  7 LKV 9
Db  10 LKV 12

RESULT 74
Q54298          PRELIMINARY; PRT; 15 AA.
ID  Q54298
AC  Q54298;
DT  01-JUN-1998 (TrEMBLrel. 06, Created)
DT  01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  RNA polymerase alpha subunit (Fragment).
GN  RPOA.
OS  Salmonella typhimurium.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Salmonella.
OX  NCB1_TaxID=602;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=LT2;
RX  MEDLINE=98188310; PubMed=9520473;
RA  Bjorkman J., Hughes D., Anderson D.;
RT  "Virulence of antibiotic resistant Salmonella typhimurium.";
RL  Proc. Natl. Acad. Sci. U.S.A. 95:3949-3953(1998).
DR  EMBL; AJ223236; CAA11204.1; -.

```

```

FT  NON_TER 15 15
SQ  SEQUENCE 15 AA; 1720 MW; D1E381FC9FBC3D10 CRC64;

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LKP 3
Db  9 LKP 11

RESULT 75
Q52304          PRELIMINARY; PRT; 15 AA.
ID  Q52304
AC  Q52304; Q52634;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE  TRAL protein (Fragment).
OS  Escherichia coli.
OC  Plasmid IncFII R1, and Plasmid IncFII R1-19 (R1 drd-19).
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Escherichia.
OX  NCB1_TaxID=562;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86059219; PubMed=2999074;
RA  Frost L.S., Finlay B.B., Opgenorth A., Paranchych W., Lee J.S.;
RT  "Characterization and sequence analysis of pilin from F-like
RT  plasmids";
RL  J. Bacteriol. 164:1238-1247(1985).
DR  EMBL; M19710; AAA92660.1; -.
DR  EMBL; K03091; AAA92757.1; -.
KW  Plasmid.
FT  NON_TER 15 15
SQ  SEQUENCE 15 AA; 1844 MW; 5CCA91188EB3511A CRC64;

Query Match      20.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  6 KLK 8
Db  8 KLK 10

Search completed: November 25, 2003, 18:25:25
Job time : 38.1936 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 48.5904 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKPPFKLKEVFPFP 15

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	22	AA872253 Colostrinin derive
2	15	100.0	15	22	AA872507 Colostrinin peptid
3	15	100.0	15	22	AA872539 Colostrinin peptid
4	15	100.0	15	22	AA859313 Ewe colostrinin pe
5	15	100.0	15	23	AA820235 Colostrinin consti
6	15	100.0	15	23	AA851043 Colostrinin consti
7	15	100.0	15	23	AA014584 Neural cell regula
8	15	100.0	16	22	AA859344 Ewe colostrinin pe
9	7	46.7	10	22	AA807188 Colostrinin peptid

7	46.7	11	22	AA807198 Modified colostrin
5	33.3	9	21	AA870257 Peptide encoded by
5	33.3	9	23	ABJ01751 158PID7 related HL
5	33.3	9	23	ABJ01752 158PID7 related HL
5	33.3	9	23	ABJ01851 158PID7 related HL
5	33.3	9	23	ABJ01855 158PID7 related HL
5	33.3	9	23	ABJ01996 158PID7 related HL
5	33.3	10	23	ABJ01366 158PID7 related HL
5	33.3	10	23	ABJ01907 158PID7 related HL
5	33.3	10	23	ABJ01929 158PID7 related HL
5	33.3	11	19	AAW48881 Cyclic peptide gra
5	33.3	16	21	AAW59323 Tyrosine phosphata
5	33.3	16	24	ABP82437 G protein-coupled
5	33.3	17	21	AB830278 CD4+ T-cell activa
5	33.3	19	24	ABP83371 G protein-coupled
4	26.7	5	19	AAW65794 Polyprolyl inhibit
4	26.7	6	23	AAE22869 Carrot red leaf lu
4	26.7	7	20	AAW49731 Compact structure
4	26.7	7	23	ABG32211 Sheep colostrinin
4	26.7	7	23	ABB77133 Classical swine fe
4	26.7	7	23	ABB07085 Hepatitis C virus
4	26.7	8	15	AAW59968 Peptide signal seq
4	26.7	9	17	AAW07412 Antibacterial/anti
4	26.7	9	17	AAW07413 Antibacterial/anti
4	26.7	9	17	AAW07414 Antibacterial/anti
4	26.7	9	17	AAW07415 Antibacterial/anti
4	26.7	9	22	ABB14478 Human C35 peptide
4	26.7	9	22	AAW62673 Influenza virus im
4	26.7	9	22	AAE31250 Human mace9 peptid
4	26.7	9	23	ABJ01633 158PID7 related HL
4	26.7	9	23	ABB79424 Human MMP-2 PEX pe
4	26.7	10	17	AAW91324 Dynorphin A analog
4	26.7	10	22	AAW43031 Mycoplasma genital
4	26.7	10	22	AAW83581 Arabidopsis thalia
4	26.7	10	22	AAW84280 Arabidopsis thalia
4	26.7	10	22	AAW85870 Saccharomyces cere
4	26.7	10	22	AAW88260 Saccharomyces cere
4	26.7	10	22	AAW88261 Saccharomyces cere
4	26.7	10	22	AAW88262 Saccharomyces cere
4	26.7	10	22	AAW88263 Saccharomyces cere
4	26.7	10	23	ABG69566 Opioid peptide SEQ
4	26.7	10	23	ABG69566 Human CRPI tryptic
4	26.7	10	23	ABJ01569 158PID7 related HL
4	26.7	10	23	ABJ01656 158PID7 related HL
4	26.7	10	24	ABR47212 Staphylococcus aur
4	26.7	10	24	ABR47212 Staphylococcus aur
4	26.7	10	24	ABR47279 Staphylococcus aur
4	26.7	10	24	ABR47286 Staphylococcus aur
4	26.7	10	24	ABR47290 Staphylococcus aur
4	26.7	11	15	AAW45216 Des-Tyr Dynorphin
4	26.7	11	17	AAW91341 Dynorphin A analog
4	26.7	11	17	AAW91323 Dynorphin A analog
4	26.7	11	19	AAW65968 Des-Tyr-Gly dynorp
4	26.7	11	19	AAW65968 Specific factor VI
4	26.7	11	21	AAW15261 Specific factor VI
4	26.7	11	21	AAW15262 Specific factor VI
4	26.7	11	21	AAW15263 Specific factor VI
4	26.7	11	21	AAW15264 Specific factor VI
4	26.7	11	21	AAW15266 Specific factor VI
4	26.7	11	22	AAE02349 Ctenorhabditis ele
4	26.7	11	22	AAW91600 Opioid peptide SEQ
4	26.7	11	22	AAW91619 Opioid peptide SEQ
4	26.7	11	22	AAW91621 Opioid peptide SEQ
4	26.7	12	2	AAW10402 Analgesic peptide.
4	26.7	12	15	AAW45205 des-Tyr Dynorphin
4	26.7	12	15	AAW45215 des-Tyr Dynorphin
4	26.7	12	15	AAW45215 Dynorphin A analog
4	26.7	12	17	AAW91331 Dynorphin A analog
4	26.7	12	17	AAW91322 Dynorphin A analog
4	26.7	12	19	AAW65958 Des-Tyr dynorphin
4	26.7	12	19	AAW65957 Des-Tyr-Gly dynorp
4	26.7	12	20	AAW02595 Dynorphin analogue
4	26.7	12	21	AAW30277 CD4+ T-cell activa

83 Human chemokine de
84 Opioid peptide SEQ
85 Opioid peptide SEQ
86 Opioid peptide SEQ
87 Opioid peptide SEQ
88 Protease Cleavage
89 Tumour necrosis fa
90 Tumour necrosis fa
91 Tumour necrosis fa
92 Analgesic peptide.
93 Analgesic peptide.
94 Sequence of dynorp
95 des-Tyr Dynorphin
96 des-Tyr Dynorphin
97 Dynorphin A(1-13)
98 Dynorphin-A. Synt
99 Dynorphin A analog
100 Dynorphin A analog

ALIGNMENTS

RESULT 1
AAB72253
ID AAB72253 standard; peptide; 15 AA.
XX
AC AAB72253;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 8.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
FN WO20011937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22818.
XX
PR 17-AUG-1999; 99US-0149311.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
PA (REGG-) REGEN THERAPEUTICS PLC.
XX
PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
XX WPI; 2001-202804/20.
XX
PT Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -
XX
PS Claim 1; Page 34; 50pp; English.
XX
CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX SQ Sequence 15 AA;
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKPPPKLKVEVFPFP 15
Db 1 LKPPPKLKVEVFPFP 15
RESULT 2
AAB72507
ID AAB72507 standard; Peptide; 15 AA.
XX
AC AAB72507;
XX
DT 09-MAY-2001 (first entry)
XX
DE Colostrinin peptide #8.
XX
KW Dermatological; oxidative stress regulator; colostrinin.
XX
OS Unidentified.
XX
FN WO200112650-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US22665.
XX
PR 17-AUG-1999; 99US-0149310.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LKPPPKLKVEVFPFP 15
Db 1 LKPPPKLKVEVFPFP 15
RESULT 3
AAB72539
ID AAB72539 standard; Peptide; 15 AA.
XX
AC AAB72539;
XX
DT 09-MAY-2001 (first entry)
XX

```

DE Colostrinin peptide #8.
XX Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
XX Unidentified.
XX OS
XX WO200112651-A2.
XX PN
XX 22-FEB-2001.
XX PD
XX 17-AUG-2000; 2000WO-US222774.
XX PF
XX 17-AUG-1999; 99US-0149633.
XX PR
XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA
XX Boldogh I;
XX PI
XX WPI; 2001-226545/23.
XX DR
XX Use of colostrinin, its constituent peptide or analog as a neural cell
PT regulator, for promoting neural cell differentiation and treating
PT damaged neural cells in a patient -
XX
XX Claim 6; Page 21; 35pp; English.
XX PS
XX The present invention relates to a method for promoting neural cell
CC differentiation and treating damaged neural cells, using colostrinin and
CC colostrinin constituent peptides (e.g. the present peptide) as a neural
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX
XX
XX Query Match 100.0%; Score 15; DB 22; Length 15;
DE Best Local Similarity 100.0%; Pred. No. 3.6e-09;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LKFPFKLKVEVFPPF 15
QY |||||
DB 1 LKFPFKLKVEVFPPF 15
XX
XX
XX RESULT 4
XX AAB59313
ID AAB59313 standard; Peptide; 15 AA.
XX AC
XX AAB59313;
XX DT
XX 21-MAR-2001 (first entry)
XX DE
XX Ewe colostrinin peptide fragment A-4.
XX
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
XX Ovis sp.
XX
XX WO200075173-A2.
XX PN
XX 14-DEC-2000.
XX PD
XX 02-JUN-2000; 2000WO-GB02128.
XX PF
XX 02-JUN-1999; 99GB-0012852.
XX PR
XX (REG-) REGEN THERAPEUTICS PLC.
XX PA
XX Georgiades JA;
XX PI
XX WPI; 2001-071058/09.
XX DR
XX Peptides having an N-terminal amino acid sequence isolated from
PT

```

```

PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
XX characterized by amyloid plaques -
XX
XX Claim 7; Page 27; 63pp; English.
XX PS
XX
XX The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
XX
XX Query Match 100.0%; Score 15; DB 22; Length 15;
DE Best Local Similarity 100.0%; Pred. No. 3.6e-09;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LKFPFKLKVEVFPPF 15
QY |||||
DB 1 LKFPFKLKVEVFPPF 15
XX
XX
XX RESULT 5
XX AAE20235
ID AAE20235 standard; peptide; 15 AA.
XX AC
XX AAE20235;
XX DT
XX 18-JUN-2002 (first entry)
XX DE
XX Colostrinin constituent peptide #8.
XX
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
XX Unidentified.
XX OS
XX
XX Key Location/Qualifiers
FH Modified-site 15
FT /note= "Optionally C-terminal amide"
XX
XX WO200213850-A1.
XX PN
XX 21-FEB-2002.
XX PD
XX 17-AUG-2000; 2000WO-US22776.
XX PF
XX 17-AUG-2000; 2000WO-US22776.
XX PR
XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA
XX Stanton GJ, Hughes TK, Boldogh I;
XX PI
XX WPI; 2002-269151/31.
XX DR
XX
XX Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
XX Claim 6; Page 25; 51pp; English.
XX PS
XX The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidizing species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LKPPFKLKVEVFPP 15
 |||||
 Db 1 LKPPFKLKVEVFPP 15
 |||||

RESULT 6
 AAM51043
 ID AAM51043 standard; Peptide: 15 AA.

AC AAM51043;

DT 30-MAY-2002 (first entry)

XX Colostrinin constituent peptide.

DE Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 15 /note= "optional C-terminal amidation"

XX WO200213849-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.

XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

DR Modulation of blood cell proliferation in a patient involves use of
 XX blood cell regulator selected from colostrinin, its constituent peptide
 XX and/or analogue -

PS Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is preferred for use as an immunological regulator and as a
 CC blood cell regulator in claimed methods of the invention. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patient. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide. Cytokines induced by this peptide in human
 CC leucocyte cultures include interferon-gamma, tumour necrosis
 CC factor-alpha, interleukin-6 and interleukin-10.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.6e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPFKLKVEVFPP 15
 |||||

Db 1 LKPPFKLKVEVFPP 15
 |||||

RESULT 7

AAO14584

ID AAO14584 standard; peptide; 15 AA.

XX AC AAO14584;

XX DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 8.

DE Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 XX neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 15 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.

XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 XX regulator selected from colostrinin, its constituent peptide and/or
 XX analog -

PS Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid

CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 15; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPPPKLKVEVPPFP 15
|||||
Db 1 LKPPPKLKVEVPPFP 15

RESULT 8
AAB59344
ID AAB59344 standard; Peptide; 16 AA.

XX AC AAB59344;
XX DT 21-MAR-2001 (first entry)

XX DE Ewe colostrinin peptide fragment derived sequence #4.

XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS Ovis sp.

XX FN WO200075173-A2.

XX PD 14-DEC-2000.

XX PF 02-JUN-2000; 200WO-GB02128.

XX PR 02-JUN-1999; 99GB-0012852.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-071058/08.

XX PT Peptides having an N-terminal amino acid sequence isolated from
XX PT colostrinin for treating e.g. disorders of the central nervous system
XX PT and immune system, viral and bacterial infections, and diseases
XX PT characterized by amyloid plaques -

XX PS Claim 8; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.

XX SQ Sequence 16 AA;
Query Match 100.0%; Score 15; DB 22; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPPPKLKVEVPPFP 15
|||||
Db 2 LKPPPKLKVEVPPFP 16

RESULT 9
AAE07188
ID AAE07188 standard; peptide; 10 AA.

XX AAE07188;
XX DT 06-NOV-2001 (first entry)
XX KW Colostrinin peptide 4.
XX KW Colostrinin; nontropic; neuroprotective; immunomodulatory; antibacterial;
XX KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
XX KW central nervous system disorder; neurodegenerative disorder; weight loss;
XX KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
XX KW acquired immunological deficiency; neurological disorder; dementia;
XX KW antiviral.

XX OS Unidentified.

XX FN WO200155199-A1.

XX PD 02-AUG-2001.

XX PF 26-JAN-2001; 2001WO-GB00329.

XX PR 26-JAN-2000; 2000GB-0001825.

XX PA (REG-) REGEN THERAPEUTICS PLC.

XX PI Georgiades JA;

XX DR WPI; 2001-488775/53.

XX PT Peptide useful as an inter alia in the treatment of e.g. disorders of
XX PT the immune system and the central nervous system comprises ten
XX PT amino-terminal amino acid sequence derived from peptides present in
XX PT colostrinin -

XX PS Claim 1; Page 15; 40pp; English.

CC The invention relates to colostrinin peptide fragments which are useful,
CC inter alia, in the treatment of chronic disorders of the immune system
CC and the central nervous system. Colostrinin peptides are used as a
CC medicament in the treatment of neurological disorders e.g., dementia,
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC neurosis, in acquired immunological deficiencies, chronic bacterial and
CC viral infections and diseases characterised by the presence of beta-
CC amyloid plaques and as a dietary supplement for babies, small children,
CC adults and senile persons, who have been subjected to chemotherapy or
CC have suffered from cachexia or weight loss due to the chronic disease.
CC Colostrinin peptides are also used as food additives and as an auxiliary
CC withdrawal treatment for drug addicts, after a period of detoxification
CC and in persons dependent on stimulants. Colostrinin peptides are used to
CC prepare antibodies and to treat emotional disturbances, e.g. emotional
CC disturbances of psychiatric patients in a state of depression. These
CC colostrinin peptides improves the development of immune system in a new
CC born child and to correct the immunological deficiencies in a child.
CC The present sequence is colostrinin peptide 4 related to the invention.

XX SQ Sequence 10 AA;

Query Match 46.7%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PCLKVEV 11
|||||
Db 1 PCLKVEV 7

RESULT 10
AAE07198
ID AAE07198 standard; peptide; 11 AA.
XX AC AAE07198;

XX 06-NOV-2001 (first entry)
 XX Modified colostrinin cyclic peptide #4.
 XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
 XX Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
 KW central nervous system disorder; neurodegenerative disorder; weight loss;
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
 KW acquired immunological deficiency; neurological disorder; dementia;
 KW antiviral; cyclic.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetyl"; this residue forms a cyclic
 FT linkage with Pro found at the C-terminal end"
 FT
 XX WO200155199-A1.
 XX 02-AUG-2001.
 XX 26-JAN-2001; 2001WO-GB00329.
 XX 26-JAN-2000; 2000GB-0001825.
 XX (REG-) REGEN THERAPEUTICS PLC.
 XX Georgiades JA;
 XX WPI; 2001-486775/53.
 XX Peptide useful as an inter alia in the treatment of e.g. disorders of
 PT the immune system and the central nervous system comprises ten
 PT amino-terminal amino acid sequence derived from peptides present in
 PT colostrinin -
 XX
 PS Example 2; Page 8; 40pp; English.
 XX
 CC The invention relates to colostrinin peptide fragments which are useful,
 CC inter alia, in the treatment of chronic disorders of the immune system
 CC and the central nervous system. Colostrinin peptides are used as a
 CC medicament in the treatment of neurological disorders e.g., dementia,
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and
 CC viral infections and diseases characterised by the presence of beta-
 CC amyloid plaques and as a dietary supplement for babies, small children,
 CC adults and senile persons, who have been subjected to chemotherapy or
 CC have suffered from cachexia or weight loss due to the chronic disease.
 CC Colostrinin peptides are also used as food additives and as an auxiliary
 CC withdrawal treatment for drug addicts, after a period of detoxification
 CC and in persons dependent on stimulants. Colostrinin peptides are used to
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional
 CC disturbances of psychiatric patients in a state of depression. These
 CC colostrinin peptides improves the development of immune system in a new
 CC born child and to correct the immunological deficiencies in a child.
 CC The present sequence is modified colostrinin cyclic peptide #4 related to
 CC the invention.
 XX
 SQ Sequence 11 AA;
 Query Match 46.7%; Score 7; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PKLKVEV 11
 Db 2 PKLKVEV 8
 |||||
 |||||
 RESULT 11

AAV70257
 ID AAV70257 standard; peptide; 9 AA.
 XX
 AC AAV70257;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Peptide encoded by forward primer-2 for human Fc-Angiostatin immunofusin.
 XX
 KW Human; immunoglobulin gamma Fc fragment; angiostatin; immunofusin;
 KW angiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic;
 KW antipsoriatic; antidiabetic; ophthalmological; immunosuppressant;
 KW vasotropic; vulnery; treatment; antiarteriosclerosis; tumour;
 KW metastasis; atherosclerosis; psoriasis; rheumatoid arthritis;
 KW ocular angiogenic disease; diabetic retinopathy; macular degeneration;
 KW myocardial angiogenesis; plaque neovascularisation; telangiectasia;
 KW wound granulation; keloid scar; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200011033-A2.
 XX
 PD 02-MAR-2000.
 XX
 PF 25-AUG-1999; 99WO-US19329.
 XX
 PR 25-AUG-1998; 98US-0097883.
 XX
 PA (LEXI-) LEXINGEN PHARM CORP.
 XX
 PI Lo K, Li Y, Gillies SD;
 XX
 DR WPI; 2000-237616/20.
 DR N-PSDB; AA251297.
 XX
 PT Novel fusion protein of angiostatin or endostatin and an immunoglobulin
 PT Fc region, useful for treating conditions mediated by angiogenesis,
 PT such as rheumatoid arthritis, tumors and macular degeneration -
 XX
 PS Example 4; Page 47; 68pp; English.
 XX
 CC The patent discloses a DNA molecule encoding a fusion protein comprising
 CC a signal sequence, an immunoglobulin Fc region, and an angiogenesis
 CC inhibitor selected from angiostatin, endostatin, a plasminogen fragment
 CC having angiostatin activity, a collagen XVIII fragment having endostatin
 CC activity, or combinations of them. The fusion protein (immunofusin) is
 CC used to inhibit angiogenesis and to treat diseases or conditions mediated
 CC by angiogenesis. Conditions that may be treated include solid tumours,
 CC blood born tumours, tumour metastasis, benign tumours including
 CC haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic
 CC granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases
 CC e.g. diabetic retinopathy, retinopathy of prematurity, macular
 CC degeneration, corneal graft rejection, neovascular glaucoma, retrolental
 CC fibroplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis,
 CC plaque neovascularisation, telangiectasia, haemophilic joints,
 CC angiofibroma, wound granulation, and excessive or abnormal stimulation of
 CC endothelial cells, intestinal cells, atherosclerosis, sclerodermal and
 CC hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in
 CC gene therapy. The present sequence is a peptide encoded by forward primer
 CC used in the construction of immunofusin comprising human immunoglobulin
 CC gamma (IgG) Fc fragment and human angiostatin (Fc-Angio fusion protein).
 XX
 SQ Sequence 9 AA;
 Query Match 33.3%; Score 5; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PKLKV 9
 Db 1 PKLKV 5
 |||||
 |||||

```

RESULT 12'
ABJ01751
ID  ABOJ1751 standard; Peptide; 9 AA.
XX
XX  AC  ABOJ1751;
XX  DT  19-SEP-2002 (first entry)
XX  DE  158P1D7 related HLA peptide SEQ ID No 451.
XX  KW  Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  KW  HLA.
XX
XX  OS  Homo sapiens.
XX  PN  WO200216593-A2.
XX  PD  28-FEB-2002.
XX  PF  22-AUG-2001; 2001WO-US26276.
XX  PR  22-AUG-2000; 2000US-227098P.
XX  PR  10-APR-2001; 2001US-282739P.
XX  PA  (AGEN-) AGENSYS INC.
XX  PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX  PI  Challita-eid PM, Jakobovits A;
XX  DR  WPI; 2002-425659/45.
XX  PT  New compositions comprising a gene (designated 158P1D7), its encoded
XX  PT  protein or their modulators, useful for treating or diagnosing cancers,
XX  PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX  PT  or humans)
XX  PS  Disclosure; Page 142; 181pp; English.
XX  CC  The invention relates to a novel nucleic acid, designated 158P1D7. The
XX  CC  compositions are useful for treating or diagnosing cancers, particularly
XX  CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX  CC  horses or humans). The compositions are also useful for monitoring
XX  CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX  CC  of the invention can be used in gene therapy to treat the said disorders.
XX  CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
XX  CC  to the 158P1D7 protein of the invention.
XX  SQ  Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PRLKV 9
Db 4 PRLKV 8

RESULT 13
ABJ01752
ID  ABOJ1752 standard; Peptide; 9 AA.
XX
XX  AC  ABOJ1752;
XX  DT  19-SEP-2002 (first entry)
XX  DE  158P1D7 related HLA peptide SEQ ID No 452.
XX  KW  Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  KW  HLA.
XX  PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;

```

```

OS  Homo sapiens.
XX  PN  WO200216593-A2.
XX  PD  28-FEB-2002.
XX  PF  22-AUG-2001; 2001WO-US26276.
XX  PR  22-AUG-2000; 2000US-227098P.
XX  PR  10-APR-2001; 2001US-282739P.
XX  PA  (AGEN-) AGENSYS INC.
XX  PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX  PI  Challita-eid PM, Jakobovits A;
XX  DR  WPI; 2002-425659/45.
XX  PT  New compositions comprising a gene (designated 158P1D7), its encoded
XX  PT  protein or their modulators, useful for treating or diagnosing cancers,
XX  PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX  PT  or humans)
XX  PS  Disclosure; Page 142; 181pp; English.
XX  CC  The invention relates to a novel nucleic acid, designated 158P1D7. The
XX  CC  compositions are useful for treating or diagnosing cancers, particularly
XX  CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX  CC  horses or humans). The compositions are also useful for monitoring
XX  CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX  CC  of the invention can be used in gene therapy to treat the said disorders.
XX  CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
XX  CC  to the 158P1D7 protein of the invention.
XX  SQ  Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PRLKV 9
Db 2 PRLKV 6

RESULT 14
ABJ01851
ID  ABOJ1851 standard; Peptide; 9 AA.
XX
XX  AC  ABOJ1851;
XX  DT  19-SEP-2002 (first entry)
XX  DE  158P1D7 related HLA peptide SEQ ID No 551.
XX  KW  Cytostatic; 158P1D7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  KW  HLA.
XX  OS  Homo sapiens.
XX  PN  WO200216593-A2.
XX  PD  28-FEB-2002.
XX  PF  22-AUG-2001; 2001WO-US26276.
XX  PR  22-AUG-2000; 2000US-227098P.
XX  PR  10-APR-2001; 2001US-282739P.
XX  PA  (AGEN-) AGENSYS INC.
XX  PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;

```

```

PI Challita-eid PM, Jakobovits A;
XX
DR WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT or humans)
XX
PS Disclosure; Page 146; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 2 PKLKV 6
|||||

RESULT 15
ABJ01855
ID ABJ01855 standard; Peptide; 9 AA.
XX
AC ABJ01855;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide SEQ ID No 555.
XX
KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
FN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US26276.
XX
PR 22-AUG-2000; 2000US-227098P.
XX
PT 10-APR-2001; 2001US-282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Challita-eid PM, Jakobovits A;
XX
WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT or humans)
XX
PS Disclosure; Page 146; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 2 PKLKV 6
|||||

RESULT 16
ABJ01996
ID ABJ01996 standard; Peptide; 9 AA.
XX
AC ABJ01996;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide #37.
XX
KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
FN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US26276.
XX
PR 22-AUG-2000; 2000US-227098P.
XX
PT 10-APR-2001; 2001US-282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Challita-eid PM, Jakobovits A;
XX
WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT or humans)
XX
PS Disclosure; Page 140; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
|||||

```

```

CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 4 PKLKV 8
|||||

RESULT 16
ABJ01996
ID ABJ01996 standard; Peptide; 9 AA.
XX
AC ABJ01996;
XX
DT 19-SEP-2002 (first entry)
XX
DE 158PID7 related HLA peptide #37.
XX
KW Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW HLA.
XX
OS Homo sapiens.
XX
FN WO200216593-A2.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-US26276.
XX
PR 22-AUG-2000; 2000US-227098P.
XX
PT 10-APR-2001; 2001US-282739P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI Challita-eid PM, Jakobovits A;
XX
WPI; 2002-425659/45.
XX
PT New compositions comprising a gene (designated 158PID7), its encoded
PT protein or their modulators, useful for treating or diagnosing cancers,
PT particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT or humans)
XX
PS Disclosure; Page 140; 181pp; English.
XX
CC The invention relates to a novel nucleic acid, designated 158PID7. The
CC compositions are useful for treating or diagnosing cancers, particularly
CC bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC horses or humans). The compositions are also useful for monitoring
CC genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC of the invention can be used in gene therapy to treat the said disorders.
CC This sequence represents a human leukocyte antigen (HLA) peptide relating
CC to the 158PID7 protein of the invention.
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
|||||

```

```

Db      .      4 PKLKV 8

RESULT 17
ABJ01366
ID  ABJ01366 standard; Peptide; 10 AA.
XX
XX  AC  ABJ01366;
XX
XX  DT  19-SEP-2002 (first entry)
XX
XX  DE  158PID7 related HLA peptide SEQ ID No 66.
XX
XX  KW  Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  KW  HLA.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200216593-A2.
XX
XX  PD  28-FEB-2002.
XX
XX  PF  22-AUG-2001; 2001WO-US26276.
XX
XX  PR  22-AUG-2000; 2000US-227098P.
XX
XX  PR  10-APR-2001; 2001US-282739P.
XX
XX  PA  (AGEN-) AGENSYS INC.
XX
XX  PI  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
XX  PI  Challita-eid PM, Jakobovits A;
XX
XX  DR  WPI; 2002-425659/45.
XX
XX  PT  New compositions comprising a gene (designated 158PID7), its encoded
XX  PT  protein or their modulators, useful for treating or diagnosing cancers,
XX  PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
XX  PS  or humans) -
XX
XX  PS  Disclosure; Page 147; 181pp; English.
XX
XX  CC  The invention relates to a novel nucleic acid, designated 158PID7. The
XX  CC  compositions are useful for treating or diagnosing cancers, particularly
XX  CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
XX  CC  horses or humans). The compositions are also useful for monitoring
XX  CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
XX  CC  of the invention can be used in gene therapy to treat the said disorders.
XX  CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
XX  CC  to the 158PID7 protein of the invention.
XX
XX  SQ  Sequence 10 AA;

Query Match      33.3%; Score 5; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      |||||
        4 PKLKV 8

RESULT 19
ABJ01929
ID  ABJ01929 standard; Peptide; 10 AA.
XX
XX  AC  ABJ01929;
XX
XX  DT  19-SEP-2002 (first entry)
XX
XX  DE  158PID7 related HLA peptide SEQ ID No 629.
XX
XX  KW  Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
XX  KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
XX  KW  HLA.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200216593-A2.
XX
XX  PD  28-FEB-2002.
XX
XX  PF  22-AUG-2001; 2001WO-US26276.
XX
XX  PR  22-AUG-2000; 2000US-227098P.
XX
XX  PR  10-APR-2001; 2001US-282739P.
XX
XX

```


CC islet-cell transplant to alleviate their pre-existing diabetes. The
 CC peptides can be used therapeutically to protect against or ameliorate the
 CC symptoms associated with type 1 diabetes. The vaccines can be used for
 CC raising an immune response against Rotavirus. T-cell epitopes in
 CC autoantigens have potential diagnostic and therapeutic applications and
 CC may hold clues to environmental agents that could trigger or exacerbate
 CC autoimmune diseases. The present invention identified T-cell epitopes
 CC that may provide such clues.

XX Sequence 16 AA;

Query Match 33.3%; Score 5; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLVKE 10
 |||||

Db 8 KLVKE 12

RESULT 22

ABP82437

ID ABP82437 standard; Peptide; 16 AA.

XX AC ABP82437;

XX 04-MAR-2003 (first entry)

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1110.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

XX Homo sapiens.

XX WO200261087-A2.

XX 08-AUG-2002.

XX 19-DEC-2001; 2001WO-US50107.

XX 19-DEC-2000; 2000US-257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

XX Burmer GC, Roush CL, Brown JP;

XX WPI; 2003-046718/04.

XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -

XX Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:

CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific

CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

SQ Sequence 16 AA;

Query Match 33.3%; Score 5; DB 24; Length 16;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPFPK 6

|||||

Db 9 KPFPK 13

RESULT 23

AAB30278

ID AAB30278 standard; Peptide; 17 AA.

XX AC AAB30278;

XX 12-FEB-2001 (first entry)

XX CD4+ T-cell activation methods peptide ligand #40.

DE CD4+ T-cell activation; peptide epitope; autoimmune disease;
 KW infectious disease; cancer; immunological mass fingerprinting.

XX Synthetic.

XX WO2000063702-A1.

XX 26-OCT-2000.

XX 20-APR-2000; 2000WO-US10888.

XX 21-APR-1999; 99US-0130355.

XX 21-APR-1999; 99US-0295868.

XX (ZYCO-) ZYCOS INC.

XX (UNLO) KINGS COLLEGE LONDON.

XX Peakman M, Chicx RM;

XX WPI; 2000-665270/64.

XX Identifying a class II major histocompatibility complex-binding fragment
 of a polypeptide useful for diagnosing and protecting against diabetes
 PT comprises contacting a ligand, a polypeptide and a mammalian antigen
 PT presenting cell -

XX Claim 35; Page 96; 118pp; English.

XX The present invention is concerned with a method, designated
 CC immunological mass fingerprinting, which enables the identification of
 CC peptide epitopes that activate CD4+ T-cells. Peptides of this kind are
 CC also given. CD4+ cells are involved in the pathogenesis of disease, and
 CC the peptides can be used in the prevention and treatment of autoimmune
 CC diseases such as diabetes, multiple sclerosis, rheumatoid arthritis,

CC myasthenia gravis, systemic lupus erythematosus, autoimmune premature
 CC ovarian failure, Graves' thyroiditis, Hashimoto's thyroiditis, primary
 CC hypothyroidism, coeliac disease, primary biliary cirrhosis, autoimmune
 CC hepatitis, Addison's disease, vitiligo, systemic sclerosis and
 CC anti-glomerular basement membrane disease, infectious diseases including
 CC leprosy, measles, hepatitis C, HIV and parasitic diseases, and cancer.
 XX
 XX Sequence 17 AA;
 Query Match 33.3%; Score 5; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 KLVKE 10
 Db 1 KLVKE 5
 |||||
 |||||
 RESULT 24
 ABP83371
 ID ABP83371 standard; Peptide; 19 AA.
 XX
 AC ABP83371;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:2044.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW Graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US50107.
 XX
 PR 19-DEC-2000; 2000US-257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 PI Burner GC, Roush CL, Brown JP;
 XX
 DR WPI; 2003-046718/04.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases -
 XX
 PS Claim 1; Fig 2; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 19 AA;
 Query Match 33.3%; Score 5; DB 24; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LKVEV 11
 Db 4 LKVEV 8
 |||||
 |||||
 RESULT 25
 AAW65794
 ID AAW65794 standard; peptide; 5 AA.
 XX
 AC AAW65794;
 XX
 DT 19-OCT-1998 (first entry)
 XX
 DE Polypeptidyl inhibitor of cyclophilin.
 XX
 KW polypeptidyl; cyclophilin; inhibitor; neurotrophic compound; PPI;
 KW peptidyl-prolyl isomerase; rotamase; immunophilin protein; degeneration;
 KW neuronal damage.
 XX
 OS Synthetic.
 XX
 PN WO9825950-A1.
 XX
 PD 18-JUN-1998.
 XX
 PF 08-DEC-1997; 97WO-US23102.
 XX
 PR 09-DEC-1996; 96US-0761902.
 XX
 PA (GUIL-) GUILFORD PHARM INC.
 XX
 PI Hamilton GS, Steiner JP, Wei L;
 XX
 DR WPI; 1998-348444/30.
 XX
 PT Effecting neuronal activity in mammals - by administering tetra-
 PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,
 PT useful in treatment of neuronal damage or degeneration disorders
 XX
 PS Claim 11; Page 41; 70pp; English.
 XX
 CC The invention relates to a method of effecting a neuronal activity. It
 CC comprises administering a neurotrophic compound with an affinity for a
 CC cyclophilin type immunophilin. The immunophilin shows peptidyl-prolyl
 CC isomerase (rotamase) activity. The neurotrophic compound achieves the
 CC stimulation of damaged neurons, promotion of neuronal regeneration or
 CC prevention of neurodegeneration, and treatment of neurological disorder.
 CC The neurotrophic compounds are potent peptidyl-proline isomerase
 CC (rotamase) inhibitors. They are of use in disorders which include
 CC peripheral neuropathy caused by physical injury or disease state, i.e.
 CC physical injury to the brain or spinal cord, stroke, or neurological


```

XX 25-JUN-2002 (first entry)
DT Hepatitis C virus NS3-serine protease inhibitor related peptide #9.
DE Hepatitis C virus; HCV; NS3-serine protease inhibitor; hepatitis;
KW HCV protease inhibitor; infection; virucide; hepatotropic.
XX
OS Hepatitis C virus.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 6 /note= "nVal-(CO)"
FT
XX WO200208256-A2.
XX
XX 31-JAN-2002.
PD
XX 19-JUL-2001; 2001WO-US22826.
XX
XX 21-JUL-2000; 2000US-220109P.
PR
XX (SCHE ) SCHERING CORP.
PA (CORV-) CORVAS INT INC.
XX
XX Sakena AK, Girijavallabhan VM, Lovey RG, Jao EE, Bennett F;
PI McCormick J, Wang H, Pike RE, Bogen SL, Liu Y, Arasappan A;
PI Parekh T, Pinto FA, Njoroge FG, Ganguly AK, Brunck TK, Kemp SJ;
PI Levy OE, Lim-Wilby M;
XX
XX WPI; 2002-361644/39.
DR
XX Novel peptide inhibitor compounds of hepatitis virus NS3/NS4a serine
PT protease, useful for treating hepatitis C virus disorders -
XX
XX Example 1; Page 107; 196pp; English.
XX
XX The present invention describes a peptide compound (I) exhibiting
CC hepatitis C virus (HCV) protease inhibitory activity, including
CC enantiomers, stereoisomers, rotomers and tautomers, pharmaceutically
CC acceptable salts, solvates or derivatives. Also described are: (I) a
CC pharmaceutical composition (II) comprising (I); and (2) preparing (II)
CC for treating disorders associated with HCV protease involving bringing
CC into intimate contact (I) and a carrier. (I) has virucide and
CC hepatotropic activities and can be used as HCV NS3/NS4a serine protease
CC inhibitors. (I) is useful for manufacturing a medicament to treat
CC disorders associated with HCV protease. (I) can be used for modulating
CC activity of HCV protease preferably, HCV NS3/NS4a protease and for
CC modulating the processing of HCV polypeptide. (II) is useful for
CC treating disorders associated with HCV and for treating disorders
CC associated with HCV protease. (I) is useful for treating hepatitis
CC caused by HCV. The present sequence represents a peptide given in an
XX example from the present invention.
XX
XX Sequence 7 AA;
XX
Query Match 26.7%; Score 4; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 10 EVFP 13
DB 2 EVFP 5
XX
RESULT 31
AAR59968
ID AAR59968 standard; peptide; 8 AA.
XX
AC AAR59968;
XX

```

```

DT 25-MAR-2003 (updated)
DT 14-FEB-1995 (first entry)
XX
DE Peptide signal sequence of platelet derived growth factor A.
XX
KW Therapeutic; metabolic interactions; PSS; analogues.
XX
OS Synthetic.
XX
XX WO9416328-A1.
XX
XX 21-JUL-1994.
PD
XX 30-DEC-1993; 93WO-US12679.
PF
XX 30-DEC-1992; 92US-0997727.
PR
XX (RATH/) RATH M.
PA
XX Rath M;
XX
XX WPI; 1994-249399/30.
DR
XX Identifying peptide signal sequences in a protein - and use of
PT their synthetic analogues for treating or preventing, e.g.
PT cardiovascular and auto-immune disease, infections and cancer.
XX
XX Claim 38; Page 17; 28pp; English.
XX
XX The sequence is that of a signal sequence analogous to that of
CC platelet derived growth factor chain A.
CC See also AAR59944-83.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 8 AA;
XX
Query Match 26.7%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 PKLK 8
DB 4 PKLK 7
XX
RESULT 32
AAR07412
ID AAR07412 standard; peptide; 9 AA.
XX
AC AAR07412;
XX
XX 20-JAN-1997 (first entry)
DT
XX Antibacterial/antifungal, synthetic peptide.
DE
XX Antimicrobial; food additive; preservative; low toxicity; fungus;
KW bacterium; treatment; inhibitory.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 9 /note= "opt. amidated"
FT
XX JP08134096-A.
XX
XX 28-MAY-1996.
PD
XX 01-NOV-1994; 94JP-0268723.
PF
XX 01-NOV-1994; 94JP-0268723.
PR
XX (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
PA

```

```

XX WPI; 1996-306572/31.
XX
XX New antimicrobial nona:peptide(s) - useful for treating bacterial
PT and fungal diseases and as preservatives for food and feedstuffs
XX
XX Example 4; Page 8; 10pp; Japanese.
XX
XX AAW07406-W07418 are peptides which have both antifungal and
CC antibacterial properties. The peptides can be synthesised by solid phase
CC synthesis or chemical synthesis in large amounts at a low cost. The
CC peptides are specific examples of a generic peptide KXXXXXXX (see
CC AAW07405) and can be used as microbial additives for foods and animal
CC feeds. The peptides were shown to have minimum inhibitory concns. of
CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an
CC amidated N-terminus are preferred).
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 KLKV 9
XX Db 1 KLKV 4
XX
XX RESULT 33
XX AAW07413
XX ID AAW07413 standard; peptide; 9 AA.
XX AC AAW07413;
XX
XX DT 20-JAN-1997 (first entry)
XX
XX Antibacterial/antifungal, synthetic peptide.
XX
XX Antimicrobial; food additive; preservative; low toxicity; fungus;
XX bacterium; treatment; inhibitory.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 9 /note= "opt. amidated"
XX
XX JF08134096-A.
XX
XX PD 28-MAY-1996.
XX
XX PF 01-NOV-1994; 94JP-0268723.
XX
XX PR 01-NOV-1994; 94JP-0268723.
XX
XX PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX
XX WPI; 1996-306572/31.
XX
XX New antimicrobial nona:peptide(s) - useful for treating bacterial
PT and fungal diseases and as preservatives for food and feedstuffs
XX
XX Example 4; Page 8; 10pp; Japanese.
XX
XX AAW07406-W07418 are peptides which have both antifungal and
CC antibacterial properties. The peptides can be synthesised by solid phase
CC synthesis or chemical synthesis in large amounts at a low cost. The
CC peptides are specific examples of a generic peptide KXXXXXXX (see
CC AAW07405) and can be used as microbial additives for foods and animal
CC feeds. The peptides were shown to have minimum inhibitory concns. of
CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an
CC amidated N-terminus are preferred).
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 KLKV 9
XX Db 1 KLKV 4
XX
XX RESULT 33
XX AAW07413
XX ID AAW07413 standard; peptide; 9 AA.
XX AC AAW07413;
XX
XX DT 20-JAN-1997 (first entry)
XX
XX Antibacterial/antifungal, synthetic peptide.
XX
XX Antimicrobial; food additive; preservative; low toxicity; fungus;
XX bacterium; treatment; inhibitory.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 9 /note= "opt. amidated"
XX
XX JF08134096-A.
XX
XX PD 28-MAY-1996.
XX
XX PF 01-NOV-1994; 94JP-0268723.
XX
XX PR 01-NOV-1994; 94JP-0268723.
XX
XX PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX
XX WPI; 1996-306572/31.
XX
XX New antimicrobial nona:peptide(s) - useful for treating bacterial
PT and fungal diseases and as preservatives for food and feedstuffs
XX
XX Example 4; Page 8; 10pp; Japanese.
XX
XX AAW07406-W07418 are peptides which have both antifungal and
CC antibacterial properties. The peptides can be synthesised by solid phase
CC synthesis or chemical synthesis in large amounts at a low cost. The
CC peptides are specific examples of a generic peptide KXXXXXXX (see
CC AAW07405) and can be used as microbial additives for foods and animal
CC feeds. The peptides were shown to have minimum inhibitory concns. of
CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an

```

```

CC amidated N-terminus are preferred).
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 KLKV 9
XX Db 1 KLKV 4
XX
XX RESULT 34
XX AAW07414
XX ID AAW07414 standard; peptide; 9 AA.
XX AC AAW07414;
XX
XX DT 20-JAN-1997 (first entry)
XX
XX Antibacterial/antifungal, synthetic peptide.
XX
XX Antimicrobial; food additive; preservative; low toxicity; fungus;
XX bacterium; treatment; inhibitory.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 9 /note= "opt. amidated"
XX
XX JF08134096-A.
XX
XX PD 28-MAY-1996.
XX
XX PF 01-NOV-1994; 94JP-0268723.
XX
XX PR 01-NOV-1994; 94JP-0268723.
XX
XX PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX
XX WPI; 1996-306572/31.
XX
XX New antimicrobial nona:peptide(s) - useful for treating bacterial
PT and fungal diseases and as preservatives for food and feedstuffs
XX
XX Example 4; Page 8; 10pp; Japanese.
XX
XX AAW07406-W07418 are peptides which have both antifungal and
CC antibacterial properties. The peptides can be synthesised by solid phase
CC synthesis or chemical synthesis in large amounts at a low cost. The
CC peptides are specific examples of a generic peptide KXXXXXXX (see
CC AAW07405) and can be used as microbial additives for foods and animal
CC feeds. The peptides were shown to have minimum inhibitory concns. of
CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an
CC amidated N-terminus are preferred).
XX
XX Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 KLKV 9
XX Db 1 KLKV 4
XX
XX RESULT 35
XX AAW07415
XX ID AAW07415 standard; peptide; 9 AA.

```

```

XX AC AAW07415;
XX XX
XX DT 20-JAN-1997 (first entry)
XX DE Antibacterial/antifungal, synthetic peptide.
XX DE
XX KW Antimicrobial; food additive; preservative; low toxicity; fungus;
XX KW bacterium; treatment; inhibitory.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 9
XX FT /note= "opt. amidated"
XX PN JP08134096-A.
XX XX
XX PD 28-MAY-1996.
XX XX
XX PF 01-NOV-1994; 94JP-0268723.
XX XX
XX PR 01-NOV-1994; 94JP-0268723.
XX PA (SANW ) SANWA KAGAKU KENKYUSHO CO LTD.
XX XX
XX DR WPI; 1996-306572/31.
XX XX
XX PT New antimicrobial nona;peptide(s) - useful for treating bacterial
XX PT and fungal diseases and as preservatives for food and feedstuffs
XX XX
XX PS Example 4; Page 8; 10pp; Japanese.
XX CC
XX CC AAW07406-W07418 are peptides which have both antifungal and
XX CC antibacterial properties. The peptides can be synthesised by solid phase
XX CC synthesis or chemical synthesis in large amounts at a low cost. The
XX CC peptides are specific examples of a generic peptide KXXXXXXX (see
XX CC AAW07405) and can be used as microbial additives for foods and animal
XX CC feeds. The peptides were shown to have minimum inhibitory concns. of
XX CC between 1 and 2 microgram/ml against S. aureus ATCC 6538P and Candida
XX CC albicans and 4 microgram/ml against E. coli K12 594 (peptides having an
XX CC amidated N-terminus are preferred).
XX XX
XX SQ Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 17; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 KLKV 9
XX Db ||||
XX 1 KLKV 4
XX
XX RESULT 36
XX ABB14478
XX ID ABB14478 standard; Peptide; 9 AA.
XX XX
XX AC ABB14478;
XX XX
XX DT 22-JAN-2002 (first entry)
XX XX
XX DE Human C35 peptide epitope #1982.
XX XX
XX KW Human; C35; cytostatic; gene therapy; vaccine; tumour antigen;
XX KW breast cancer; bladder cancer; tumour immunotherapy; epitope;
XX KW major histocompatibility complex binding peptide; MHC.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200174859-A2.
XX XX
XX PD 11-OCT-2001.

```

```

XX XX
XX PF 04-APR-2001; 2001WO-US10855.
XX XX
XX PR 04-APR-2000; 2000US-194463P.
XX XX
XX PA (UYRP ) UNIV ROCHESTER.
XX XX
XX PI Zauderer M, Evans EE, Borrello MA;
XX XX WPI; 2001-626383/72.
XX DR
XX PS Novel C35 polypeptides and C35 genes useful in immunogenic compositions
XX PT and vaccines, for inducing antibody and cell-mediated immunity against
XX PT target cells, such as tumor cells that express C35 gene
XX XX
XX PS Disclosure; Page 166; 331pp; English.
XX XX
XX CC The present invention relates to human C35 (see AAG78997). C35 is a novel
XX CC tumour antigen that is overexpressed in human breast and bladder
XX CC carcinoma. C35 is thought to be a promising candidate for tumour
XX CC immunotherapy, in immunogenic compositions and vaccines, to induce
XX CC antibody and cell-mediated immunity against target cells such as tumour
XX CC cells that express C35 genes. The present sequence is a C35 peptide
XX CC epitope. This peptide is predicted to be a major histocompatibility
XX CC complex (MHC) binding peptide.
XX XX
XX SQ Sequence 9 AA;
XX
XX Query Match 26.7%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 FPKL 7
XX Db ||||
XX 1 FPKL 4
XX
XX RESULT 37
XX AAB91625
XX ID AAB91625 standard; Peptide; 9 AA.
XX XX
XX AC AAB91625;
XX XX
XX DT 22-JUN-2001 (first entry)
XX XX
XX DE Opioid peptide SEQ ID NO:801.
XX XX
XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX KW blood component; modification; succinimidyl; maleimido group; amino;
XX KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX XX
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN WO200069900-A2.
XX XX
XX PD 23-NOV-2000.
XX XX
XX PF 17-MAY-2000; 2000WO-US13576.
XX XX
XX PR 17-MAY-1999; 99US-0134406.
XX PR 10-SEP-1999; 99US-0153406.
XX PR 15-OCT-1999; 99US-0159783.
XX XX
XX PA (CONJ-) CONJUCHEM INC.
XX XX
XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX XX WPI; 2001-112059/12.
XX DR
XX KW Modifying and attaching therapeutic peptides to albumin prevents
XX PT peptidase degradation, useful for increasing length of in vivo activity
XX PT

```

XX Disclosure; Page 457; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimide and maleimide groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidease stabilised therapeutic peptide composed of 3-50 amino acids.

XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

XX Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes.

XX AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
| | | |
Db 2 PKLK 5

RESULT 38
AAB76273
ID AAB76273 standard; Peptide; 9 AA.
XX AC
XX AAB76273;
DT 10-APR-2001 (first entry)
DE Influenza virus immunogenic peptide.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC; cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
KW HLA binding peptide; immune response; glycoprotein; cytostatic;
KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
KW human immunodeficiency virus; protozoicide; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV; cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
KW renal carcinoma; cervical carcinoma; lymphoma; malaria; condyloma acuminatum.
XX
OS Influenza virus.
XX
PN WO200100225-A1.
XX
PD 04-JAN-2001.
XX
PF 28-JUN-2000; 2000WO-US17842.
XX
PR 29-JUN-1999; 99US-0141422.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S;
XX
DR WPI; 2001-112389/12.
XX
PT Composition comprising human leukocyte antigen binding peptide which comprises isolated, prepared epitope useful for treating viral infections such as acquired immunodeficiency syndrome, and cancer -
XX
PS Claim 1; Page 51; 58pp; English.

XX The present invention describes a composition (I) which comprises at least one human leukocyte antigen (HLA) binding peptide comprising an isolated, prepared epitope comprising one of 547 8-11 residue amino acid sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic, virucide, hepatotropic, antiinflammatory, anti-HIV (human immunodeficiency virus) and protozoicide activities, which can be used in vaccine production and is an inducer of cytotoxic T-cell response.

XX (I) is useful for inducing a cytotoxic T cell response against a preselected antigen in a patient expressing a specific major histocompatibility complex (MHC) class I allele, by contacting cytotoxic T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to treat and/or prevent viral infection and cancer such as prostate cancer, hepatitis B, hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma acuminatum.

XX Sequence 9 AA;

Query Match 26.7%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
| | | |
Db 2 PKLK 5

RESULT 39
AAE31250
ID AAE31250 standard; peptide; 9 AA.
XX AC
XX AAE31250;
DT 24-FEB-2003 (first entry)
DE Human mages9 peptide #3.
KW Human; T-lymphocyte; vaccine; viral infection; gene therapy; cancer.
XX
OS Homo sapiens.
XX
PN WO200272627-A2.
XX
PD 19-SEP-2002.
XX
PF 11-MAR-2002; 2002WO-EP02666.
XX
PR 09-MAR-2001; 2001US-274250P.
PR 14-MAY-2001; 2001US-290353P.
PR 18-MAY-2001; 2001US-291610P.
XX
PA (CALL-) CALLISTOGEN AG.
XX
PI Wrede P, Walden P, Eichler-Mertens M, Filter M;
XX
DR WPI; 2002-759836/82.
XX
PT Providing, identifying or optimizing peptides for inducing cytotoxic T-lymphocytes and for treating cancer, comprises selecting conserved PT regions in antigenic proteins and identifying CD8+ T-cell epitopes in the protein -
PT
XX
PS Disclosure; Page 10; 32pp; English.
XX
XX The invention relates to a method for providing, identifying or/and optimising peptides which induce cytotoxic T-lymphocytes and to the uses of the obtained peptides for vaccination. The method is useful for providing, identifying and/or optimising peptides that are useful in manufacturing a pharmaceutical composition for the induction of cytotoxic T-lymphocytes, and for the prevention, treatment or diagnosis of cancer or viral infections. The invention is also used in gene

CC	therapy. The present sequence is human mage9 peptide used to illustrate	
CC	the method of the invention.	
XX		
SQ	Sequence 9 AA;	
	Query Match 26.7%; Score 4; DB 23; Length 9;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	6 KLKV 9	
Db	3 KLKV 6	
RESULT 40		
ABJ01633		
ID	ABJ01633 standard; Peptide; 9 AA.	
XX		
AC	ABJ01633;	
XX		
DT	19-SEP-2002 (first entry)	
XX		
DE	158PID7 related HLA peptide SEQ ID No 333.	
XX		
KW	Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;	
KW	cat; cow; horse; human; vaccine; Gene therapy; human leukocyte antigen;	
KW	HLA.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200216593-A2.	
XX		
PD	28-FEB-2002.	
XX		
PF	22-AUG-2001; 2001WO-US26276.	
XX		
PR	22-AUG-2000; 2000US-227098P.	
PR	10-APR-2001; 2001US-282739P.	
XX		
PA	(AGEN-) AGENSYS INC.	
XX		
PI	Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;	
PI	Challita-eid PM, Jakobovits A;	
XX		
DR	WPI; 2002-425659/45.	
XX		
PT	New compositions comprising a gene (designated 158PID7), its encoded	
PT	protein or their modulators, useful for treating or diagnosing cancers,	
PT	particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses	
PT	or humans)	
XX		
PS	Disclosure; Page 137; 181pp; English.	
XX		
CC	The invention relates to a novel nucleic acid, designated 158PID7. The	
CC	compositions are useful for treating or diagnosing cancers, particularly	
CC	bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,	
CC	horses or humans). The compositions are also useful for monitoring	
CC	genetic abnormalities and in preparing cancer vaccines. The nucleic acid	
CC	of the invention can be used in gene therapy to treat the said disorders.	
CC	This sequence represents a human leukocyte antigen (HLA) peptide relating	
CC	to the 158PID7 protein of the invention.	
XX		
SQ	Sequence 9 AA;	
	Query Match 26.7%; Score 4; DB 23; Length 9;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	5 PKLK 8	
Db	6 PKLK 9	
RESULT 41		
ABB79424		
ID	ABB79424 standard; peptide; 9 AA.	
XX		
AC	ABB79424;	
XX		
DT	08-JUL-2002 (first entry)	
XX		
DE	Human MMP-2 PEX peptide 8.	
XX		
KW	Human; matrix metalloproteinase-2; MMP-2; enzyme; thrombolytic;	
KW	anticoagulant; cardiant; antiarteriosclerotic; cytostatic; osteopathic;	
KW	antiinflammatory; antibacterial; virucide; fungicide; anipisoriatic;	
KW	vulnary; cerebroprotective; antiangular; ophthalmological;	
KW	antirheumatic; antiarthritic; antiulcer; vasotropic; nephrotropic;	
KW	alpha-v-beta-3 integrin receptor; thrombosis; tumour; osteoporosis;	
KW	infection; veterinary medicine; rheumatoid arthritis; Crohn's disease;	
KW	antimicrobial; antiseptic.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	WO200220566-A2.	
XX		
PD	14-MAR-2002.	
XX		
PF	28-AUG-2001; 2001WO-EP09899.	
XX		
PR	07-SEP-2000; 2000DE-1044325.	
XX		
PA	(MERE) MERCK PATENT GMBH.	
XX		
PI	Jonczyk A, Diefenbach B, Groth U, Zischinsky G;	
XX		
DR	WPI; 2002-329868/36.	
XX		
PT	New matrix metalloproteinase-2 derivative peptides, are alpha-v-beta-3	
PT	integrin receptor inhibitors useful e.g. for treating thrombosis,	
PT	cardiac infarction, tumors, osteoporosis, inflammation or infections	
XX		
PS	Examples; Page 24; 35pp; German.	
XX		
CC	The invention relates to peptides (ABB79414-ABB79426) derived from the	
CC	C-terminal fragment PEX of matrix metalloproteinase-2 (MMP-2). Matrix MMP-2	
CC	derivatives of formula X-Y-Z (I) and their salts and solvates are	
CC	described.	
CC	X = H, 1-10C alkanoyl or peptide fragment consisting of 1-20 naturally	
CC	occurring amino acid residues;	
CC	Y = peptide fragment selected from the sequence region 466-660 of human	
CC	Pro-MMP-2; and	
CC	Z = OH, NH ₂ , NH-1-10C alkyl N(1-10C alkyl) ₂ or peptide fragment	
CC	consisting of 1-20 naturally occurring amino acid residues.	
CC	Primary amino groups are optionally protected conventionally. The	
CC	peptides and MMP-2 derivatives are used for combating diseases involving	
CC	interaction of ligands (specifically MMP-2) with the alpha-v-beta-3	
CC	integrin receptor, especially pathological processes supported or	
CC	propagated by angiogenesis, thrombosis, cardiac infarction, coronary	
CC	heart disease, arteriosclerosis, tumours, osteoporosis, fibrosis,	
CC	inflammation, infections, psoriasis or wound healing deficiency. More	
CC	generally the peptides and MMP-2 derivatives are useful in human and	
CC	veterinary medicine for the treatment and/or prophylaxis of thrombosis,	
CC	myocardial infarction, apoplexy, angina pectoris, tumour diseases,	
CC	osteolytic diseases (e.g. osteoporosis or hypercalcaemia), pathological	
CC	angiogenic diseases (e.g. inflammation), ophthalmological diseases (e.g.	
CC	diabetic retinopathy, macular degeneration, myopia, ocular histioplasmosis	
CC	or rubotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative	
CC	colitis, Crohn's disease, atherosclerosis, psoriasis, restenosis after	
CC	angioplasty, viral, bacterial or fungal infections, acute renal failure	
CC	or wound healing deficiency; as antimicrobial/antiseptic agents in	
CC	operations involving biomaterials, implants, catheters or cardiac	
CC	pacemakers); or as diagnostic agents or reagents. The present sequence is	
CC	that of a human MMP-2 PEX peptide useful in examples of the invention.	
XX		

SQ Sequence 9 AA;

Query Match 26.7%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPKL 7
|||
Db 3 FPKL 6

RESULT 42

AAR91324
ID AAR91324 standard; peptide; 10 AA.

XX
AC AAR91324;

DT 10-OCT-1996 (first entry)

XX Dynorphin A analogue Dyn A (4-13).

DE Analogue; dynorphin A; endogenous opioid; proenkephalin B; truncation;
KW receptor; binding; nociceptive; analgesic; pain-killer; resistance; burn;
KW neuropathic; neurogenic; allodynia; post-operative pain; side effect;
KW drowsiness; addiction.

XX Synthetic.

OS WO9606626-A1.

PN 07-MAR-1996.

PD 26-AUG-1994; 94WO-US09563.

XX 26-AUG-1994; 94WO-US09563.

XX (GOLD/) GOLDSTEIN A.

PA (LEEN/) LEE N M.

XX Goldstein A, Lee NM;

XX WPI; 1996-160138/16.

DR N-terminally truncated dynorphin A analogues - useful for treating
PT pain, esp. for pain resistant to opioid analgesics

PS Claim 13; Page 17; 22pp; English.

XX The peptides AAR91320-45 represent analogues of dynorphin A, a member of
CC the dynorphin group of endogenous opioids derived from proenkephalin B.
CC The novel peptides contain N- and C-terminal truncations as compared to
CC the 17 amino acid natural dynorphin A. The peptides AAR91320-7 have a
CC truncation of the N-terminal Tyr-Gly-Gly amino acids and serial
CC deletions of the C-terminal amino acids. It has been shown that
CC dynorphin A analogues having the N-terminal Tyr residue deleted do not
CC bind to mu, delta or kappa opioid receptors. The peptides presented here
CC are analogues that do not bind to opioid receptors but retain an
CC anti-nociceptive (i.e. analgesic) activity. The peptides can be used to
CC treat pain which is resistant to opioid analgesics e.g. neuropathic or
CC neurogenic pain, allodynia, post-operative pain or burns. Since the
CC peptides do not interact with the opioid receptors, side effects
CC associated with opioid analgesics, e.g. drowsiness or addiction are
CC avoided.

SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
|||
Db 7 PKLK 10

RESULT 43

AAM43031

ID AAM43031 standard; Peptide; 10 AA.

XX AAM43031;

DT 22-OCT-2001 (first entry)

XX Mycoplasma genitalium intermolecular complementary peptide, SEQ ID 340.

DE Mycoplasma genitalium; complementary peptide; ligand;
KW protein-protein interaction; drug design; intermolecular;
KW intramolecular.

XX Mycoplasma genitalium.

OS WO200142278-A2.

PN 14-JUN-2001.

PD 13-DEC-2000; 2000WO-GB04778.

XX 13-DEC-1999; 99GB-0029466.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-514238/56.

DR Complementary peptide ligands as reagents and drugs for drug discovery

XX programs and as lead ligands to facilitate drug design and development,
XX are generated from microbial genome sequences -
XX Example 2; Page 96; 161pp; English.

XX The present sequence is one of a large number of complementary peptide

CC ligands generated from Mycoplasma genitalium genome sequences. These
CC specific complementary peptides interact with their relevant target
CC proteins encoded by the microbial genome. They are capable of
CC antagonising or agonising specific interaction of a protein with
CC another protein or receptor and are thus useful as reagents and drugs,
CC and as lead ligands to facilitate drug design and development. They
CC are useful as tools for functional genomic studies, reagents for the
CC configuration of high-throughput screens, as a starting point for
CC medicinal chemistry manipulation, for peptide mimetics and as
CC therapeutic agents. The analysis and acquisition of peptide sequences
CC facilitates understanding of protein-protein interactions. The method
CC allows for analysis of an entire database at a time, thus overcoming
CC sampling problems. The set of complementary peptides includes both
CC intermolecular (between proteins) and intermolecular (within a
CC protein) sequences.

SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPKL 7
|||
Db 5 FPKL 8

RESULT 44

AAG83581

ID AAG83581 standard; Peptide; 10 AA.

XX AAG83581;

AC AAG83581;

XX


```
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12
Db 1 VEVF 4

RESULT 47
AAG88260
ID AAG88260 standard; Peptide; 10 AA.
XX
AC AAG88260;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 3209.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX
PS Example 5; Page 472; 488pp; English.
XX
CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;
Query Match 26.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10
Db 5 LKVE 8

RESULT 48
AAG88261
ID AAG88261 standard; Peptide; 10 AA.
XX
AC AAG88261;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 3210.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
```

```
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX
PS Example 5; Page 472; 488pp; English.
XX
CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;
Query Match 26.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10
Db 5 LKVE 8

RESULT 49
AAG88262
ID AAG88262 standard; Peptide; 10 AA.
XX
AC AAG88262;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 3211.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB04773.
XX
PR 13-DEC-1999; 99GB-0029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and
```

PT nucleotide sequence databases, useful in drug design -
PS Example 5; Page 472; 488pp; English.
XX

CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX

SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10
| | | |
Db 4 LKVE 7

RESULT 50
AAG88263
ID AAG88263 standard; Peptide; 10 AA.

XX AC AAG88263;

XX DT 11-SEP-2001 (first entry)

XX DE Saccharomyces cerevisiae peptide, SEQ ID NO: 3212.

XX KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX drug discovery; drug design.

XX OS Saccharomyces cerevisiae.

XX PN WO200142276-A1.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB04773.

XX PR 13-DEC-1999; 99GB-0029471.

XX PA (PROT-) PROTEOM LTD.

XX PI Roberts GW, Heal JR;

XX DR WPI; 2001-367863/38.

XX PT Identifying complementary peptides by analysis of protein and
XX nucleotide sequence databases, useful in drug design -

PS Example 5; Page 473; 488pp; English.

XX CC The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX

SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10
| | | |
Db 6 LKVE 9

RESULT 51

AAB91622
ID AAB91622 standard; Peptide; 10 AA.

XX AC AAB91622;

XX DT 22-JUN-2001 (first entry)

XX DE Opioid peptide SEQ ID NO: 798.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimide; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 456; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimide and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.

SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
| | | |
Db 3 PKLK 6

RESULT 52
ABG69388
ID ABG69388 standard; peptide; 10 AA.
XX AC ABG69388;
XX DT 21-OCT-2002 (first entry)
XX Vascular response-associated protein isoform tryptic digest peptide #19.
XX DE
XX KW Vascular response; VR; vascular response-associated feature; VRP;
KW Vascular response-associated protein isoform; VRPI; blood; serum;
KW plasma; aneurysm; stenosis; atherosclerosis; congestion; oedema;
KW haemorrhage; shock; stroke; varicose vein; vasculitis; angilitis;
KW VRPI tryptic digest peptide; antiatherosclerotic; haemostatic;
KW cerebroprotective; antiinflammatory; vasotropic.
XX OS Unidentified.
XX PN WO200254080-A2.
XX PD 11-JUL-2002.
XX PF 24-DEC-2001; 2001WO-GB05774.
XX PR 29-DEC-2000; 2000US-260387P.
XX PR 24-OCT-2001; 2001US-0260387.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Herman EH, Holt GD, Sistare FD, Zhang J;
XX WPI; 2002-583636/62.
XX PT Screening, diagnosis or prognosis of vascular response including shock,
PT stroke, in subject, by detecting vascular response-associated features
PT or vascular response-associated protein isoforms in body fluid from
PT subject -
XX PS Disclosure; Page 35; 156pp; English.
XX CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of vascular response (VR) in a
CC subject. The method comprises analysing a test sample of body fluid
CC from the subject by two-dimensional electrophoresis to generate a 2D
CC array of vascular response-associated features (VRPs), whose relative
CC abundance correlates with presence, absence, stage or severity of VR
CC and comparing the abundance of each feature with the abundance of that
CC chosen feature in body fluid from persons free from VR. The invention
CC also describes vascular response-associated protein isoforms (VRPIs)
CC detectable in blood, serum or plasma. The methods and compositions of
CC the invention are useful for the screening, diagnosis or prognosis of
CC VR in a subject, for determining the stage or severity of VR in a
CC subject, for identifying a subject at risk of developing VR, or for
CC monitoring the effect of therapy administered to a subject having VR.
CC Antibodies capable of binding to VRPIs are useful for treating or
CC preventing VR. An agent that modulates the activity of VRPI is useful
CC in the manufacture of a medicament for the treatment or prevention of
CC VR in a subject. The vascular response includes aneurysm, stenosis,
CC atherosclerosis, congestion, oedema, haemorrhage, shock, stroke,
CC varicose veins, and vasculitis (angilitis). ABG69370-ABG69449 represent
CC VRPI tryptic digest peptides.
XX SQ Sequence 10 AA;
Query Match 26.7%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 VEVF 12
| | | |
Db 6 VEVF 9

RESULT 53
ABG69566
ID ABG69566 standard; Peptide; 10 AA.
XX AC ABG69566;
XX DT 21-OCT-2002 (first entry)
XX Human CRPI tryptic digest peptide #47.
XX DE
XX KW Human; cardiac response; CR; cardiac response-associated protein isoform;
KW CRPI; aneurysm; angina; arrhythmia; cardiomyopathy; cardiac arrest;
KW myocardial infarction; coronary; atherosclerosis; oedema; endocarditis;
KW haemorrhage; stenosis; shock; tryptic digest peptide.
XX OS Homo sapiens.
XX PN WO200254079-A2.
XX PD 11-JUL-2002.
XX PF 24-DEC-2001; 2001WO-GB05763.
XX PR 29-DEC-2000; 2000US-260389P.
XX PR 24-OCT-2001; 2001US-0260389.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Herman EH, Holt GD, Sistare FD, Zhang J;
XX WPI; 2002-583635/62.
XX PT Screening, diagnosis or prognosis of cardiac response in a subject, by
PT detecting cardiac response-associated features or cardiac
PT response-associated protein isoforms in body fluid or tissue from the
PT subject -
XX PS Disclosure; Page 30; 138pp; English.
XX CC The present invention relates to a new method for screening, diagnosis or
CC prognosis of cardiac response (CR) in a subject. The method of the
CC invention involves analysing a test sample of body fluid or tissue from
CC subject by 2D electrophoresis to generate a 2D array of features, whose
CC relative abundance correlates with the presence, absence, stage or
CC severity of CR and comparing abundance of each feature with the abundance
CC of that chosen feature in body fluid from persons free from CR. The
CC method is useful for screening, diagnosis or prognosis of CR in a
CC subject, for determining the stage or severity of CR in a subject, for
CC identifying a subject at risk of developing CR, or for monitoring the
CC effect of therapy administered to a subject with CR. The method is also
CC useful for screening agents that interact with one or more of the CRPIs
CC (cardiac response-associated protein isoforms). The invention is useful
CC for diagnosis or to determine the efficacy of a given treatment regimen.
CC The cardiac response includes aneurysm, angina, arrhythmia,
CC cardiomyopathy, cardiac arrest (myocardial infarction), coronary
CC atherosclerosis, oedema, endocarditis, haemorrhage, stenosis, and shock.
CC The present amino acid sequence represents one of a collection (ABG69520-
CC ABG69591) of human CRPI tryptic digest peptides, as described in the
CC specification.
XX SQ Sequence 10 AA;
Query Match 26.7%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 VEVF 12
| | | |
Db 6 VEVF 9

```

RESULT 54
ABJ01569
ID  ABJ01569 standard; Peptide; 10 AA.
XX
XX  AC  ABJ01569;
XX
DT  19-SEP-2002 (first entry)
XX
DE  158PID7 related HLA peptide SEQ ID No 269.
XX
KW  Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW  HLA.
XX
XX  Homo sapiens.
OS
XX  WO200216593-A2.
PN
XX
XX  28-FEB-2002.
PD
XX
XX  22-AUG-2001; 2001WO-US26276.
PF
XX
XX  22-AUG-2000; 2000US-227098P.
PR
XX  10-APR-2001; 2001US-282739P.
PR
XX  (AGEN-) AGENSYS INC.
XX
XX  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI  Challita-eid PM, Jakobovits A;
PI
XX
XX  WPI; 2002-425659/45.
DR
XX
XX  New compositions comprising a gene (designated 158PID7), its encoded
PT  protein or their modulators, useful for treating or diagnosing cancers,
PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT  or humans)
XX
XX  Disclosure; Page 135; 181pp; English.
PS
XX
XX  The invention relates to a novel nucleic acid, designated 158PID7. The
CC  compositions are useful for treating or diagnosing cancers, particularly
CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC  horses or humans). The compositions are also useful for monitoring
CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC  of the invention can be used in gene therapy to treat the said disorders.
CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
CC  to the 158PID7 protein of the invention.
XX
XX  Sequence 10 AA;
SQ
XX
Query Match 26.7%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 7 PKLK 10
|||||

RESULT 55
ABJ01656
ID  ABJ01656 standard; Peptide; 10 AA.
XX
XX  AC  ABJ01656;
XX
XX
XX  19-SEP-2002 (first entry)
DT
XX
DE  158PID7 related HLA peptide SEQ ID No 356.
XX
KW  Cytostatic; 158PID7; cancer; bladder cancer; mouse; rat; rabbit; dog;
KW  cat; cow; horse; human; vaccine; gene therapy; human leukocyte antigen;
KW  HLA.
XX
XX  Homo sapiens.
OS
XX  WO200216593-A2.
PN
XX
XX  28-FEB-2002.
PD
XX
XX  22-AUG-2001; 2001WO-US26276.
PF
XX
XX  22-AUG-2000; 2000US-227098P.
PR
XX  10-APR-2001; 2001US-282739P.
PR
XX  (AGEN-) AGENSYS INC.
XX
XX  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI  Challita-eid PM, Jakobovits A;
PI
XX
XX  WPI; 2002-425659/45.
DR
XX
XX  New compositions comprising a gene (designated 158PID7), its encoded
PT  protein or their modulators, useful for treating or diagnosing cancers,
PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT  or humans)
XX
XX  Disclosure; Page 135; 181pp; English.
PS
XX
XX  The invention relates to a novel nucleic acid, designated 158PID7. The
CC  compositions are useful for treating or diagnosing cancers, particularly
CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC  horses or humans). The compositions are also useful for monitoring
CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC  of the invention can be used in gene therapy to treat the said disorders.
CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
CC  to the 158PID7 protein of the invention.
XX
XX  Sequence 10 AA;
SQ
XX
Query Match 26.7%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 7 PKLK 10
|||||

```

```

XX  Homo sapiens.
OS
XX  WO200216593-A2.
PN
XX
XX  28-FEB-2002.
PD
XX
XX  22-AUG-2001; 2001WO-US26276.
PF
XX
XX  22-AUG-2000; 2000US-227098P.
PR
XX  10-APR-2001; 2001US-282739P.
PR
XX  (AGEN-) AGENSYS INC.
XX
XX  Faris M, Hubert RS, Raitano AB, Afar DEH, Levin E;
PI  Challita-eid PM, Jakobovits A;
PI
XX
XX  WPI; 2002-425659/45.
DR
XX
XX  New compositions comprising a gene (designated 158PID7), its encoded
PT  protein or their modulators, useful for treating or diagnosing cancers,
PT  particularly bladder cancer, in mammals (e.g. dogs, cats, cows, horses
PT  or humans)
XX
XX  Disclosure; Page 138; 181pp; English.
PS
XX
XX  The invention relates to a novel nucleic acid, designated 158PID7. The
CC  compositions are useful for treating or diagnosing cancers, particularly
CC  bladder cancer, in mammals (e.g. mice, rats, rabbits, dogs, cats, cows,
CC  horses or humans). The compositions are also useful for monitoring
CC  genetic abnormalities and in preparing cancer vaccines. The nucleic acid
CC  of the invention can be used in gene therapy to treat the said disorders.
CC  This sequence represents a human leukocyte antigen (HLA) peptide relating
CC  to the 158PID7 protein of the invention.
XX
XX  Sequence 10 AA;
SQ
XX
Query Match 26.7%; Score 4; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 7 PKLK 10
|||||

RESULT 56
ABR47212
ID  ABR47212 standard; Peptide; 10 AA.
XX
XX  AC  ABR47212;
XX
XX  10-JUN-2003 (first entry)
DT
XX
XX  Staphylococcus aureus CHIPS-related peptide #2401.
DE
XX
XX  CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW  formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW  inflammation; cardiovascular disease; central nervous system disease;
KW  gastrointestinal disease; skin disease; genitourinary disease;
KW  joint disease; respiratory disease; HIV infection; antiinflammatory;
KW  cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW  gynecological; immunosuppressive; anti-HIV.
XX
XX  Staphylococcus aureus.
OS
XX  Synthetic.
XX
XX  WO2003006048-A1.
PN
XX
XX  23-JAN-2003.
PD
XX
XX  11-JUL-2001; 2001WO-EP08004.
PF
XX
XX

```

```

PR 11-JUL-2001; 2001WO-EP08004.
XX (JARI-) JARI PHARM BV.
XX Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX WPI; 2003-247783/25.
DR
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases -
XX
XX Example 1; Page 55; 89pp; English.
PS
XX
XX The present invention relates to peptides (ABR44811-ABR47162 and
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC from Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
CC neutrophils, monocytes and endothelial cells or involving acute or
CC chronic inflammation reactions. The diseases or disorders include
CC cardiovascular diseases, disease of the central nervous system,
CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
CC diseases, respiratory diseases and HIV infection.
XX
SQ Sequence 10 AA;
Query Match 26.7%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PPKK 6
Db ||||
5 PPKK 8
RESULT 57
ABR47279
ID ABR47279 standard; Peptide; 10 AA.
XX
XX ABR47279;
XX
XX 10-JUN-2003 (first entry)
DT
DE Staphylococcus aureus CHIPS-related peptide #2458.
XX
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
XX Staphylococcus aureus.
OS
OS Synthetic.
XX
XX WO2003006048-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 11-JUL-2001; 2001WO-EP08004.
PF
XX
XX 11-JUL-2001; 2001WO-EP08004.
PR
XX
XX (JARI-) JARI PHARM BV.
PA
XX
XX Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
XX WPI; 2003-247783/25.
PS
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases -
XX
XX Example 1; Page 56; 89pp; English.
PS
XX
XX The present invention relates to peptides (ABR44811-ABR47162 and
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC from Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
CC neutrophils, monocytes and endothelial cells or involving acute or
CC chronic inflammation reactions. The diseases or disorders include
CC cardiovascular diseases, disease of the central nervous system,
CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
CC diseases, respiratory diseases and HIV infection.
XX
SQ Sequence 10 AA;
Query Match 26.7%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 EVFP 13
Db ||||
4 EVFP 7
RESULT 58
ABR47286
ID ABR47286 standard; Peptide; 10 AA.
XX
XX ABR47286;
XX
XX 10-JUN-2003 (first entry)
DT
DE Staphylococcus aureus CHIPS-related peptide #2475.
XX
XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
XX Staphylococcus aureus.
OS
OS Synthetic.
XX
XX WO2003006048-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 11-JUL-2001; 2001WO-EP08004.
PF
XX
XX 11-JUL-2001; 2001WO-EP08004.
PR
XX
XX (JARI-) JARI PHARM BV.
PA
XX
XX Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
XX WPI; 2003-247783/25.
PS
XX
XX Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases -
XX
XX Example 1; Page 56; 89pp; English.
PS
XX

```

CC The present invention relates to peptides (ABR44811-ABR47162 and
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC from Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
CC neutrophils, monocytes and endothelial cells or involving acute or
CC chronic inflammation reactions. The diseases or disorders include
CC cardiovascular diseases, disease of the central nervous system,
CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
CC diseases, respiratory diseases and HIV infection.
XX
XX
SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 FPPF 15
Db 4 FPPF 7

RESULT 59
ABR47290
ID ABR47290 standard; Peptide; 10 AA.
XX
AC ABR47290;
XX
DT 10-JUN-2003 (first entry)
DE Staphylococcus aureus CHIPS-related peptide #2479.
XX
KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
KW inflammation; cardiovascular disease; central nervous system disease;
KW gastrointestinal disease; skin disease; genitourinary disease;
KW joint disease; respiratory disease; HIV infection; antiinflammatory;
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
KW gynecological; immunosuppressive; anti-HIV.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
PN WO2003006048-A1.
XX
PD 23-JAN-2003.
XX
PF 11-JUL-2001; 2001WO-EP08004.
XX
PR 11-JUL-2001; 2001WO-EP08004.
XX
PA (JARI-) JARI PHARM BV.
XX
PI Van Kessel CPM, Gosselaar-de Haas CUC, Kruijtzer JAW;
PI Van Strijp JAG;
XX
DR WPI; 2003-247783/25.
XX
PT Combination of peptides derived from chemotaxis inhibiting protein from
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
PT prophylaxis and treatment of inflammation, cardiovascular, skin and
PT kidney diseases -
XX
XX Example 1; Page 56; 89pp; English.
XX
CC The present invention relates to peptides (ABR44811-ABR47162 and
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)
CC from Staphylococcus aureus. The peptide fragments are useful in the
CC prophylaxis or treatment of diseases or disorders involving the
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or
CC neutrophils, monocytes and endothelial cells or involving acute or
CC chronic inflammation reactions. The diseases or disorders include
CC cardiovascular diseases, disease of the central nervous system,

CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint
CC diseases, respiratory diseases and HIV infection.
XX
SQ Sequence 10 AA;

Query Match 26.7%; Score 4; DB 24; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KPFP 5
Db 4 KPFP 7

RESULT 60
AAR45216
ID AAR45216 standard; Protein; 11 AA.
XX
AC AAR45216;
XX
DT 25-MAR-2003 (updated)
DT 01-JAN-1980 (first entry)
XX
DE des-Tyr Dynorphin A (1-17) analogue #14.
XX
KW Analogue; dynorphin; dynorphin A (1-17); des-Tyr; cerebral; spinal;
KW ischemia; respiratory depression; gastroenteric spasm;
KW narcotic analgesic; anti-inflammation; immune system.
XX
OS Homo sapiens.
XX
PN WO9325217-A1.
XX
PD 23-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US05161.
XX
PR 12-JUN-1992; 92US-0897920.
XX
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (TAKE/) TAKEMORI A E.
XX
PI Lee NM, Loh HH, Takemori AE;
XX WPI; 1994-007185/01.
DR
PT Des-Tyr dynorphin analogues - potentiate activity of narcotic
PT analgesics and/or block withdrawal symptoms; are more stable in
PT vivo than native dynorphin
XX
PS Claim 2; Page 8; 24pp; English.
XX
CC The sequences given in AAR45202-21 are analogues of dynorphins based
CC on the sequence given in AAR45211. This sequence represents the first
CC of the dynorphins to be isolated and is designated "dynorphin A (1-
CC 17)". The claimed peptides of the invention have at least six amino
CC acids, but are des-Tyr with respect to dynorphin A (1-17). These
CC peptides may be used to reverse at least some neurological deficit
CC in treating cerebral and spinal ischemia, in inhibiting respiratory
CC depression or gastroenteric spasms produced by narcotic analgesics
CC to a naive host, as an adjunct for anti-inflammatory medication, and
CC in blocking narcotic-induced impairment in a host whose immune
CC system has been damaged by narcotic analgesics.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 11 AA;
SQ

Query Match 26.7%; Score 4; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8

```

Db      8 PKLK 11
|||||
RESULT 61
AAR91341
ID   AAR91341 standard; peptide; 11 AA.
XX   AC      AAR91341;
XX   DT      10-OCT-1996 (first entry)
XX   DE      Dynorphin A analogue Dyn A (3-13).
XX   KW      Analogue; dynorphin A; endogenous opioid; proenkephalin B; truncation;
XX   KW      receptor; binding; nociceptive; analgesic; pain-killer; resistance; burn;
XX   KW      neuropathic; neurogenic; allodynia; post-operative pain; side effect;
XX   KW      drowsiness; addiction.
XX   OS      Synthetic.
XX   PN      WO9606626-A1.
XX   PD      07-MAR-1996.
XX   PF      26-AUG-1994; 94WO-US09563.
XX   PR      26-AUG-1994; 94WO-US09563.
XX   PA      (GOLD/) GOLDSTEIN A.
XX   PA      (LEEN/) LEE N M.
XX   PI      Goldstein A, Lee NM;
XX   DR      WPI; 1996-160138/16.
XX   PT      N-terminally truncated dynorphin A analogues - useful for treating
XX   FT      pain, esp. for pain resistant to opioid analgesics
XX   PS      Disclosure; Page 8; 22pp; English.
XX   CC      The peptides AAR91320-45 represent analogues of dynorphin A, a member of
XX   CC      the dynorphin group of endogenous opioids derived from proenkephalin B.
XX   CC      The novel peptides contain N- and C-terminal truncations as compared to
XX   CC      the 17 amino acid natural dynorphin A. The peptides AAR91337-45 have a
XX   CC      truncation of the N-terminal Tyr-Gly amino acids and serial deletions of
XX   CC      the C-terminal amino acids. It has been shown that dynorphin A
XX   CC      analogues having the N-terminal Tyr residue deleted do not bind to mu,
XX   CC      delta or kappa opioid receptors. The peptides presented here are
XX   CC      analogues that do not bind to opioid receptors but retain an
XX   CC      anti-nociceptive (i.e. analgesic) activity. The peptides can be used to
XX   CC      treat pain which is resistant to opioid analgesics e.g. neuropathic or
XX   CC      neurogenic pain, allodynia, post-operative pain or burns. Since the
XX   CC      peptides do not interact with the opioid receptors, side effects
XX   CC      associated with opioid analgesics, e.g. drowsiness or addiction, are
XX   CC      avoided.
XX   SQ      Sequence 11 AA;
Query Match 26.7%; Score 4; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
|||||
Db      8 PKLK 11

RESULT 62
AAR91323
ID   AAR91323 standard; peptide; 11 AA.
XX   AC      AAR91323;
XX   DT      12-NOV-1998 (first entry)
XX   DE      Des-Tyr-Gly dynorphin analogue #17.
XX   KW      dynorphin A; narcotic; analgesic; withdrawal symptoms; opiate addict;
XX   KW      morphine; pain.
XX   OS      Synthetic.
XX   PN      WO9606626-A1.
XX   PD      07-MAR-1996.
XX   PF      26-AUG-1994; 94WO-US09563.
XX   PR      26-AUG-1994; 94WO-US09563.
XX   PA      (GOLD/) GOLDSTEIN A.
XX   PA      (LEEN/) LEE N M.
XX   PI      Goldstein A, Lee NM;
XX   DR      WPI; 1996-160138/16.
XX   PT      N-terminally truncated dynorphin A analogues - useful for treating
XX   FT      pain, esp. for pain resistant to opioid analgesics
XX   PS      Disclosure; Page 8; 22pp; English.
XX   CC      The peptides AAR91320-45 represent analogues of dynorphin A, a member of
XX   CC      the dynorphin group of endogenous opioids derived from proenkephalin B.
XX   CC      The novel peptides contain N- and C-terminal truncations as compared to
XX   CC      the 17 amino acid natural dynorphin A. The peptides AAR91337-45 have a
XX   CC      truncation of the N-terminal Tyr-Gly amino acids and serial deletions of
XX   CC      the C-terminal amino acids. It has been shown that dynorphin A
XX   CC      analogues having the N-terminal Tyr residue deleted do not bind to mu,
XX   CC      delta or kappa opioid receptors. The peptides presented here are
XX   CC      analogues that do not bind to opioid receptors but retain an
XX   CC      anti-nociceptive (i.e. analgesic) activity. The peptides can be used to
XX   CC      treat pain which is resistant to opioid analgesics e.g. neuropathic or
XX   CC      neurogenic pain, allodynia, post-operative pain or burns. Since the
XX   CC      peptides do not interact with the opioid receptors, side effects
XX   CC      associated with opioid analgesics, e.g. drowsiness or addiction, are
XX   CC      avoided.
XX   SQ      Sequence 11 AA;
Query Match 26.7%; Score 4; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
|||||
Db      7 PKLK 10

RESULT 63
AAW65968
ID   AAW65968 standard; peptide; 11 AA.
XX   AC      AAW65968;
XX   DT      12-NOV-1998 (first entry)
XX   DE      Des-Tyr-Gly dynorphin analogue #17.
XX   KW      dynorphin A; narcotic; analgesic; withdrawal symptoms; opiate addict;
XX   KW      morphine; pain.
XX   OS      Synthetic.

```


OS Homo sapiens.
PN US5607827-A.
XX
XX 15-SEP-1998.
XX
XX PF 14-MAY-1997; 97US-0856053.
XX
XX 27-SEP-1993; 93US-0127132.
PR 12-JUN-1992; 92US-0897920.
PR 20-DEC-1995; 95US-0581479.
PR 14-MAY-1997; 97US-0856053.
PA (DST-) DES-TYR DYNORPHIN PARTNERSHIP.
XX
PI Lee NM, Loh HH, Takemori AE;
XX
XX WPI; 1998-520169/44.
XX
XX Treatment of narcotic analgesic tolerance with dynorphin analogues -
PT useful for treating narcotics addicts and allowing the use of lower
PT doses of e.g. morphine to treat chronic pain
XX
XX Example 1; Column 4; 12pp; English.
XX
XX The invention relates to the treatment of narcotic analgesic tolerance.
CC It comprises administering a dynorphin analogue that is des-tyr or des-
CC Tyr-Glu at the N terminus and which has at least 7 amino acid residues.
CC The dynorphin analogue, which potentiates analgesic actions, is useful
CC when administered in a solution in conjunction with a narcotic analgesic
CC for: (a) blocking withdrawal symptoms in e.g. opiate addicts, and (b)
CC allowing lower doses of e.g. morphine to be used in treating chronic
CC pain. The present sequence represents a dynorphin analogue, which is
CC without the N-terminal tyrosine-glycine residues (des-Tyr-Gly) with
CC respect to endogenous dynorphin.
XX
XX Sequence 11 AA;
SQ
Query Match 26.7%; Score 4; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 PKLK 8
Db 8 PKLK 11
RESULT 64
AAB15261
ID AAB15261 standard; peptide; 11 AA.
XX
AC AAB15261;
XX
DT 19-DEC-2000 (first entry)
XX
DE Specific factor VIII binding peptide #24.
XX
KW Factor VIII binding peptide; factor VIII purification; haemophilia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 2..10
XX
PN WO200040602-A1.
XX
PD 13-JUL-2000.
XX
PF 03-JAN-2000; 2000WO-US00043.
XX
PR 04-JAN-1999; 99US-0224785.
XX
PA (DYAX-) DYAX CORP.
XX
PI Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;
XX
XX WPI; 2000-475816/41.
XX
XX New polypeptides which bind Factor VIII and/or Factor VIII-like
PT polypeptides, useful for the detection and purification of human Factor
PT VIII and/or Factor VIII-like polypeptides -
XX
XX Claim 2; Page 28; 57pp; English.
XX
XX The present sequence is the sequence of a peptide which can
CC be used to bind Factor VIII and Factor VIII-like proteins. The two
CC cysteine residues present cause it to form a disulphide bond, thus
CC creating a stable loop structure. The Factor VIII isolated by this
CC peptide can then be used in the treatment of Haemophilia A.
XX
XX Sequence 11 AA;
SQ

XX Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;
PI WPI; 2000-475816/41.
XX
XX New polypeptides which bind Factor VIII and/or Factor VIII-like
PT polypeptides, useful for the detection and purification of human Factor
PT VIII and/or Factor VIII-like polypeptides -
XX
XX Claim 2; Page 28; 57pp; English.
XX
XX The present sequence is the sequence of a peptide which can
CC be used to bind Factor VIII and Factor VIII-like proteins. The two
CC cysteine residues present cause it to form a disulphide bond, thus
CC creating a stable loop structure. The Factor VIII isolated by this
CC peptide can then be used in the treatment of Haemophilia A.
XX
XX Sequence 11 AA;
SQ
Query Match 26.7%; Score 4; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 VFPF 14
Db 4 VFPF 7
RESULT 65
AAB15262
ID AAB15262 standard; peptide; 11 AA.
XX
AC AAB15262;
XX
DT 19-DEC-2000 (first entry)
XX
DE Specific factor VIII binding peptide #25.
XX
KW Factor VIII binding peptide; factor VIII purification; haemophilia.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 2..10
XX
PN WO200040602-A1.
XX
PD 13-JUL-2000.
XX
PF 03-JAN-2000; 2000WO-US00043.
XX
PR 04-JAN-1999; 99US-0224785.
XX
PA (DYAX-) DYAX CORP.
XX
PI Yu J, Potter MD, Kelley BD, Deetz JS, Booth JE;
XX
XX WPI; 2000-475816/41.
XX
XX New polypeptides which bind Factor VIII and/or Factor VIII-like
PT polypeptides, useful for the detection and purification of human Factor
PT VIII and/or Factor VIII-like polypeptides -
XX
XX Claim 2; Page 28; 57pp; English.
XX
XX The present sequence is the sequence of a peptide which can
CC be used to bind Factor VIII and Factor VIII-like proteins. The two
CC cysteine residues present cause it to form a disulphide bond, thus
CC creating a stable loop structure. The Factor VIII isolated by this
CC peptide can then be used in the treatment of Haemophilia A.
XX
XX Sequence 11 AA;
SQ

DR WPI; 2000-475816/41.
XX
PT New polypeptides which bind Factor VIII and/or Factor VIII-like
PT polypeptides, useful for the detection and purification of human Factor
PT VIII and/or Factor VIII-like polypeptides -
XX
PS Claim 2; Page 28; 57pp; English.
XX
XX
CC The present sequence is the sequence of an example of a peptide which can
CC be used to bind Factor VIII and Factor VIII-like proteins. The two
CC cysteine residues present cause it to form a disulphide bond, thus
CC creating a stable loop structure. The Factor VIII isolated by this
CC peptide can then be used in the treatment of Haemophilia A.
XX
SQ Sequence 11 AA;

Query Match 26.7%; Score 4; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPF 14
Db 4 VFPF 7

RESULT 69
AAE02349
ID AAE02349 standard; Protein; 11 AA.
XX
AC AAE02349;
XX
DT 10-AUG-2001 (first entry)
XX
DE Caenorhabditis elegans Ras suppressor SUR-5 AMP binding motif #2.
XX
KW Ras suppressor; SUR-5; cytostatic; Ras signalling; gene therapy;
KW cell growth; differentiation; proliferation; transgenic animal;
KW cancer; nematode; AMP binding motif.
XX
OS Caenorhabditis elegans.
XX
FN US6225456-B1.
XX
PD 01-MAY-2001.
XX
PF 06-MAY-1999; 99US-0307265.
XX
PR 07-MAY-1998; 98US-0084590.
XX
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Gu T, Orita S, Han M;
XX
PS WPI; 2001-342417/36.
XX
XX Novel Ras suppressor SUR-5 polynucleotides from human, murine,
PT Caenorhabditis elegans, for treating Ras-mediated effects, especially
PT cancer and producing SUR-5 polypeptides for screening drugs altering
PT Ras signaling -
XX
XX Example 12; Column 71; 50pp; English.
XX
XX The invention relates to Ras suppressor sur-5 polynucleotides and
CC polypeptides (SUR-5) from human, murine and Caenorhabditis elegans
CC (nematode). SUR-5 polynucleotides are useful for producing poly-
CC peptides by recombinant techniques, which are useful as targets for
CC screening drugs that alter Ras signalling and the physiological
CC effects of Ras such as effects on cell growth, differentiation and
CC proliferation. SUR-5 genes are useful in gene therapy for treating
CC diseases or altering physiological states characterised by unwanted
CC proliferation of cells or other Ras-mediated effects, especially
CC cancer. The invention also provides methods of producing transgenic
CC animals expressing SUR-5.

CC The present sequence is C. elegans Ras suppressor SUR-5 AMP
CC binding motif.
XX
SQ Sequence 11 AA;

Query Match 26.7%; Score 4; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVEV 11
Db 8 KVEV 11

RESULT 70
AAB91600
ID AAB91600 standard; Peptide; 11 AA.
XX
AC AAB91600;
XX
DT 22-JUN-2001 (first entry)
XX
DE Opioid peptide SEQ ID NO:776.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
PS WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
XX Disclosure; Page 449; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.
SQ Sequence 11 AA;

Query Match 26.7%; Score 4; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
 ||||
 DB 8 PKLK 11

RESULT 71
 AAB91619
 ID AAB91619 standard; Peptide; 11 AA.

XX AC AAB91619;

XX DT 22-JUN-2001 (first entry)

DE DE Opioid peptide SEQ ID NO:795.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WP1; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 455; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the CC exemplification of the present invention.

SQ Sequence 11 AA;

Query Match 26.7%; Score 4; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8

DB 8 PKLK 11
 ||||

RESULT 72
 AAB91621
 ID AAB91621 standard; Peptide; 11 AA.

XX AC AAB91621;

XX DT 22-JUN-2001 (first entry)

DE DE Opioid peptide SEQ ID NO:797.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WP1; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 456; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. CC AAB90829 to AAB92441 represent peptides which can be used in the CC exemplification of the present invention.

SQ Sequence 11 AA;

Query Match 26.7%; Score 4; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8

DB 4 PKLK 7

RESULT 73

AAP10402
 ID AAP10402 standard; peptide; 12 AA.
 XX
 AC AAP10402;
 XX
 DT 16-DEC-1992 (first entry)
 XX
 DE Analgesic peptide.
 XX
 KW Dynorphin; enkephalin; endorphin; opioid receptor; neurotransmitter;
 KW radioimmunoassay; mood altering; muscle relaxing; regulatory.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 2
 FT /label= D-form
 FT Modified-site 12
 FT /label= amidated
 XX
 PN EP29300-A.
 XX
 PN 27-MAY-1981.
 XX
 PD 20-OCT-1980; 80EP-0303698.
 XX
 PF 05-NOV-1979; 79US-0091615.
 XX
 PR (ADDI) ADDI-COLOR AG.
 XX
 PA Goldstein A;
 XX
 PI WPI; 1981-40572D/23 (40572D).
 XX
 DR Oligopeptide contg. alternating basic hydrophilic and hydrophobic
 PT unit - useful e.g. as analgesics and for raising antisera
 XX
 PS Claim 5; Page 20; 4lpp; English.
 XX
 CC The synthetic peptide is an example of an extremely generic
 CC oligopeptide having a chain of at least 5 amino acids with
 CC alternating basic hydrophilic and hydrophobic amino acids. The
 CC peptide is a dynorphin analogue, having greater potency than leu-
 CC enkephalin and beta-endorphin. The peptide is an intermediate for
 CC an analgesic, an analgesic itself, and an opioid antagonist which is
 CC useful for studying the structure of opioid binding sites. By
 CC interaction with opioid receptor sites, they provide analgesic, mood
 CC altering, muscle relaxing and blood-flow regulating effects.
 CC See also AAP10403-5.
 XX
 SQ Sequence 12 AA;
 Query Match 26.7%; Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 PKLK 8
 Db |||||
 9 PKLK 12
 RESULT 74
 AAR45205
 ID AAR45205 standard; Protein; 12 AA.
 XX
 AC AAR45205;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-JAN-1980 (first entry)
 XX
 DE des-Tyr Dynorphin A (1-17) analogue #4.
 XX
 KW Analogue; dynorphin; dynorphin A (1-17); des-Tyr; cerebral; spinal;
 XX

KW ischemia; respiratory depression; gastroenteric spasm;
 KW narcotic analgesic; anti-inflammation; immune system.
 XX
 OS Homo sapiens.
 XX
 PN WO9325217-A1.
 XX
 PD 23-DEC-1993.
 XX
 PF 01-JUN-1993; 93WO-US05161.
 XX
 PR 12-JUN-1992; 92US-0897920.
 XX
 PA (LEEN/) LEE N M.
 PA (LOHH/) LOH H H.
 PA (TAKE/) TAKEMORI A E.
 XX
 PI Lee NM, Loh HH, Takemori AE;
 XX
 DR WPI; 1994-007185/01.
 XX
 PT Des-Tyr dynorphin analogues - potentiate activity of narcotic
 PT analgesics and/or block withdrawal symptoms; are more stable in
 PT vivo than native dynorphin
 XX
 PS Claim 1; Page 7; 24pp; English.
 XX
 CC The sequences given in AAR45202-21 are analogues of dynorphins based
 CC on the sequence given in AAR45211. This sequence represents the first
 CC of the dynorphins to be isolated and is designated "dynorphin A (1-
 CC 17)". The claimed peptides of the invention have at least six amino
 CC acids, but are des-Tyr with respect to dynorphin A (1-17). These
 CC peptides may be used to reverse at least some neurological deficit
 CC in treating cerebral and spinal ischemia, in inhibiting respiratory
 CC depression or gastroenteric spasms produced by narcotic analgesics
 CC to a naive host, as an adjunct for anti-inflammatory medication, and
 CC in blocking narcotic-induced impairment in a host whose immune
 CC system has been damaged by narcotic analgesics.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 12 AA;
 Query Match 26.7%; Score 4; DB 15; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 PKLK 8
 Db |||||
 9 PKLK 12
 RESULT 75
 AAR45215
 ID AAR45215 standard; Protein; 12 AA.
 XX
 AC AAR45215;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-JAN-1980 (first entry)
 XX
 DE des-Tyr Dynorphin A (1-17) analogue #13.
 XX
 KW Analogue; dynorphin; dynorphin A (1-17); des-Tyr; cerebral; spinal;
 KW ischemia; respiratory depression; gastroenteric spasm;
 KW narcotic analgesic; anti-inflammation; immune system.
 XX
 OS Homo sapiens.
 XX
 PN WO9325217-A1.
 XX
 PD 23-DEC-1993.
 XX
 PF 01-JUN-1993; 93WO-US05161.
 XX

XX 12-JUN-1992; 92US-0897920.
PR (LEEN/) LEE N M.
XX (LOHH/) LOH H H.
PA (TAKE/) TAKEMORI A E.
XX
PI Lee NM, Loh HH, Takemori AE;
XX WPI; 1994-007185/01.
XX
XX Des-Tyr dynorphin analogues - potentiate activity of narcotic
PT analgesics and/or block withdrawal symptoms; are more stable in
PT vivo than native dynorphin
XX
XX Claim 2; Page 8; 24pp; English.
XX
XX The sequences given in AAR45202-21 are analogues of dynorphins based
CC on the sequence given in AAR45211. This sequence represents the first
CC of the dynorphins to be isolated and is designated "dynorphin A (1-
CC 17)". The claimed peptides of the invention have at least six amino
CC acids, but are des-tyr with respect to dynorphin A (1-17). These
CC peptides may be used to reverse at least some neurological deficit
CC in treating cerebral and spinal ischemia, in inhibiting respiratory
CC depression or gastroenteric spasms produced by narcotic analgesics
CC to a naive host, as an adjunct for anti-inflammatory medication, and
CC in blocking narcotic-induced impairment in a host whose immune
CC system has been damaged by narcotic analgesics.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 12 AA;
SQ
Query Match 26.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PKLK 8
Db 8 PKLK 11
Search completed: November 25, 2003, 18:15:49
Job time : 49.5904 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 29.8404 Seconds
(without alignments)
92.715 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKPPFKLKVVEVFPFP 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCR_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	US-10-281-652-8	Sequence 8, Appli
2	5	33.3	9	US-10-292-418-15	Sequence 15, Appli
3	5	33.3	9	US-10-277-292-451	Sequence 41, App
4	5	33.3	9	US-10-277-292-452	Sequence 452, App
5	5	33.3	9	US-10-277-292-551	Sequence 551, App
6	5	33.3	9	US-10-277-292-555	Sequence 555, App
7	5	33.3	9	US-10-280-340-451	Sequence 451, App
8	5	33.3	9	US-10-280-340-452	Sequence 452, App
9	5	33.3	9	US-10-280-340-551	Sequence 551, App
10	5	33.3	9	US-10-280-340-555	Sequence 555, App
11	5	33.3	10	US-10-277-292-66	Sequence 66, Appl
12	5	33.3	10	US-10-277-292-607	Sequence 607, App
13	5	33.3	10	US-10-277-292-629	Sequence 629, App
14	5	33.3	10	US-10-280-340-66	Sequence 66, Appl
15	5	33.3	10	US-10-280-340-607	Sequence 607, App

16	5	33.3	10	US-10-280-340-629	Sequence 629, App
17	5	33.3	16	US-10-225-567A-1110	Sequence 1110, Ap
18	5	33.3	19	US-10-225-567A-2044	Sequence 2044, Ap
19	4	26.7	4	US-09-750-736-4	Sequence 4, Appli
20	4	26.7	5	US-09-992-124A-7	Sequence 7, Appli
21	4	26.7	7	US-09-909-062-13	Sequence 13, Appli
22	4	26.7	7	US-10-293-371-15	Sequence 15, Appl
23	4	26.7	7	US-10-293-371-30	Sequence 30, Appl
24	4	26.7	7	US-10-293-371-32	Sequence 32, Appl
25	4	26.7	7	US-10-293-371-40	Sequence 40, Appl
26	4	26.7	7	US-10-293-371-41	Sequence 41, Appl
27	4	26.7	7	US-10-293-371-42	Sequence 42, Appl
28	4	26.7	9	US-09-393-634-91	Sequence 91, Appl
29	4	26.7	9	US-09-824-787B-124	Sequence 124, App
30	4	26.7	9	US-10-383-982-91	Sequence 91, Appl
31	4	26.7	9	US-10-277-292-333	Sequence 333, App
32	4	26.7	9	US-10-280-340-333	Sequence 333, App
33	4	26.7	10	US-09-572-270A-221	Sequence 221, App
34	4	26.7	10	US-09-572-270A-920	Sequence 920, App
35	4	26.7	10	US-09-573-822C-340	Sequence 340, App
36	4	26.7	10	US-10-277-292-269	Sequence 269, App
37	4	26.7	10	US-10-277-292-356	Sequence 356, App
38	4	26.7	10	US-10-280-340-269	Sequence 269, App
39	4	26.7	10	US-10-280-340-356	Sequence 356, App
40	4	26.7	10	US-10-033-741-52	Sequence 52, Appl
41	4	26.7	10	US-10-033-662-47	Sequence 47, Appl
42	4	26.7	11	US-09-756-594-27	Sequence 27, Appl
43	4	26.7	11	US-09-756-594-28	Sequence 28, Appl
44	4	26.7	11	US-09-756-594-29	Sequence 29, Appl
45	4	26.7	11	US-09-756-594-30	Sequence 30, Appl
46	4	26.7	11	US-09-756-594-32	Sequence 32, Appl
47	4	26.7	11	US-10-272-497-27	Sequence 27, Appl
48	4	26.7	11	US-10-272-497-28	Sequence 28, Appl
49	4	26.7	11	US-10-272-497-29	Sequence 29, Appl
50	4	26.7	11	US-10-272-497-30	Sequence 30, Appl
51	4	26.7	11	US-10-272-497-32	Sequence 32, Appl
52	4	26.7	11	US-10-272-497-72	Sequence 72, Appl
53	4	26.7	11	US-10-272-497-74	Sequence 74, Appl
54	4	26.7	11	US-10-272-497-76	Sequence 76, Appl
55	4	26.7	11	US-10-272-497-79	Sequence 79, Appl
56	4	26.7	12	US-08-927-939-38	Sequence 38, Appl
57	4	26.7	12	US-09-798-119-3	Sequence 3, Appli
58	4	26.7	12	US-09-798-121-3	Sequence 3, Appli
59	4	26.7	12	US-09-813-329-37	Sequence 37, Appl
60	4	26.7	12	US-09-813-329-47	Sequence 47, Appl
61	4	26.7	12	US-09-813-329-58	Sequence 58, Appl
62	4	26.7	13	US-09-798-119-2	Sequence 2, Appli
63	4	26.7	13	US-09-798-121-2	Sequence 2, Appli
64	4	26.7	13	US-09-366-955A-31	Sequence 31, Appl
65	4	26.7	13	US-09-966-955A-32	Sequence 32, Appl
66	4	26.7	13	US-10-300-215-10	Sequence 10, Appl
67	4	26.7	13	US-10-300-215-32	Sequence 32, Appl
68	4	26.7	14	US-09-876-904A-194	Sequence 194, App
69	4	26.7	14	US-10-312-691-6	Sequence 6, Appli
70	4	26.7	14	US-10-145-206-29	Sequence 29, Appl
71	4	26.7	16	US-09-880-748-2262	Sequence 2262, Ap
72	4	26.7	16	US-10-234-816-98	Sequence 98, Appl
73	4	26.7	16	US-10-161-791-181	Sequence 181, App
74	4	26.7	16	US-10-225-567A-1075	Sequence 1075, Ap
75	4	26.7	17	US-09-170-919-7	Sequence 7, Appli
76	4	26.7	17	US-09-798-119-1	Sequence 1, Appli
77	4	26.7	17	US-09-798-121-1	Sequence 1, Appli
78	4	26.7	17	US-10-146-999-11	Sequence 11, Appl
79	4	26.7	17	US-10-197-954-46	Sequence 46, Appl
80	4	26.7	18	US-09-864-761-40786	Sequence 40786, A
81	4	26.7	18	US-10-082-014-92	Sequence 92, Appl
82	4	26.7	18	US-10-372-076-93	Sequence 93, Appl
83	4	26.7	18	US-10-281-652-22	Sequence 22, Appl
84	4	26.7	18	US-10-225-567A-1930	Sequence 1930, Ap
85	4	26.7	18	US-10-225-567A-1985	Sequence 1985, Ap
86	4	26.7	19	US-09-864-761-45349	Sequence 45349, A
87	4	26.7	20	US-09-841-132-156	Sequence 156, App
88	4	26.7	20	US-09-757-417-35	Sequence 35, Appl

89 4 26.7 20 11 US-09-983-802-664 Sequence 664, Appl
90 4 26.7 20 12 US-10-181-993A-4 Sequence 4, Appl
91 4 26.7 20 12 US-10-280-066-45 Sequence 45, Appl
92 4 26.7 20 12 US-09-171-432A-57 Sequence 57, Appl
93 4 26.7 20 12 US-10-145-206-4 Sequence 4, Appl
94 4 26.7 20 15 US-10-042-945-35 Sequence 35, Appl
95 3 20.0 4 11 US-09-300-425B-31 Sequence 31, Appl
96 3 20.0 4 12 US-10-237-160-1 Sequence 1, Appl
97 3 20.0 4 12 US-10-293-371-72 Sequence 72, Appl
98 3 20.0 4 12 US-10-087-942-5 Sequence 5, Appl
99 3 20.0 4 12 US-10-313-338A-1 Sequence 1, Appl
100 3 20.0 4 12 US-10-313-790A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-8
; Sequence 8, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-8

Query Match 100.0%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPPPKLKVEVFPPF 15
 |||||
Db 1 LKPPPKLKVEVFPPF 15

RESULT 2
US-10-292-418-15
; Sequence 15, Application US/10292418
; Publication No. US20030139365A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Li, Yue
; APPLICANT: Gillies, Stephen D
; TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
; TITLE OF INVENTION: Immunofusins
; FILE REFERENCE: LEX-006C1
; CURRENT APPLICATION NUMBER: US/10/292,418
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/383,315
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 60/097,883
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Forward primer
; OTHER INFORMATION: for human Fc-Angio
US-10-292-418-15

Query Match 33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLKV 9
 |||||
Db 1 PKLKV 5

RESULT 3
US-10-277-292-451
; Sequence 451, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-451

Query Match 33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLKV 9
 |||||
Db 4 PKLKV 8

RESULT 4
US-10-277-292-452
; Sequence 452, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA


```
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/277,292
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 452
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-452

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      2 PKLKV 6

RESULT 5
US-10-277-292-551
/ Sequence 551, Application US/10277292
/ Publication No. US20030199470A1
/ GENERAL INFORMATION:
/ APPLICANT: FARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: AFAR, DANIEL
/ APPLICANT: LEVIN, ELANA
/ APPLICANT: CHALLITA-EID, PIA
/ APPLICANT: JAKOBOVITZ, AYA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/277,292
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 551
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-551

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      2 PKLKV 6

RESULT 6
US-10-277-292-555
/ Sequence 555, Application US/10277292
/ Publication No. US20030199470A1
/ GENERAL INFORMATION:
/ APPLICANT: FARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: AFAR, DANIEL
/ APPLICANT: LEVIN, ELANA
/ APPLICANT: CHALLITA-EID, PIA
/ APPLICANT: JAKOBOVITZ, AYA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/277,292
/ CURRENT FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 555
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-555

Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      4 PKLKV 8

RESULT 7
US-10-280-340-451
/ Sequence 451, Application US/10280340
/ Publication No. US20030207835A1
/ GENERAL INFORMATION:
/ APPLICANT: FARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: AFAR, DANIEL
/ APPLICANT: LEVIN, ELANA
/ APPLICANT: CHALLITA-EID, PIA
/ APPLICANT: JAKOBOVITZ, AYA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/280,340
/ CURRENT FILING DATE: 2002-10-25
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 451
/ LENGTH: 9
/ TYPE: PRT
```

```
Query Match          33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLKV 9
Db      4 PKLKV 8

RESULT 7
US-10-280-340-451
/ Sequence 451, Application US/10280340
/ Publication No. US20030207835A1
/ GENERAL INFORMATION:
/ APPLICANT: FARIS, MARY
/ APPLICANT: HUBERT, RENE
/ APPLICANT: RAITANO, ARTHUR
/ APPLICANT: AFAR, DANIEL
/ APPLICANT: LEVIN, ELANA
/ APPLICANT: CHALLITA-EID, PIA
/ APPLICANT: JAKOBOVITZ, AYA
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
/ FILE REFERENCE: 51158-20050.00
/ CURRENT APPLICATION NUMBER: US/10/280,340
/ CURRENT FILING DATE: 2002-10-25
/ PRIOR APPLICATION NUMBER: US/09/935,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/227,098
/ PRIOR FILING DATE: 2000-08-22
/ PRIOR APPLICATION NUMBER: 60/282,739
/ PRIOR FILING DATE: 2001-04-10
/ NUMBER OF SEQ ID NOS: 700
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 451
/ LENGTH: 9
/ TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-451

Query Match      33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLKV 9
Db      4 PKLKV 8

RESULT 8
US-10-280-340-452
; Sequence 452, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 452
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-452

Query Match      33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLKV 9
Db      2 PKLKV 6

RESULT 9
US-10-280-340-551
; Sequence 551, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 452
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-452

Query Match      33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLKV 9
Db      2 PKLKV 6

RESULT 9
US-10-280-340-551
; Sequence 551, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
```

```
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 551
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-551

Query Match      33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLKV 9
Db      2 PKLKV 6

RESULT 10
US-10-280-340-555
; Sequence 555, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 555
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-555

Query Match      33.3%; Score 5; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLKV 9
Db      4 PKLKV 8

RESULT 11
US-10-277-292-66
; Sequence 66, Application US/10277292
```

; Publication No. US20030199470A1

; GENERAL INFORMATION:

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

; TITLE OF INVENTION: OTHER CANCERS

; FILE REFERENCE: 51158-20050.00

; CURRENT APPLICATION NUMBER: US/10/277,292

; CURRENT FILING DATE: 2002-10-21

; PRIOR APPLICATION NUMBER: US/09/935,430

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/227,098

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: 60/282,739

; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 700

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 66

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-277-292-66

Query Match 33.3%; Score 5; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 59;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9

Db |||||

4 PKLKV 8

RESULT 12

US-10-277-292-607

; Sequence 607, Application US/10277292

; Publication No. US20030199470A1

; GENERAL INFORMATION:

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

; TITLE OF INVENTION: OTHER CANCERS

; FILE REFERENCE: 51158-20050.00

; CURRENT APPLICATION NUMBER: US/10/277,292

; CURRENT FILING DATE: 2002-10-21

; PRIOR APPLICATION NUMBER: US/09/935,430

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/227,098

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: 60/282,739

; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 700

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 607

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-277-292-607

Query Match

Best Local Similarity 33.3%; Score 5; DB 12; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9

Db |||||

4 PKLKV 8

RESULT 13

US-10-277-292-629

; Sequence 629, Application US/10277292

; Publication No. US20030199470A1

; GENERAL INFORMATION:

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

; TITLE OF INVENTION: OTHER CANCERS

; FILE REFERENCE: 51158-20050.00

; CURRENT APPLICATION NUMBER: US/10/277,292

; CURRENT FILING DATE: 2002-10-21

; PRIOR APPLICATION NUMBER: US/09/935,430

; PRIOR FILING DATE: 2001-08-22

; PRIOR APPLICATION NUMBER: 60/227,098

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: 60/282,739

; PRIOR FILING DATE: 2001-04-10

; NUMBER OF SEQ ID NOS: 700

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 629

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif

US-10-277-292-629

Query Match

Best Local Similarity 33.3%; Score 5; DB 12; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9

Db |||||

2 PKLKV 6

RESULT 14

US-10-280-340-66

; Sequence 66, Application US/10280340

; Publication No. US20030207835A1

; GENERAL INFORMATION:

; APPLICANT: FARIS, MARY

; APPLICANT: HUBERT, RENE

; APPLICANT: RAITANO, ARTHUR

; APPLICANT: AFAR, DANIEL

; APPLICANT: LEVIN, ELANA

; APPLICANT: CHALLITA-EID, PIA

; APPLICANT: JAKOBOVITZ, AYA

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND

; TITLE OF INVENTION: OTHER CANCERS

; FILE REFERENCE: 51158-20050.00

; CURRENT APPLICATION NUMBER: US/10/280,340

; CURRENT FILING DATE: 2002-10-25

; PRIOR APPLICATION NUMBER: US/09/935,430

; PRIOR FILING DATE: 2001-08-22

```
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-66

Query Match      33.3%; Score 5; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLV 9
Db      4 PKLV 8

RESULT 15
US-10-280-340-607
; Sequence 607, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-607

Query Match      33.3%; Score 5; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLV 9
Db      4 PKLV 8

RESULT 16
US-10-280-340-629
; Sequence 629, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
```

```
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 629
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-629

Query Match      33.3%; Score 5; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLV 9
Db      2 PKLV 6

RESULT 17
US-10-225-567A-1110
; Sequence 1110, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1110
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1110

Query Match      33.3%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 KPFPK 6
Db      9 KPFPK 13

RESULT 18
US-10-225-567A-2044
; Sequence 2044, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
```

```

; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2044
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-2044

Query Match      33.3%; Score 5; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LKVEV 11
    |||||
Db 4 LKVEV 8

RESULT 19
US-09-750-726-4
; Sequence 4, Application US/09750726
; Patent No. US20010010817A1
; GENERAL INFORMATION:
; APPLICANT: Platt, David
; TITLE OF INVENTION: TUMOR DERIVED CARBOHYDRATE BINDING
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gifford, Krass, et al
; STREET: 280 No. US20010010817A1th Woodward Ave., Suite 400
; CITY: Birmingham
; STATE: Michigan
; COUNTRY: US
; ZIP: 48009
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/750,726
; FILING DATE: 28-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Citkowski, Ronald W.
; REGISTRATION NUMBER: 31,005
; REFERENCE/POCKET NUMBER: DPL-00102/16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-647-6000
; TELEFAX: 810-647-5210
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-750-726-4

Query Match      26.7%; Score 4; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPP 14
    |||||
Db 1 VFPP 4

RESULT 20
US-09-992-124A-7
; Sequence 7, Application US/09992124A
; Publication No. US20030162289A1
; GENERAL INFORMATION:
; APPLICANT: Heidaran, Mohammad A.
; APPLICANT: Haaland, Perry D.
; APPLICANT: Wilkins, Jamie H.
; APPLICANT: Spargo, Catherine A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: Peptides Promoting Cell Adherence, Growth and Secretion
; FILE REFERENCE: 102-410
; CURRENT APPLICATION NUMBER: US/09/992,124A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide selected for biological activity
US-09-992-124A-7

Query Match      26.7%; Score 4; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPP 14
    |||||
Db 1 VFPP 4

RESULT 21
US-09-909-062-13
; Sequence 13, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Sakseena, Anil K
; APPLICANT: Girijavaliabhan, Viyyor M
; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephane L
; APPLICANT: Liu, Yi-Tsung
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Gadguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT APPLICATION NUMBER: US/09/909,062
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
```

```
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6).-(6)
; OTHER INFORMATION: norvaline-C(-O)
US-09-909-062-13

Query Match          26.7%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVFP 13
    ||||
Db 2 EVFP 5

RESULT 22
US-10-293-371-15
; Sequence 15, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; TITLE OF INVENTION: Interaction Screens
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-15

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPFP 5
    ||||
Db 2 KPFP 5

RESULT 23
US-10-293-371-30
; Sequence 30, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; TITLE OF INVENTION: Interaction Screens
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPFP 5
    ||||
Db 2 KPFP 5

RESULT 24
US-10-293-371-32
; Sequence 32, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; TITLE OF INVENTION: Interaction Screens
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-32

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPFP 15
    ||||
Db 2 FPFP 5

RESULT 25
US-10-293-371-40
; Sequence 40, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; TITLE OF INVENTION: Interaction Screens
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPFP 15
    ||||
Db 2 FPFP 5
```

```
; SEQ ID NO 40
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-40

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPFP 15
DB 2 FPFP 5

RESULT 26
US-10-293-371-41
; Sequence 41, Application US/10293371
; Publication NO. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-41

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPFP 15
DB 2 FPFP 5

RESULT 27
US-10-293-371-42
; Sequence 42, Application US/10293371
; Publication NO. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAU, ALAIN
; APPLICANT: KORNELUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-42

Query Match          26.7%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FPFP 15
DB 2 FPFP 5

RESULT 28
US-09-393-634-91
; Sequence 91, Application US/09393634
; Patent No. US20020051997A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a NO. US20020051997A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Sf01 signature
; OTHER INFORMATION: sequence 4, amino acids encoded by PCR primers
; OTHER INFORMATION: identifying polymorphic variants, interspecies
; OTHER INFORMATION: homologs and alleles of Sf family members
US-09-393-634-91

Query Match          26.7%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
DB 6 PKLK 9

RESULT 29
US-09-824-787B-124
; Sequence 124, Application US/09824787B
; Patent No. US2002015547A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
```

```
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-787B-124

Query Match      26.7%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PPKL 7
Db 1 PPKL 4

RESULT 30
US-10-383-982-91
; Sequence 91, Application US/10383982
; Publication No. US20030157568A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. US20030157568A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/10/383.982
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US/09/393.634
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sf01 signature
; OTHER INFORMATION: sequence 4, amino acids encoded by PCR primers
; OTHER INFORMATION: identifying polymorphic variants, interspecies
; OTHER INFORMATION: homologs and alleles of Sf family members
US-10-383-982-91

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPKL 8
Db 6 PPKL 9

RESULT 31
US-10-277-292-333
; Sequence 333, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
```

```
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-333

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPKL 8
Db 6 PPKL 9

RESULT 32
US-10-280-340-333
; Sequence 333, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-333

Query Match      26.7%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PPKL 8
Db 6 PPKL 9

RESULT 33
```



```
US-09-572-270A-221
; Sequence 221, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 221
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in CYP88A3 OR YUP8H12.23. at 402-411 and
US-09-572-270A-221

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 EVVF 13
Db      4 EVVF 7

RESULT 34
US-09-572-270A-920
; Sequence 920, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 920
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in AH1. at 339-348 and may interact with
US-09-572-270A-920

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VEVF 12
Db      7 VEVF 10

RESULT 35
US-09-573-822C-340
; Sequence 340, Application US/09573822C
; Publication No. US20030199011A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
; FILE REFERENCE: Microbe patent
; CURRENT APPLICATION NUMBER: US/09/573,822C
; CURRENT FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 804
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 340
; LENGTH: 10
; TYPE: PRT
; ORGANISM: mycoplasma genitalium
; FEATURE:
; OTHER INFORMATION: Sequence located in MG370 at 287-296 and may interact with Sequen
```

```
; OTHER INFORMATION: in this patent.
US-09-573-822C-340

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPKL 7
Db      5 FPKL 8

RESULT 36
US-10-277-292-269
; Sequence 269, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-269

Query Match      26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLK 8
Db      7 PKLK 10

RESULT 37
US-10-277-292-356
; Sequence 356, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
```

; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 356
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-277-292-356

Query Match 26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
|||
Db 7 PKLK 10

RESULT 38
US-10-280-340-269
; Sequence 269, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:
; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-269

Query Match 26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
|||
Db 7 PKLK 10

RESULT 39
US-10-280-340-356
; Sequence 356, Application US/10280340
; Publication No. US20030207835A1
; GENERAL INFORMATION:

; APPLICANT: PARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PID7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/280,340
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 356
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-10-280-340-356

Query Match 26.7%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
|||
Db 7 PKLK 10

RESULT 40
US-10-033-741-52
; Sequence 52, Application US/10033741
; Publication No. US20030049640A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of V.
; TITLE OF INVENTION: Response
; FILE REFERENCE: 9195-079
; CURRENT APPLICATION NUMBER: US/10/033,741
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-741-52

Query Match 26.7%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VEVF 12
|||
Db 6 VEVF 9

RESULT 41
US-10-033-662-47
; Sequence 47, Application US/10033662
; Publication No. US20030092197A1
; GENERAL INFORMATION:
; APPLICANT: Herman, et al.
; TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of C.

; TITLE OF INVENTION: Response
; FILE REFERENCE: 9195-081
; CURRENT APPLICATION NUMBER: US/10/033,662
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-033-662-47

Query Match 26.7%; Score 4; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12
|||
Db 6 VEVF 9

RESULT 42
US-09-756-594-27
; Sequence 27, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-756-594-27

Query Match 26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 43
US-09-756-594-28
; Sequence 28, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-756-594-28

Query Match 26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 44
US-09-756-594-29
; Sequence 29, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-756-594-29

Query Match 26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 45
US-09-756-594-30
; Sequence 30, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594

; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-756-594-30

Query Match 26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 46

US-09-756-594-32
; Sequence 32, Application US/09756594
; Patent No. US20010014456A1
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: dyax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09756,594
; FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-756-594-32

Query Match 26.7%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 47

US-10-272-497-27
; Sequence 27, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; TITLE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009

; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phage Display Sequence
US-10-272-497-27

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 48

US-10-272-497-28
; Sequence 28, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; TITLE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phage Display Sequence
US-10-272-497-28

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 49

US-10-272-497-29
; Sequence 29, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.

; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; FILE OF INVENTION: and Factor VIII-like Proteins
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phase Display Sequence
US-10-272-497-29

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 50
US-10-272-497-30
; Sequence 30, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phase Display Sequence
US-10-272-497-30

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 51
US-10-272-497-32
; Sequence 32, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel

; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phase Display Sequence
US-10-272-497-32

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 52
US-10-272-497-72
; Sequence 72, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phase Display Sequence
US-10-272-497-72

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 53
US-10-272-497-74
; Sequence 74, Application US/10272497
; Publication No. US20030165822A1

US-10-272-497-76

GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phage Display Sequence

US-10-272-497-74

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
Db 4 VFPF 7

RESULT 54

US-10-272-497-76

Sequence 76, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phage Display Sequence

US-10-272-497-76

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
Db 4 VFPF 7

RESULT 55

US-10-272-497-79

Sequence 79, Application US/10272497
; Publication No. US20030165822A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jinan
; APPLICANT: Potter, M. Daniel
; APPLICANT: Kelley, Brian D.
; APPLICANT: Deetz, Jeffrey S.
; APPLICANT: Booth, James E.
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII
; FILE REFERENCE: 3421.1004-009
; CURRENT APPLICATION NUMBER: US/10/272,497
; CURRENT FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/756,594
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US 09/224,785
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected Phage Display Sequence

US-10-272-497-79

Query Match 26.7%; Score 4; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
Db 4 VFPF 7

RESULT 56

US-08-927-939-38

Sequence 38, Application US/08927939
; Publication No. US20010006640A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatallick, Lauen Marie
; TITLE OF INVENTION: Compounds and methods to inhibit or
; FILE REFERENCE: 295.022US1
; CURRENT APPLICATION NUMBER: US/08/927,939
; CURRENT FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Selected Phage Display Sequence

US-08-927-939-38

Query Match 26.7%; Score 4; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 6 PKLK 9

RESULT 57

US-09-798-119-3

Sequence 3, Application US/09798119
; Patent No. US20010018420A1
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EZRIN, ALAN M.

```
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: HOLMES, DARREN L.
; APPLICANT: MILNER, PETER G.
; TITLE OF INVENTION: A METHOD FOR ALLEVIATING PAIN OR PROVIDING AN ANALGESIC EFFECT IN
; TITLE OF INVENTION: PATIENT
; FILE REFERENCE: 500862000610
; CURRENT APPLICATION NUMBER: US/09/798,119
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/445,986
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
; OTHER INFORMATION: analogue A(2-13)
US-09-798-119-3

Query Match      26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
      ||||
Db      9 PKLK 12

RESULT 58
US-09-798-121-3
; Sequence 3, Application US/09798121
; Patent No. US20010018421A1
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EZRIN, ALAN M.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: HOLMES, DARREN L.
; APPLICANT: MILNER, PETER G.
; TITLE OF INVENTION: A CONJUGATE COMPRISING AN ANTINOCEPTIVE AGENT COVALENTLY BONDE
; TITLE OF INVENTION: BLOOD COMPONENT
; FILE REFERENCE: 500862000612
; CURRENT APPLICATION NUMBER: US/09/798,121
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/445,986
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
; OTHER INFORMATION: analogue A(2-13)
US-09-798-121-3

Query Match      26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
      ||||
Db      9 PKLK 12

RESULT 59
US-09-813-329-37
```

```
; Sequence 37, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Subb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class M
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 37
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-37

Query Match      26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKPF 4
      ||||
Db      6 LKPF 9

RESULT 60
US-09-813-329-47
; Sequence 47, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Subb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class M
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 47
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-47

Query Match      26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKPF 4
      ||||
Db      6 LKPF 9

RESULT 61
US-09-813-329-58
; Sequence 58, Application US/09813329
; Patent No. US20020012968A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Subb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class M
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.0
```

; SEQ ID NO 58
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-58

Query Match 26.7%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPF 4
|||
Db 6 LKPF 9

RESULT 62
US-09-798-119-2
; Sequence 2, Application US/09798119
; Patent No. US20010018420A1
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EZRIN, ALAN M.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: HOLMES, DARREN L.
; APPLICANT: MILNER, PETER G.

; TITLE OF INVENTION: A METHOD FOR ALLEVIATING PAIN OR PROVIDING AN ANALGESIC EFFECT
; FILE REFERENCE: 500862000610
; CURRENT APPLICATION NUMBER: US/09/798,119
; CURRENT FILING DATE: 2001-03-01
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
; OTHER INFORMATION: analogue A(1-13)
US-09-798-119-2

Query Match 26.7%; Score 4; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 10 PKLK 13

RESULT 63
US-09-798-121-2
; Sequence 2, Application US/09798121
; Patent No. US20010018421A1
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EZRIN, ALAN M.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: HOLMES, DARREN L.
; APPLICANT: MILNER, PETER G.
; TITLE OF INVENTION: A CONJUGATE COMPRISING AN ANTINOCEPTIVE AGENT COVALENTLY BONDED
; FILE REFERENCE: 500862000612
; CURRENT APPLICATION NUMBER: US/09/798,121
; CURRENT FILING DATE: 2001-03-01
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
; OTHER INFORMATION: analogue A(1-13)
US-09-798-121-2

Query Match 26.7%; Score 4; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 10 PKLK 13

RESULT 64
US-09-966-955A-31
; Sequence 31, Application US/09966955A
; Patent No. US20020155563A1
; GENERAL INFORMATION:

; APPLICANT: Perez-Villar, Juan J.
; APPLICANT: Chang, Han
; APPLICANT: Yang, Wen-Pin
; APPLICANT: Wu, Yuli
; APPLICANT: Whitney, Gena S.
; APPLICANT: Kanner, Steven B.
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human
; TITLE OF INVENTION: Clnk-related Gene, MIST (Mast Cell Immunoreceptor)
; TITLE OF INVENTION: Signal Transducer
; FILE REFERENCE: 3053-4113US1
; CURRENT APPLICATION NUMBER: US/09/966,955A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/237030
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: HUMAN
US-09-966-955A-31

Query Match 26.7%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFPK 6
|||
Db 10 PFPK 13

RESULT 65
US-09-966-955A-32
; Sequence 32, Application US/09966955A
; Patent No. US20020155563A1
; GENERAL INFORMATION:

; APPLICANT: Perez-Villar, Juan J.
; APPLICANT: Chang, Han
; APPLICANT: Yang, Wen-Pin
; APPLICANT: Wu, Yuli
; APPLICANT: Whitney, Gena S.
; APPLICANT: Kanner, Steven B.
; TITLE OF INVENTION: Identification and Cloning of a Full-length Human
; TITLE OF INVENTION: Clnk-related Gene, MIST (Mast Cell Immunoreceptor)
; TITLE OF INVENTION: Signal Transducer
; FILE REFERENCE: 3053-4113US1
; CURRENT APPLICATION NUMBER: US/09/966,955A
; CURRENT FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: 60/237030
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: HUMAN
US-09-966-955A-32

Query Match 26.7%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPK 6
Db 1 PPK 4

RESULT 66
US-10-300-215-10
; Sequence 10, Application US/10300215
; Publication No. US20030153043A1
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: ADAIR, Fiona Suzanne
; APPLICANT: HAMILTON, Anita Anne
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
; FILE REFERENCE: MER-104-Con.1
; CURRENT APPLICATION NUMBER: US/10/300,215
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 09/438,136
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: GB 9710480.6
; PRIOR FILING DATE: 1997-05-21
; PRIOR APPLICATION NUMBER: GB 9716197.0
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: GB 9725270.4
; PRIOR FILING DATE: 1997-11-28
; PRIOR APPLICATION NUMBER: GB 9807751.4
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/067,235
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: humanized monoclonal antibody fragments
US-10-300-215-10
Query Match 26.7%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 KVEV 11
Db 8 KVEV 11
RESULT 67
US-10-300-215-32
; Sequence 32, Application US/10300215
; Publication No. US20030153043A1
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: ADAIR, Fiona Suzanne

; APPLICANT: HAMILTON, Anita Anne
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
; FILE REFERENCE: MER-104-Con.1
; CURRENT APPLICATION NUMBER: US/10/300,215
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 09/438,136
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: GB 9710480.6
; PRIOR FILING DATE: 1997-05-21
; PRIOR APPLICATION NUMBER: GB 9716197.0
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: GB 9725270.4
; PRIOR FILING DATE: 1997-11-28
; PRIOR APPLICATION NUMBER: GB 9807751.4
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/067,235
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: humanized monoclonal antibody fragments
US-10-300-215-32

Query Match 26.7%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVEV 11
Db 8 KVEV 11

RESULT 68

US-09-876-904A-194
; Sequence 194, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 194
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-194

Query Match 26.7%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVK 9
Db 6 KLVK 9

```
RESULT 69
US-10-312-691-6
; Sequence 6, Application US/10312691
; Publication No. US20030175975A1
; GENERAL INFORMATION:
; APPLICANT: CARTIER, Regis
; APPLICANT: BOTTGER, Michael
; APPLICANT: HABERLAND, Annekathrin
; APPLICANT: RESZKA, Regina
; TITLE OF INVENTION: Procedure To Improve The Transfection Efficiency
; FILE REFERENCE: 3658-0108P
; CURRENT APPLICATION NUMBER: US/10/312,691
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: PCT/DE01/02336
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: DE 100.31.900.9
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: DE 100.40.895.8
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic NLS-sequence of the K16-Cyc synthetic peptide
US-10-312-691-6

Query Match          26.7%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KLKV 9
Db      2 KLKV 5

RESULT 70
US-10-145-206-29
; Sequence 29, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZIANG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred TALL-1 Modulating Domains
US-10-145-206-29

Query Match          26.7%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 PFPF 15
Db      5 PFPF 8

RESULT 71
US-09-880-748-2262
```

```
; Sequence 2262, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2262
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2262

Query Match          26.7%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 VPFF 14
Db      10 VPFF 13

RESULT 72
US-10-234-816-98
; Sequence 98, Application US/10234816
; Publication No. US20030157514A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRIN HOMOLOG DOMAIN AND
; TITLE OF INVENTION: RICH DOMAIN CONTAINING ADAPTER PROTEIN, PKN29
; FILE REFERENCE: D0117 NP
; CURRENT APPLICATION NUMBER: US/10/234,816
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-234-816-98

Query Match          26.7%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KLKV 9
Db      8 KLKV 11

RESULT 73
US-10-161-791-181
; Sequence 181, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
```

APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-181

Query Match 26.7%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPKK 6
Db 5 PPKK 8

RESULT 74
US-10-225-567A-1075
Sequence 1075, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1075
LENGTH: 16
TYPE: PPT
ORGANISM: Homo sapiens
US-10-225-567A-1075

Query Match 26.7%; Score 4; DB 15; Length 16;

Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 12 PKLK 15

RESULT 75
US-09-170-919-7
Sequence 7, Application US/09170919
Patent No. US20010010919A1
GENERAL INFORMATION:
APPLICANT: Grisel, Judith E.
APPLICANT: Grandy, David K.
APPLICANT: Mogil, Jeffrey S.
TITLE OF INVENTION: Opioid Antagonists and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston LLP
STREET: 121 S.W. Salmon, Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: USA
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Version WP6, ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,919
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,058
FILING DATE: 11/3/95
ATTORNEY/AGENT INFORMATION:
NAME: William D. No. US20010010919Alnan, M.D.
REGISTRATION NUMBER: 30,878
REFERENCE/DOCKET NUMBER: 899-40006/WDN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-170-919-7

Query Match 26.7%; Score 4; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 10 PKLK 13

Search completed: November 25, 2003, 20:25:34
Job time : 30.8404 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 16.3564 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-8

Perfect score: 15

Sequence: 1 LKFPFKLKEVEFFFP 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	4	US-09-641-803-8
2	5	33.3	12	4	US-08-949-059A-30
3	5	33.3	17	4	US-09-552-802B-40
4	4	26.7	4	1	US-08-540-202-4
5	4	26.7	4	4	US-09-750-726-4
6	4	26.7	5	1	US-08-201-081-6
7	4	26.7	5	2	US-08-288-059-5
8	4	26.7	6	1	US-08-093-741-77
9	4	26.7	6	1	US-08-720-012-77
10	4	26.7	6	3	US-08-981-056A-1
11	4	26.7	8	5	PCT-US93-12679-25
12	4	26.7	9	4	US-09-393-634-91
13	4	26.7	10	3	US-08-649-100-32
14	4	26.7	11	1	US-08-856-053-17
15	4	26.7	11	3	US-09-224-785-27
16	4	26.7	11	3	US-09-224-785-28
17	4	26.7	11	3	US-09-224-785-29
18	4	26.7	11	3	US-09-224-785-30
19	4	26.7	11	3	US-09-224-785-32
20	4	26.7	11	3	US-09-307-265A-14
21	4	26.7	11	4	US-09-756-594-27
22	4	26.7	11	4	US-09-756-594-28
23	4	26.7	11	4	US-09-756-594-29
24	4	26.7	11	4	US-09-756-594-30
25	4	26.7	11	4	US-09-756-594-32
26	4	26.7	12	1	US-08-856-053-7
27	4	26.7	12	1	US-08-856-053-16
28	4	26.7	12	2	US-08-726-306A-136
29	4	26.7	12	4	US-09-445-986B-3
30	4	26.7	12	4	US-09-798-121-3
31	4	26.7	12	4	US-09-552-802B-39
32	4	26.7	13	1	US-08-313-547-2
33	4	26.7	13	1	US-08-482-713-2
34	4	26.7	13	1	US-08-856-053-2
35	4	26.7	13	1	US-08-856-053-6
36	4	26.7	13	1	US-08-856-053-15
37	4	26.7	13	2	US-07-984-469A-19
38	4	26.7	13	3	US-08-855-531D-47
39	4	26.7	13	3	US-08-855-526B-47
40	4	26.7	13	4	US-09-445-986B-2
41	4	26.7	13	4	US-09-798-121-2
42	4	26.7	13	5	PCT-US91-02942-10
43	4	26.7	13	5	PCT-US91-02942-11
44	4	26.7	13	5	PCT-US94-06953-2
45	4	26.7	14	1	US-08-856-053-5
46	4	26.7	14	1	US-08-856-053-14
47	4	26.7	14	1	US-08-949-059A-1
48	4	26.7	14	4	US-08-949-059A-2
49	4	26.7	14	4	US-08-949-059A-7
50	4	26.7	14	4	US-08-949-059A-8
51	4	26.7	14	4	US-08-949-059A-9
52	4	26.7	14	4	US-08-949-059A-10
53	4	26.7	14	4	US-08-949-059A-11
54	4	26.7	14	4	US-08-949-059A-12
55	4	26.7	14	4	US-08-949-059A-13
56	4	26.7	14	4	US-08-949-059A-14
57	4	26.7	14	4	US-08-949-059A-15
58	4	26.7	15	1	US-08-856-053-4
59	4	26.7	15	1	US-08-856-053-13
60	4	26.7	16	1	US-08-074-210-2
61	4	26.7	16	1	US-08-201-081-2
62	4	26.7	16	1	US-08-856-053-23
63	4	26.7	16	2	US-07-984-469A-18
64	4	26.7	16	3	US-08-602-999A-181
65	4	26.7	16	4	US-09-500-124-181
66	4	26.7	16	5	PCT-US94-06502A-1
67	4	26.7	16	5	PCT-US94-06502A-2
68	4	26.7	17	1	US-08-482-713-3
69	4	26.7	17	1	US-08-856-053-1
70	4	26.7	17	2	US-07-984-469A-17
71	4	26.7	17	2	US-08-553-058C-7
72	4	26.7	17	2	US-08-514-451A-12
73	4	26.7	17	2	US-08-436-420-1
74	4	26.7	17	2	US-08-927-328A-2
75	4	26.7	17	4	US-09-048-918B-10
76	4	26.7	17	4	US-09-445-986B-1
77	4	26.7	17	4	US-09-798-121-1
78	4	26.7	18	1	US-08-295-085-3
79	4	26.7	18	1	US-08-295-085-5
80	4	26.7	18	1	US-08-295-085-6
81	4	26.7	18	1	US-08-295-085-7
82	4	26.7	18	1	US-08-295-085-8
83	4	26.7	18	3	US-09-056-226-7
84	4	26.7	18	3	PCT-US95-10741-3
85	4	26.7	18	5	PCT-US95-10741-4
86	4	26.7	18	5	PCT-US95-10741-5
87	4	26.7	18	5	PCT-US95-10741-6
88	4	26.7	18	5	PCT-US95-10741-7
89	4	26.7	18	5	PCT-US95-10741-8
90	4	26.7	19	2	US-08-729-152-17
91	4	26.7	19	2	US-09-552-802B-42
92	4	26.7	19	2	US-08-898-885A-2
93	4	26.7	20	2	US-08-860-656B-11
94	4	26.7	20	3	US-09-227-357-664
95	4	26.7	20	4	US-09-556-877-156
96	4	26.7	20	4	US-09-620-412C-156
97	4	26.7	20	4	US-09-598-419-156
98	4	26.7	20	4	Sequence 136, Appl
99	4	26.7	20	4	Sequence 3, Appl
100	4	26.7	20	4	Sequence 39, Appl

ALIGNMENTS

```
RESULT 1
US-09-641-803-8
; Sequence 8, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDUGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-8
Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPPPKLKVVEVFPF 15
Db 1 LKPPPKLKVVEVFPF 15

RESULT 2
US-08-949-059A-30
; Sequence 30, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Premner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: .McMasters, David D.
```

```
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
US-08-949-059A-30
Query Match 33.3%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLKV 9
Db 8 PKLKV 12

RESULT 3
US-09-552-802B-40
; Sequence 40, Application US/09552802B
; Patent No. 6562943
; GENERAL INFORMATION:
; APPLICANT: Peakman, Mark
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
; TITLE OF INVENTION: CD4+ T LYMPHOCYTES
; FILE REFERENCE: 08191-009002
; CURRENT APPLICATION NUMBER: US/09/552,802B
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/295,868
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/130,355
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-802B-40
Query Match 33.3%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLKVE 10
Db 1 KLKVE 5

RESULT 4
US-08-540-202-4
; Sequence 4, Application US/08540202
; Patent No. 5681923
; GENERAL INFORMATION:
; APPLICANT: Platt, David
; TITLE OF INVENTION: TUMOR DERIVED CARBOHYDRATE BINDING
```

;; TITLE OF INVENTION: PROTEIN
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Gifford, Krass, et al
;; STREET: 280 No. 5681923th Woodward Ave., Suite 400
;; CITY: Birmingham
;; STATE: Michigan
;; COUNTRY: US
;; ZIP: 48009
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/540,202
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Citkowski, Ronald W.
;; REGISTRATION NUMBER: 31,005
;; REFERENCE/DOCKET NUMBER: DPL-00102/16
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 810-647-6000
;; TELEFAX: 810-647-5210
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;;
US-08-540-202-4

Query Match 26.7%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPF 14
Db 1 VFPF 4

RESULT 5
US-09-750-726-4
; Sequence 4, Application US/09750726
; Patent No. 6423314
; GENERAL INFORMATION:
; APPLICANT: Platt, David
; TITLE OF INVENTION: TUMOR DERIVED CARBOHYDRATE BINDING
; PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gifford, Krass, et al
; STREET: 280 No. 6423314th Woodward Ave., Suite 400
; CITY: Birmingham
; STATE: Michigan
; COUNTRY: US
; ZIP: 48009
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/750,726
; FILING DATE: 28-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Citkowski, Ronald W.
; REGISTRATION NUMBER: 31,005
; REFERENCE/DOCKET NUMBER: DPL-00102/16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 810-647-6000

;; TELEFAX: 810-647-5210
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;;
US-09-750-726-4

Query Match 26.7%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VFPF 14
Db 1 VFPF 4

RESULT 6
US-08-201-081-6
; Sequence 6, Application US/08201081
; Patent No. 5593849
; GENERAL INFORMATION:
; APPLICANT: Roy, Benjamin
; TITLE OF INVENTION: METHOD FOR DETECTING ANTIBODY AGAINST
; STAPHYLOCOCCUS AUREUS REPLICATION PROTEIN B SEQUENCE
; TITLE OF INVENTION: 275-290 ARG-LYS-LEU-LYS IN HUMAN BODY FLUIDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Levy Zito & Grandinetti
; STREET: 1730 K Street, N.W. Suite 304
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,081
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Grandinetti, Paul
; REGISTRATION NUMBER: 30,754
; REFERENCE/DOCKET NUMBER: MCG0009US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)429-4560
; TELEFAX: (202)429-4564
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-201-081-6

Query Match 26.7%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 2 PKLK 5

RESULT 7
US-08-288-059-5
; Sequence 5, Application US/08288059
; Patent No. 5827666
; GENERAL INFORMATION:

APPLICANT: FINN, OLIVERA J.
APPLICANT: FONTENOT, J. D.
APPLICANT: MONTECARO, RONALD C.
TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN
TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/288,059
FILING DATE: 08-AUG-1994

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARIANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 61137/205204
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-288-059-5

Query Match 26.7%; Score 4; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 1 PKLK 4

RESULT 8
US-08-093-741-77
Sequence 77, Application US/08093741
Patent No. 5681721
GENERAL INFORMATION:
APPLICANT: STEFFENS, GERD J.
APPLICANT: WENNDT, STEPHAN
APPLICANT: SCHNEIDER, JOHANNES
APPLICANT: HEINZEL-WIELAND, REGINA
APPLICANT: SAUNDERS, DEREK J.
TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: INHIBITING EFFECT
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N. W. Suite 700
CITY: Washington, D.C.
COUNTRY: U.S.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,741
FILING DATE: 20-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/41345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-8800
TELEFAX: (202)628-8844
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-093-741-77

Query Match 26.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVF 12
|||
Db 3 VEVF 6

RESULT 9
US-08-720-012-77
Sequence 77, Application US/08720012
Patent No. 5747291
GENERAL INFORMATION:
APPLICANT: STEFFENS, GERD J.
APPLICANT: WENNDT, STEPHAN
APPLICANT: SCHNEIDER, JOHANNES
APPLICANT: HEINZEL-WIELAND, REGINA
APPLICANT: SAUNDERS, DEREK J.
TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
TITLE OF INVENTION: INHIBITING EFFECT
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N. W. Suite 700
CITY: Washington, D.C.
COUNTRY: U.S.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,012
FILING DATE: 27-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,741
FILING DATE: 20-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, JOSEPH D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/41345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-8800
TELEFAX: (202)628-8844
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:

```
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-720-012-77

Query Match      26.7%; Score 4; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VEVP 12
Db 3 VEVP 6

RESULT 10
US-08-981-256A-1
; Sequence 1, Application US/08981256A
; Patent No. 6046042
; GENERAL INFORMATION:
; APPLICANT: Meinhard HASSLACHER et al.
; TITLE OF INVENTION: (S)-HYDROXY-NITRILE-LYASE FROM HEVEA BRASILIENSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981.256A
; FILING DATE: December 22, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew Jacob
; REGISTRATION NUMBER: 25,154
; REFERENCE/DOCKET NUMBER: 1553-OZ1112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-981-256A-1

Query Match      26.7%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EVFP 13
Db 3 EVFP 6

RESULT 11
PCT-US93-12679-25
; Sequence 25, Application PC/TUS9312679
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: SYNTHETIC OLIGOPEPTIDES ANALOGOUS TO
; PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND
```

```
; TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHELDON & MAK
; STREET: 401 Florence Street
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12679
; FILING DATE: 30-DEC-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cranfill, Raymond B
; REGISTRATION NUMBER: 32,845
; REFERENCE/DOCKET NUMBER: RATH-10016PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5333
; TELEFAX: 415-322-5499
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-12679-25

Query Match      26.7%; Score 4; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 4 PKLK 7

RESULT 12
US-09-393-634-91
; Sequence 91, Application US/09393634
; Patent No. 6558910
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Sf01 signature
; OTHER INFORMATION: sequence 4, amino acids encoded by PCR primers
; OTHER INFORMATION: identifying polymorphic variants, interspecies
; OTHER INFORMATION: homologs and alleles of Sf family members
US-09-393-634-91
```



```
Query Match          26.7%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLK 8
DB      6 PKLK 9

RESULT 13
US-08-649-100-32
; Sequence 32, Application US/08649100
; Patent No. 6114507
; GENERAL INFORMATION:
; APPLICANT: SHIRAKAWA, KAMON
; APPLICANT: MATSUE, TOMOKAZU
; APPLICANT: NATAGATA, SHIGEKAZU
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,100
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1110-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-100-32

Query Match          26.7%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 KVEV 11
DB      6 KVEV 9

RESULT 14
US-08-856-053-17
; Sequence 17, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-17

Query Match          26.7%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLK 8
DB      8 PKLK 11

RESULT 15
US-09-224-785-27
; Sequence 27, Application US/09224785A
; Patent No. 6197526
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dvax-008 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/224,785A
; CURRENT FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-224-785-27
```

Query Match 26.7%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 16
US-09-224-785-28
; Sequence 28, Application US/09224785A
; Patent No. 6197526
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/224,785A
; CURRENT FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-224-785-28

Query Match 26.7%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 17
US-09-224-785-29
; Sequence 29, Application US/09224785A
; Patent No. 6197526
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/224,785A
; CURRENT FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-224-785-29

Query Match 26.7%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 18
US-09-224-785-30
; Sequence 30, Application US/09224785A
; Patent No. 6197526
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/224,785A
; CURRENT FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-224-785-30

Query Match 26.7%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14
|||
Db 4 VFPF 7

RESULT 19
US-09-224-785-32
; Sequence 32, Application US/09224785A
; Patent No. 6197526
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: Dyax-008 US sequence listing
; CURRENT APPLICATION NUMBER: US/09/224,785A
; CURRENT FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: binding loop peptide
US-09-224-785-32

Query Match 26.7%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VFPF 14

Db |||||
 4 VEPF 7

RESULT 20

US-09-307-265A-14
; Sequence 14, Application US/09307265A
; Patent No. 6225456
; GENERAL INFORMATION:
; APPLICANT: Gu, Trent
; APPLICANT: Orita, Satoshi
; APPLICANT: Han, Min
; TITLE OF INVENTION: RAS SUPPRESSOR SUR-5
; FILE REFERENCE: UTC-03732
; CURRENT APPLICATION NUMBER: US/09/307,265A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-307-265A-14

Query Match 26.7%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KVEV 11
 |||||
Db 8 KVEV 11

RESULT 21

US-09-756-594-27
; Sequence 27, Application US/09756594
; Patent No. 6492105
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: DVax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-27

Query Match 26.7%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
 |||||
Db 4 VEPF 7

RESULT 22

US-09-756-594-28
; Sequence 28, Application US/09756594

; Patent No. 6492105
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: DVax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-28

Query Match 26.7%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
 |||||
Db 4 VEPF 7

RESULT 23

US-09-756-594-29
; Sequence 29, Application US/09756594
; Patent No. 6492105
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: DVax-008 US Div. 1 sequence listing
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-29

Query Match 26.7%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 VEPF 14
 |||||
Db 4 VEPF 7

RESULT 24

US-09-756-594-30

```
; Sequence 30, Application US/09756594
; Patent No. 6492105
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: VIII-like Proteins
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-30

Query Match          26.7%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VFPF 14
Db      4 VFPF 7

RESULT 25
US-09-756-594-32
; Sequence 32, Application US/09756594
; Patent No. 6492105
; GENERAL INFORMATION:
; APPLICANT: Potter, M. Daniel
; APPLICANT: Yu, Jinan
; APPLICANT: Kelley, Brian D
; APPLICANT: Deetz, Jeffrey S
; APPLICANT: Booth, James E
; TITLE OF INVENTION: Binding Molecules for Human Factor VIII and Factor
; FILE REFERENCE: VIII-like Proteins
; CURRENT APPLICATION NUMBER: US/09/756,594
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 09/224,785
; PRIOR FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-756-594-32

Query Match          26.7%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 VFPF 14
Db      4 VFPF 7

RESULT 26
US-09-641-801-8-oligo.ra1

US-08-856-053-7
; Sequence 7, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-7

Query Match          26.7%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 PKLK 8
Db      9 PKLK 12

RESULT 27
US-08-856-053-16
; Sequence 16, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
```

ZIP: 94111-4121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,053
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,920
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 2995.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 362-5556
TELEFAX: (415) 362-5418
TELEX: 278638 MGPS
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: porcine
US-08-856-053-16

Query Match 26.7%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 8 PKLK 11

RESULT 28
US-08-726-306A-136
Sequence 136, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-136

Query Match 26.7%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 6 PKLK 9

RESULT 29
US-09-445-986B-3
Sequence 3, Application US/09445986B
Patent No. 6437092
GENERAL INFORMATION:
APPLICANT: CONJUCHEM, INC.
APPLICANT: EZRIN, ALAN M.
APPLICANT: BRIDON, DOMINIQUE P.
APPLICANT: HOLMES, DARREN L.
APPLICANT: MILNER, PETER G.
TITLE OF INVENTION: NOVEL CONJUGATES OF OPIOIDS AND ENDOGENOUS CARRIERS
FILE REFERENCE: RDC-600 USA
CURRENT APPLICATION NUMBER: US/09/445,986B
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US98/23704
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 3
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Dynorphin
OTHER INFORMATION: analogue A(2-13)
US-09-445-986B-3

Query Match 26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 9 PKLK 12

RESULT 30
US-09-798-121-3
Sequence 3, Application US/09798121
Patent No. 6500918
GENERAL INFORMATION:
APPLICANT: CONJUCHEM, INC.
APPLICANT: EZRIN, ALAN M.
APPLICANT: BRIDON, DOMINIQUE P.
APPLICANT: HOLMES, DARREN L.
APPLICANT: MILNER, PETER G.
TITLE OF INVENTION: A CONJUGATE COMPRISING AN ANTINOCEPTIVE AGENT COVALENTLY B
TITLE OF INVENTION: BLOOD COMPONENT

```

; FILE REFERENCE: 500862000612
; CURRENT APPLICATION NUMBER: US/09/798,121
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/445,986
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
; OTHER INFORMATION: analogue A(2-13)
US-09-798-121-3

Query Match          26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 9 PKLK 12

RESULT 31
US-09-552-802B-39
; Sequence 39, Application US/09552802B
; Patent No. 6562943
; GENERAL INFORMATION:
; APPLICANT: Peakman, Mark
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
; TITLE OF INVENTION: CD4+ T LYMPHOCYTES
; FILE REFERENCE: 08191-009002
; CURRENT APPLICATION NUMBER: US/09/552,802B
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/295,868
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/130,355
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-552-802B-39

Query Match          26.7%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKVE 10
Db 1 LKVE 4

RESULT 32
US-08-313-547-2
; Sequence 2, Application US/08313547
; Patent No. 5428128
; GENERAL INFORMATION:
; APPLICANT: Mensi-Pattchi, Nahla
; APPLICANT: Molineaux, Christopher J.
; APPLICANT: Shorr, Robert G.B.
; TITLE OF INVENTION: Site Specific Synthesis of Conjugated Peptides
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite No. 5428128 600

```

```

; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,547
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/080,457
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0977.2170000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-313-547-2

Query Match          26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 10 PKLK 13

RESULT 33
US-08-482-713-2
; Sequence 2, Application US/08482713
; Patent No. 5624932
; GENERAL INFORMATION:
; APPLICANT: Qin, Bo-yi
; APPLICANT: Shen, Ke-fei
; APPLICANT: Gong, Xiong-qi
; APPLICANT: Crain, Stanley M.
; APPLICANT: Huang, Mao
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION OF
; TITLE OF INVENTION: LOW/NON-ADDICTIVE ANALGESICS AND THE USE OF SAID
; TITLE OF INVENTION: ANALGESICS FOR TREATMENT OF OPIOID ADDICTION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: M. Lisa Wilson
; STREET: 25 Davids Drive
; CITY: Hauppauge
; STATE: NY
; COUNTRY: USA
; ZIP: 11788
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,713
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, M. Lisa
; REGISTRATION NUMBER: 34,045

```

; REFERENCE/DOCKET NUMBER: 2001XC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)273-2828
; TELEFAX: (516)273-1717
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-713-2

Query Match 26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 10 PKLK 13

RESULT 34
US-08-856-053-2
; Sequence 2, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELEPHONE: (415) 362-5556
; TELEFAX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-2

Query Match 26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 10 PKLK 13

RESULT 35
US-08-856-053-6
; Sequence 6, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES

QY 5 PKLK 8
|||
Db 10 PKLK 13

RESULT 35
US-08-856-053-6
; Sequence 6, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-6

Query Match 26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 9 PKLK 12

RESULT 36
US-08-856-053-15
; Sequence 15, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES

```
;
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
; US-08-856-053-15

Query Match 26.7%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 8 PKLK 11

RESULT 37
US-07-984-469A-19
; Sequence 19, Application US/07984469A
; Patent No. 5817628
; GENERAL INFORMATION:
; APPLICANT: Mary Jeanne Kreek, M.D.
; TITLE OF INVENTION: Dynorphin A Suppression of Natural
; TITLE OF INVENTION: Killer Cell Activity
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/984,469A
; FILING DATE: 02 - Dec - 1992
```

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth H. Sonnenfeld
; REGISTRATION NUMBER: 33,285
; REFERENCE/DOCKET NUMBER: 2016-4003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-415-8513
; TELEX: (212) 751-6849
; TELEFAX: 421792
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-07-984-469A-19

Query Match 26.7%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 10 PKLK 13

RESULT 38
US-08-855-531D-47
; Sequence 47, Application US/08855531D
; Patent No. 6110467
; GENERAL INFORMATION:
; APPLICANT: PREM, PAUL S.
; HALBUR, PATRICK G.
; MENG, XIANG-JIN
; LUM, MELISSA A.
; LYOO, YOUNG S.
; TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL
; RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND
; REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAIN:
; A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCQUELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,531D
; FILING DATE: 13-May-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,071
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: LAVALLEYE, JEAN-PAUL M.P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 4625-038-55X DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
```



```
;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-08-855-531D-47

Query Match          26.7%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 7 PKLK 10

RESULT 39
US-08-855-526B-47
; Sequence 47, Application US/08055526B
; Patent No. 6251404
; GENERAL INFORMATION:
; APPLICANT: FREW, PAUL S.
; APPLICANT: HALBUR, PATRICK G.
; APPLICANT: MENG, XIANG-JIN
; APPLICANT: LUM, MELISSA A.
; APPLICANT: LYOO, YOUNG S.
; TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL
; TITLE OF INVENTION: RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND
; TITLE OF INVENTION: REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST
; TITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,526B
; FILING DATE: 13-MAY-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/969,071
; FILING DATE: 30-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: LAVALLEYE, JEAN-PAUL M.P.
; REGISTRATION NUMBER: 31,451
; REFERENCE/DOCKET NUMBER: 4625-040-55X DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-855-526B-47

Query Match          26.7%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 7 PKLK 10
```

```
RESULT 40
US-09-445-986B-2
; Sequence 2, Application US/09445986B
; Patent No. 6437092
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EZRIN, ALAN M.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: HOLMES, DARREN L.
; APPLICANT: MILNER, PETER G.
; TITLE OF INVENTION: NOVEL CONJUGATES OF OPIOIDS AND ENDOGENOUS CARRIERS
; FILE REFERENCE: REDC-600 USA
; CURRENT APPLICATION NUMBER: US/09/445,986B
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
US-09-445-986B-2

Query Match          26.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 10 PKLK 13

RESULT 41
US-09-798-121-2
; Sequence 2, Application US/09798121
; Patent No. 6500918
; GENERAL INFORMATION:
; APPLICANT: CONJUCHEM, INC.
; APPLICANT: EZRIN, ALAN M.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: HOLMES, DARREN L.
; APPLICANT: MILNER, PETER G.
; TITLE OF INVENTION: A CONJUGATE COMPRISING AN ANTINOCICEPTIVE AGENT COVALENTLY BC
; FILE REFERENCE: 500862000612
; CURRENT APPLICATION NUMBER: US/09/798,121
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/445,986
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US98/23704
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Dynorphin
US-09-798-121-2

Query Match          26.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
```

```
Db          10 PKLK 13
|||||
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US91-02942-11
;
; Query Match          26.7%; Score 4; DB 5; Length 13;
; Best Local Similarity 100.0%; Pred. No. 3.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY          8 KVEV 11
          |||||
Db          8 KVEV 11
          |||||

RESULT 44
PCT-US94-06953-2
; Sequence 2, Application PC/TUS9406953
; GENERAL INFORMATION:
; APPLICANT: Enzon, Inc.
; APPLICANT: 40 Kingsbridge Road
; APPLICANT: Piscataway, New Jersey 08854-3998
; APPLICANT: United States of America
; APPLICANT: Molineaux, Christopher J.
; APPLICANT: Shorr, Robert G.L.
; TITLE OF INVENTION: Site Specific Synthesis of Conjugated Peptides
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite No. 600
; CITY: Washington,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06953
; FILING DATE: herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,457
; FILING DATE: 21-JUN-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0977.2170000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600

;
; Query Match          26.7%; Score 4; DB 5; Length 13;
; Best Local Similarity 100.0%; Pred. No. 3.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY          8 KVEV 11
          |||||
Db          8 KVEV 11
          |||||

RESULT 43
PCT-US91-02942-11
; Sequence 11, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US91-02942-10
;
; Query Match          26.7%; Score 4; DB 5; Length 13;
; Best Local Similarity 100.0%; Pred. No. 3.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY          8 KVEV 11
          |||||
Db          8 KVEV 11
          |||||

RESULT 43
PCT-US91-02942-11
; Sequence 11, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
```

; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US94-06953-2

Query Match 26.7%; Score 4; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 PKLK 8
Db 10 PKLK 13

RESULT 45
US-08-856-053-5
; Sequence 5, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-5

Query Match 26.7%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 PKLK 8
Db 9 PKLK 12

RESULT 46
US-08-856-053-14
; Sequence 14, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-14

Query Match 26.7%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 8 PKLK 11

RESULT 47
US-08-949-059A-1
; Sequence 1, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Premner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND

```
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Where Xaa is D-Tyrosine or
; OTHER INFORMATION: D-phenylalanine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Where Xaa is D-Tyrosine or
; OTHER INFORMATION: D-phenylalanine"
; US-08-949-059A-1
;
; Query Match 26.7%; Score 4; DB 4; Length 14;
; Best Local Similarity 100.0%; Pred. No. 3.3e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 6 KLKV 9
; DB 2 KLKV 5
```

```
RESULT 48
US-08-949-059A-2
; Sequence 2, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
```

```
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Residue is a D-Valine "
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; US-08-949-059A-2
;
; Query Match 26.7%; Score 4; DB 4; Length 14;
; Best Local Similarity 100.0%; Pred. No. 3.3e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 6 KLKV 9
; DB 2 KLKV 5
```

```
RESULT 49
US-08-949-059A-7
; Sequence 7, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
```

```
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-7

Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVV 9
Db 2 KLVV 5

RESULT 50
US-08-949-059A-8
; Sequence 8, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; CORRESPONDENCE ADDRESSES: 42
; NUMBER OF SEQUENCES: 42
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-8

Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVV 9
Db 2 KLVV 5

RESULT 51
US-08-949-059A-9
; Sequence 9, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; CORRESPONDENCE ADDRESSES: 42
; NUMBER OF SEQUENCES: 42
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /note= "Residue is a D-Leucine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-9
Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKV 9
DB 2 KLKV 5

RESULT 52
US-08-949-059A-10
; Sequence 10, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 42
; TITLE OF INVENTION: METHOD
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
```

```
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "Residue is a D-Lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-10
Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKV 9
DB 2 KLKV 5

RESULT 53
US-08-949-059A-11
; Sequence 11, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; CORRESPONDENCE ADDRESS:
; NUMBER OF SEQUENCES: 42
; TITLE OF INVENTION: METHOD
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /note= "Residue is a D-Valine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; US-08-949-059A-11
;
Query Match          26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KLVV 9
        ||||
Db      2 KLVV 5

RESULT 54
US-08-949-059A-12
; Sequence 12, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
```

```
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Residue is a D-Lysine"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
; US-08-949-059A-12
;
Query Match          26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KLVV 9
        ||||
Db      2 KLVV 5

RESULT 55
US-08-949-059A-13
; Sequence 13, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
```

```
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: /note= "Residue is a D-Leucine"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-13
Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVV 9
Db 2 KLVV 5
|||||

RESULT 56
US-08-949-059A-14
; Sequence 14, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
```

```
;
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
US-08-949-059A-14
Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KLVV 9
Db 2 KLVV 5
|||||

RESULT 57
US-08-949-059A-15
; Sequence 15, Application US/08949059A
; Patent No. 6358921
; GENERAL INFORMATION:
; APPLICANT: Kondejewski, Leslie H.
; APPLICANT: Hodges, Robert S.
; APPLICANT: Wishart, David S.
; APPLICANT: Hancock, Robert E.W.
; APPLICANT: McElhaney, Ronald N.
; APPLICANT: Prenner, Elmar J.
; APPLICANT: Lewis, Ruthven N.A.H.
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE COMPOSITIONS AND
; TITLE OF INVENTION: METHOD
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,059A
; FILING DATE: 10-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 660081.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: cyclic
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: /note= "Residue is a D-Tyrosine"
;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: /note= "Residue is a D-Proline"
;
US-08-949-059A-15
```


Query Match 26.7%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKV 9
|||
Db 2 KLKV 5

RESULT 58
US-08-856-053-4
; Sequence 4, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-4

Query Match 26.7%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 9 PKLK 12

RESULT 59
US-08-856-053-13
; Sequence 13, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-4

Query Match 26.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 9 PKLK 12

RESULT 60
US-08-074-210-1
; Sequence 1, Application US/08074210
; Patent No. 5482930
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

APPLICANT: Loh, Horace H.
APPLICANT: Takemori, Akira E.
TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1450
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,053
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/897,920
FILING DATE: 12-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 2995.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 362-5556
TELEFAX: (415) 362-5418
TELEX: 278638 MGPS
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: porcine
US-08-856-053-13

Query Match 26.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 8 PKLK 11

RESULT 60
US-08-074-210-1
; Sequence 1, Application US/08074210
; Patent No. 5482930
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

Query Match 26.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
|||
Db 8 PKLK 11

RESULT 60
US-08-074-210-1
; Sequence 1, Application US/08074210
; Patent No. 5482930
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/074,210
;; FILING DATE: 19930609
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Siebert, J. Suzanne
;; REGISTRATION NUMBER: 28,758
;; REFERENCE/DOCKET NUMBER: 2500.72
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 362-5556
;; TELEFAX: (415) 362-5418
;; TELEX: 278638 MGPS
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-074-210-1

Query Match 26.7%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 9 PKLK 12

RESULT 61
US-08-074-210-2
; Sequence 2, Application US/08074210
; Patent No. 5482930
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Heue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/074,210
; FILING DATE: 19930609
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2500.72
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELEX: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-074-210-2

Query Match 26.7%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 9 PKLK 12

RESULT 62
US-08-201-081-2
; Sequence 2, Application US/08201081
; Patent No. 5593849
; GENERAL INFORMATION:
; APPLICANT: Roy, Benjamin
; TITLE OF INVENTION: METHOD FOR DETECTING ANTIBODY AGAINST
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS REPLICATION PROTEIN B SEQUENCE
; TITLE OF INVENTION: 275-290 ARG-LYS-LEU-LYS IN HUMAN BODY FLUIDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Levy, Zito & Grandinetti
; STREET: 1730 K Street, N.W. Suite 304
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/201,081
; FILING DATE: 24-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Grandinetti, Paul
; REGISTRATION NUMBER: 30,754
; REFERENCE/DOCKET NUMBER: MCG00909
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 429-4560
; TELEFAX: (202) 429-4564
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-201-081-2

Query Match 26.7%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 10 PKLK 13

RESULT 63
US-08-856-053-23
; Sequence 23, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23

;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Majestic, Parsons, Siebert & Hsue
;/ STREET: Four Embarcadero Center, Suite 1450
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: U.S.A.
;/ ZIP: 94111-4121
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent In Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/856,053
;/ FILING DATE:
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 07/897,920
;/ FILING DATE: 12-JUN-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Siebert, J. Suzanne
;/ REGISTRATION NUMBER: 28,758
;/ REFERENCE/DOCKET NUMBER: 2995.1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 362-5556
;/ TELEFAX: (415) 362-5418
;/ INFORMATION FOR SEQ ID NO: 23:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 16 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: protein
;/ HYPOTHETICAL: NO
;/ ANTI-SENSE: NO
;/ ORIGINAL SOURCE:
;/ ORGANISM: porcine
;/ US-08-856-053-23

Query Match 26.7%; Score 4; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 PKLK 8
Db 9 PKLK 12

RESULT 64
US-07-984-469A-18
;/ Sequence 18, Application US/07984469A
;/ Patent No. 5817628
;/ GENERAL INFORMATION:
;/ APPLICANT: Mary Jeanne Kreek, M.D.
;/ TITLE OF INVENTION: Dynorphin A Suppression of Natural
;/ TITLE OF INVENTION: Killer Cell Activity
;/ NUMBER OF SEQUENCES: 20
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Morgan & Finnegan
;/ STREET: 345 Park Avenue
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: USA
;/ ZIP: 10154
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
;/ COMPUTER: IBM PC Compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Wordperfect 5.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/07/984,469A
;/ FILING DATE: 02 - Dec - 1992
;/ ATTORNEY/AGENT INFORMATION:

;/ NAME: Kenneth H. Sonnenfeld
;/ REGISTRATION NUMBER: 33,285
;/ REFERENCE/DOCKET NUMBER: 2016-4003
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212-415-8513
;/ TELEFAX: (212) 751-6849
;/ TELEX: 421792
;/ INFORMATION FOR SEQ ID NO: 18:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 16 amino acids
;/ TYPE: Amino Acid
;/ STRANDEDNESS: Single
;/ TOPOLOGY: Unknown
;/ MOLECULE TYPE: Peptide
;/ FEATURE:
;/ OTHER INFORMATION: This peptide is identical to
;/ OTHER INFORMATION: the mature dynorphin A(1-17) of SEQ ID NO: 17 except
;/ OTHER INFORMATION: for the removal of the amino terminal Tyr
;/ US-07-984-469A-18

Query Match 26.7%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 9 PKLK 12

RESULT 65
US-08-602-999A-181
;/ Sequence 181, Application US/08602999A
;/ Patent No. 6184205
;/ GENERAL INFORMATION:
;/ APPLICANT: SPARKS, Andrew B.
;/ APPLICANT: KAY, Brian K.
;/ APPLICANT: THORN, Judith M.
;/ APPLICANT: QUILLIAM, Lawrence A.
;/ APPLICANT: DER, Channing J.
;/ APPLICANT: FOWLKES, Dana M.
;/ APPLICANT: RIDER, James E.
;/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;/ TITLE OF INVENTION: ISOLATING AND USING SAME
;/ NUMBER OF SEQUENCES: 467
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pennie & Edmonds
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent In Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/602,999A
;/ FILING DATE: 16-FEB-1996
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Mistrock, S. Leslie
;/ REGISTRATION NUMBER: 18,872
;/ REFERENCE/DOCKET NUMBER: 1101-202
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 790-9090
;/ TELEFAX: (212) 869-9741/8864
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 181:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 16 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: unknown

```
; MOLECULE TYPE: peptide
US-08-602-999A-181
Query Match      26.7%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPKK 6
Db      5 PPKK 8

RESULT 66
US-09-500-124-181
; Sequence 181, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/500,124
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-181
Query Match      26.7%; Score 4; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPKK 6
Db      5 PPKK 8

RESULT 67
PCT-US94-06502A-1
; Sequence 1, Application PC/TUS9406502A
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06502A
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US94-06502A-1
Query Match      26.7%; Score 4; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PKLK 8
Db      9 PKLK 12

RESULT 68
PCT-US94-06502A-2
; Sequence 2, Application PC/TUS9406502A
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06502A
; FILING DATE:
```

```
;
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Xaa (position 16) is Gln-NH2"
PCT-US94-06502A-2

Query Match 26.7%; Score 4; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 9 PKLK 12

RESULT 69
US-08-482-713-3
; Sequence 3, Application US/08482713
; Patent No. 5624932
; GENERAL INFORMATION:
; APPLICANT: Qin, Bo-yi
; APPLICANT: Shen, Ke-fei
; APPLICANT: Gong, Xiong-qi
; APPLICANT: Crain, Stanley M.
; APPLICANT: Huang, Mao
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: A METHOD FOR IDENTIFICATION OF
; TITLE OF INVENTION: LOW/NON-ADDICTIVE ANALGESICS AND THE USE OF SAID
; TITLE OF INVENTION: ANALGESICS FOR TREATMENT OF OPIOID ADDICTION
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: M. Lisa Wilson
; STREET: 25 Davids Drive
; CITY: Hauppauge
; STATE: NY
; COUNTRY: USA
; ZIP: 11788
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,713
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, M. Lisa
; REGISTRATION NUMBER: 34,045
; REFERENCE/DOCKET NUMBER: 2001XC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 273-2828
; TELEFAX: (516) 273-1717
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
```

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-713-3

Query Match 26.7%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 10 PKLK 13

RESULT 70
US-08-856-053-1
; Sequence 1, Application US/08856053
; Patent No. 5807827
; GENERAL INFORMATION:
; APPLICANT: Lee, Nancy M.
; APPLICANT: Loh, Horace H.
; APPLICANT: Takemori, Akira E.
; TITLE OF INVENTION: DES-TYR DYNORPHIN ANALOGUES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94111-4121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,053
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/897,920
; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Siebert, J. Suzanne
; REGISTRATION NUMBER: 28,758
; REFERENCE/DOCKET NUMBER: 2995.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 362-5556
; TELEFAX: (415) 362-5418
; TELE: 278638 MGPS
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: porcine
US-08-856-053-1

Query Match 26.7%; Score 4; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
Db 10 PKLK 13

RESULT 71
```

US-07-984-469A-17
; Sequence 17, Application US/07984469A
; Patent No. 5817628
; GENERAL INFORMATION:
; APPLICANT: Mary Jeanne Kreek, M.D.
; TITLE OF INVENTION: Dynorphin A Suppression of Natural
; TITLE OF INVENTION: Killer Cell Activity
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/984,469A
; FILING DATE: 02 - Dec - 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth H. Sonnenfeld
; REGISTRATION NUMBER: 33,285
; REFERENCE/DOCKET NUMBER: 2016-4003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-415-8513
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-07-984-469A-17

Query Match 26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 10 PKLK 13

RESULT 72
US-08-553-058C-7
; Sequence 7, Application US/08553058C
; Patent No. 5821219
; GENERAL INFORMATION:
; APPLICANT: Grisel, Judith B.
; APPLICANT: Grandy, David K.
; APPLICANT: Mogil, Jeffrey S.
; TITLE OF INVENTION: Opioid Antagonists and Methods of Their Use
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston LLP
; STREET: 121 S.W. Salmon, Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Version WP6, ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,058C

; FILING DATE: 11/3/95
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5821219nan, M.D.
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-40006/WDN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-553-058C-7

Query Match 26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKLK 8
Db 10 PKLK 13

RESULT 73
US-08-514-451A-12
; Sequence 12, Application US/08514451A
; Patent No. 5837809
; GENERAL INFORMATION:
; APPLICANT: Bunzow, James R.
; APPLICANT: Grandy, David K.
; APPLICANT: Civelli, Olivier
; APPLICANT: Reinscheid, Rainer K.
; APPLICANT: Monsma, Frederick J.
; TITLE OF INVENTION: A NOVEL MAMMALIAN OPIOID
; TITLE OF INVENTION: RECEPTOR LIGAND AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klarquist Sparkman Campbell
; ADDRESSEE: Leigh & Whinston LLP
; STREET: 121 S.W. Salmon, Suite 1600
; CITY: Portland
; STATE: Oregon
; COUNTRY: USA
; ZIP: 97204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WP5.1 ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/514,451A
; FILING DATE: 08/11/95
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/553,058
; FILING DATE: 11/13/95
; ATTORNEY/AGENT INFORMATION:
; NAME: William D. No. 5837809nan, M.D.
; REGISTRATION NUMBER: 30,878
; REFERENCE/DOCKET NUMBER: 899-45995/WDN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
US-08-514-451A-12

Query Match 26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
| | | |
Db 10 PKLK 13

RESULT 74

US-08-436-420-10
; Sequence 10; Application US/08436420
; Patent No. 5840524
; GENERAL INFORMATION:
; APPLICANT: VAN DAMME, Jo; and
; APPLICANT: PROOST, Paul
; TITLE OF INVENTION: GRANULOCYTE CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE and DORR LLP
; STREET: 1455 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: DISTRICT OF COLUMBIA
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPC)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436.420
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03330
; FILING DATE: 26-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/982,539
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102378.215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8400
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-436-420-10

Query Match 26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KVEV 11
| | | |
Db 12 KVEV 15

RESULT 75

US-08-927-328A-2
; Sequence 2; Application US/08927328A
; Patent No. 5840696
; GENERAL INFORMATION:
; APPLICANT: HOWARD LIPPTON
; TITLE OF INVENTION: DIURETIC AND ANTINATRIURETIC
; TITLE OF INVENTION: RESPONSES PRODUCED BY ANALOGS OF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,328A
; FILING DATE: September 11, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 42740/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acids
; STRANDEDNESS: SINGLE
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-927-328A-2

Query Match 26.7%; Score 4; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKLK 8
| | | |
Db 10 PKLK 13

Search completed: November 25, 2003, 20:16:04
Job time : 17.3564 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 4.60106 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-9

Perfect score: 5

Sequence: 1 VMEV 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	60.0	13	PL0157	Ig kappa chain V-I
2	3	60.0	16	S29137	aminopyrine N-deme
3	3	60.0	18	PL0025	T-cell surface gly
4	3	60.0	18	S48862	murine cyclin H -
5	2	40.0	4	A61300	22K superhelical D
6	2	40.0	4	I57745	D-mannosate hydrol
7	2	40.0	4	E44823	synaptosomal-assoc
8	2	40.0	6	S02617	alcohol dehydrogen
9	2	40.0	6	B44510	hypothetical prote
10	2	40.0	6	A49792	acylaminoacyl-pept
11	2	40.0	6	A20186	fatty-acid synthas
12	2	40.0	7	B34818	vicilin 57K chain
13	2	40.0	7	PQ0727	H2 class I protein
14	2	40.0	7	P70246	Ig heavy chain CRD
15	2	40.0	7	I48086	DNA topoisomerase
16	2	40.0	7	S15597	orf 4 rara 5'-regi
17	2	40.0	8	S16324	hypothetical prote
18	2	40.0	8	A21440	variant surface gl
19	2	40.0	8	G33098	205K exoantigen -
20	2	40.0	8	A05169	neuropeptide M-I -
21	2	40.0	8	P70298	Ig heavy chain CRD
22	2	40.0	8	A54823	olfactory receptor
23	2	40.0	8	A35768	T-cell receptor al
24	2	40.0	8	B54823	olfactory receptor
25	2	40.0	8	I49404	prealbumin - weste
26	2	40.0	8	I57532	gene TnIsIow prote
27	2	40.0	8	B47594	aspartate kinase (
28	2	40.0	9	D24180	fibrinogen beta ch
29	2	40.0	9	PA0033	protein QA300033 -

30	2	40.0	9	D48186	ATPase R1 subunit
31	2	40.0	9	S70345	amine oxidase (cop
32	2	40.0	9	A56029	N-methylpurine DNA
33	2	40.0	10	S39392	calpain (EC 3.4.22
34	2	40.0	10	JC1367	thyloliberin poten
35	2	40.0	10	A47593	mercury resistance
36	2	40.0	10	Q00943	hypothetical 1.3K
37	2	40.0	10	B39517	probable methionin
38	2	40.0	10	C35389	urease (EC 3.5.1.5
39	2	40.0	10	JN0440	peptide-N4-(N-acet
40	2	40.0	10	P80209	24K protein 4407 -
41	2	40.0	10	S19296	16K protein - poul
42	2	40.0	10	A43977	PMRFamide-like pro
43	2	40.0	10	C39111	Ig heavy chain C r
44	2	40.0	10	B56899	serum heterodimer,
45	2	40.0	10	S77980	cytochrome-c oxida
46	2	40.0	10	B45482	platelet activatin
47	2	40.0	10	B49033	T-cell receptor ga
48	2	40.0	10	S71948	matrix metalloprot
49	2	40.0	10	S36849	Ig heavy chain V r
50	2	40.0	10	B86128	hypothetical prote
51	2	40.0	11	S68392	H4-transporing tw
52	2	40.0	11	A40693	transgelin - sheep
53	2	40.0	11	A57458	gene Gax protein -
54	2	40.0	11	A55149	tetracenomycin A2
55	2	40.0	11	S33519	probable secreted
56	2	40.0	11	H54346	pyruvate synthase
57	2	40.0	11	PQ0731	unidentified 5.7/3
58	2	40.0	11	PC2173	triacylglycerol li
59	2	40.0	11	S45698	gamma-MSH-like pro
60	2	40.0	11	I52980	glucocerebrosidase
61	2	40.0	11	S23364	T-cell receptor al
62	2	40.0	11	S09024	carboxylesterase (
63	2	40.0	11	PH0891	T-cell receptor be
64	2	40.0	11	PH0924	T-cell receptor be
65	2	40.0	11	PH0922	T-cell receptor be
66	2	40.0	11	I52708	ENAV-like neuronal
67	2	40.0	12	S09082	proteasome chain 1
68	2	40.0	12	S26558	T-cell receptor be
69	2	40.0	12	S26559	T-cell receptor be
70	2	40.0	12	A39233	myosin heavy chain
71	2	40.0	12	S65629	protoporphyrinogen
72	2	40.0	12	S69123	proton-translocati
73	2	40.0	12	S36899	ribosomal protein
74	2	40.0	12	S52561	5-enolpyruvylshiki
75	2	40.0	12	PA0019	acidic ribosomal p
76	2	40.0	12	PA0037	plastocyanin 2 - A
77	2	40.0	12	PQ0730	unidentified 5.4/3
78	2	40.0	12	S70344	amine oxidase (cop
79	2	40.0	12	A33099	163K exoantigen -
80	2	40.0	12	S16204	6-phosphofructokin
81	2	40.0	12	I39390	acetylcholine rece
82	2	40.0	12	PT0257	Ig heavy chain CRD
83	2	40.0	12	S21205	Ig heavy chain V r
84	2	40.0	12	A60528	insulin-like growt
85	2	40.0	12	A33520	inhibitory diffusi
86	2	40.0	12	PH1466	T-cell receptor be
87	2	40.0	12	S39762	T-cell receptor be
88	2	40.0	12	PH0930	T-cell receptor be
89	2	40.0	12	A53252	pollen major aller
90	2	40.0	12	JX0315	aminotransferase c
91	2	40.0	13	MTMAD	melanotropin alpha
92	2	40.0	13	A32734	melanotropin alpha
93	2	40.0	13	A32734	enkephalin precurs
94	2	40.0	13	S39413	tubulin beta chain
95	2	40.0	13	A61288	spore proteinase g
96	2	40.0	13	S20578	ribosomal protein
97	2	40.0	13	PC1149	equinatoxin 1A - s
98	2	40.0	13	D61458	Ig kappa chain V-I
99	2	40.0	13	E61458	Ig kappa chain V-I
100	2	40.0	13	S65612	tubulin alpha-chai

ALIGNMENTS

RESULT 1
 PLO157
 Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PEC) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997
 C:Accession: PLO157; C61458
 R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
 J. Exp. Med. 170, 1551-1558, 1989
 A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-associated glycoprotein
 A:Reference number: A61458; MUID:90039128; PMID:2478651
 A:Accession: PLO157
 A:Molecule type: protein
 A:Residues: 1-13 <BRO>
 A:Accession: C61458
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <BR2>
 C:Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 60.0%; Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
 |||
 Db 2 VWM 4

RESULT 2
 S29137
 aminopyrine N-demethylase (EC 1.14.14.-) cytochrome P450 betaNF-B - chicken (fragment)
 N:Alternate names: aniline monooxygenase
 C:Species: Gallus gallus (chicken)
 C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 05-Mar-1999
 C:Accession: S29137
 R:Gupta, R.P.; Lapadula, D.M.; Abou-Donia, M.B.
 Arch. Biochem. Biophys. 282, 170-182, 1990
 A:Title: Purification and characterization of cytochrome P450 isozymes from beta-naphthol
 A:Reference number: S13263; MUID:91024193; PMID:2171427
 A:Accession: S29137
 A:Molecule type: protein
 A:Residues: 1-16 <GUP>
 C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology
 C:Keywords: heme; membrane protein; microsome; monooxygenase; oxidoreductase

Query Match 60.0%; Score 3; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
 |||
 Db 1 MEV 3

RESULT 3
 PLO025
 T-cell surface glycoprotein rta - rabbit (fragment)
 N:Alternate names: thymocyte specific class I-like antigen, heavy chain
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 07-Feb-1997
 C:Accession: PLO025
 R:Wang, C.R.; Chen, G.H.; Newkirk, M.; Capra, J.D.; Mandy, W.J.
 Mol. Immunol. 25, 945-952, 1988
 A:Title: Biochemical properties of a novel rabbit thymocyte specific class I-like antigen
 A:Reference number: PLO025; MUID:89096985; PMID:3264985
 A:Accession: PLO025
 A:Molecule type: protein
 A:Residues: 1-18 <WAN>
 A:Experimental source: thymus

C;Keywords: glycoprotein; surface antigen

Query Match 60.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
 |||
 Db 12 VME 14

RESULT 4
 S48862
 murine cyclin H - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S48862
 R:Hall, F.L.; Wu, L.
 Submitted to the EMBL Data Library, October 1994
 A:Reference number: S48862
 A:Accession: S48862
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-18 <HAL>
 A:Cross-references: EMBL:X82441; NID:G563899; PIDN:CAAS7822.1; PID:G563900

Query Match 60.0%; Score 3; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
 |||
 Db 5 VME 7

RESULT 5
 A61300
 22k superhelical DNA-binding protein - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 C:Accession: A61300
 R:Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
 J. Biochem. 92, 1059-1068, 1982
 A:Title: Purification and characterization of a protein from Escherichia coli which forms a DNA-protein complex
 A:Reference number: A61300; MUID:83082696; PMID:6294066
 A:Accession: A61300
 A:Molecule type: protein
 A:Residues: 1-4 <KIS>
 C:Comment: This protein resembles some of the histone-like protein of bacteria in amino acid sequence
 C:Keywords: DNA binding; monomer

Query Match 40.0%; Score 2; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
 |||
 Db 1 ME 2

RESULT 6
 I57745
 D-mannanase hydrolase (uxuA) - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999
 C:Accession: I57745
 R:Blanco, C.; Ritzenthaler, P.; Kolb, A.
 Mol. Gen. Genet. 202, 112-119, 1986
 A:Title: The regulatory region of the uxuAB operon in Escherichia coli K12.
 A:Reference number: I57745; MUID:86174344; PMID:3083215
 A:Accession: I57745
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A;Residues: 1-4 <RES>
A;Cross-references: EMBL:X03411; NID:G43300; PIDN:CAA27147.1; PID:G581254

Query Match 40.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
||
Db 1 ME 2

RESULT 7
E44823
synaptosomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N:Alternate names: superprotein peptide 1
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: E44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A;Reference number: A44823; MUID:92044785; PMID:1941090
A;Accession: E44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <LOE>
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64247)
C;Keywords: membrane trafficking

Query Match 40.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
||
Db 2 ME 3

RESULT 8
S02617
alcohol dehydrogenase (EC 1.1.1.1) chi - horse (fragment)
C;Species: Equus caballus (domestic horse)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-1997
C;Accession: S02617
R;Fairwell, T.; Julia, P.; Kaiser, R.; Holmquist, B.; Pares, X.; Vallee, B.L.; Joernvall
FEBS Lett. 222, 99-103, 1987
A;Title: Acetylated N-terminal structures of class III alcohol dehydrogenases. Differenc
A;Reference number: S02617; MUID:88005160; PMID:3653405
A;Accession: S02617
A;Molecule type: protein
A;Residues: 1-6 <FAI>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
||
Db 3 EV 4

RESULT 9
B44510
hypothetical protein C (mler 3' region) - Lactococcus lactis (fragment)
C;Species: Lactococcus lactis
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
C;Accession: B44510
R;Renault, P.; Gaillardin, C.; Heslot, H.
J. Bacteriol. 171, 3108-3114, 1989

A;Title: Product of the Lactococcus lactis gene required for malolactic fermentation i;
A;Reference number: A44510; MUID:89255069; PMID:2498286

A;Accession: B44510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6 <REN>
A;Cross-references: EMBL:M90762

Query Match 40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
||
Db 1 ME 2

RESULT 10
A49792
acylaminoacyl-peptidase (EC 3.4.19.1) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: A49792
R;Krishna, R.G.; Chin, C.C.O.; Wold, F.
Anal. Biochem. 199, 45-50, 1991
A;Title: N-terminal sequence analysis of N(alpha)-acetylated proteins after unblocking
A;Reference number: A49792; MUID:92222120; PMID:1807161
A;Accession: A49792
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <KRI>
C;Keywords: acetylated amino end; hydrolase; omega peptidase
F;I/Modified site: acetylated amino end (Met) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
||
Db 1 ME 2

RESULT 11
A20186
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 05-May-2000
C;Accession: A20186
R;McCarthy, A.D.; Aitken, A.; Hardie, G.; Santikarn, S.; Williams, D.H.
FEBS Lett. 160, 296-300, 1983
A;Title: Amino acid sequence around the active serine in the acyl transferase domain o;
A;Reference number: A20186; MUID:83287768; PMID:6554204
A;Accession: A20186
A;Molecule type: protein
A;Residues: 1-6 <MCC>
C;Keywords: acyltransferase; coenzyme A

Query Match 40.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
||
Db 4 EV 5

RESULT 12
B34818
vicilin 57K chain - pigeon pea (fragment)
C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Accession: B34818

R.Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
 Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
 A>Title: Unusual denaturation properties of vicilin from Cajanus cajan.
 A:Reference number: A34818; MUID:90165956; PMID:2306256
 A:Accession: B34818
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <MAW>

Query Match 40.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 3 ME 4
 ||
 Db 4 ME 5

RESULT 13
 PQ0727
 H2 class I protein [imported] - rice (fragment)
 C:Species: Oryza sativa (rice)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: PQ0727
 R.Komatsu, S.; Kajiwara, H.; Hirano, H.
 Theor. Appl. Genet. 86, 935-942, 1993
 A>Title: A rice protein library; a data-file of rice proteins separated by two-dimension
 A:Reference number: PQ0696
 A:Accession: PQ0727
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <KOM>

Query Match 40.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 1 VV 2
 ||
 Db 5 VV 6

RESULT 14
 PT0246
 Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0246
 R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and f
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0246
 A:Molecule type: DNA
 A:Residues: 1-7 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 4 EV 5
 ||
 Db 2 EV 3

RESULT 15
 I48086
 DNA topoisomerase II alpha - Chinese hamster (fragment)
 C:Species: Cricetus griseus (Chinese hamster)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I48086

R.Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.
 J. Biol. Chem. 270, 25850-25858, 1995
 A>Title: Molecular cloning and characterization of the promoter for the Chinese hamste
 A:Reference number: I48086; MUID:96029684; PMID:7592770
 A:Accession: I48086
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-7 <RES>
 A:Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232

Query Match 40.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 3 ME 4
 ||
 Db 1 ME 2

RESULT 16
 S15597
 orf 4 rara 5'-region - human
 C:Species: Homo sapiens (man)
 C>Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
 C:Accession: S15597
 R.Brand, N.J.; Petkovich, M.; Chambon, P.
 Nucleic Acids Res. 18, 6799-6806, 1990
 A>Title: Characterization of a functional promoter for the human retinoic acid recepto
 A:Reference number: S15594; MUID:91088249; PMID:2175878
 A:Accession: S15597
 A:Molecule type: DNA
 A:Residues: 1-7 <BRA>
 A:Cross-references: EMBL:X56058; NID:g35876
 A>Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0
 C:Comment: This sequence is not thought to be translated.
 C:Genetics:
 A:Gene: GDB:RARA
 A:Cross-references: GDB:I20337; OMIM:180240
 A:Map position: 17q12-17q12

Query Match 40.0%; Score 2; DB 4; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 1 VV 2
 ||
 Db 6 VV 7

RESULT 17
 S16324
 hypothetical protein 2 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jul-2000
 C:Accession: S16324
 R.Ruberti, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
 EMBO J. 10, 1787-1791, 1991
 A>Title: A novel class of plant proteins containing a homeodomain with a closely linke
 A:Reference number: S16323; MUID:91266907; PMID:1675603
 A:Accession: S16324
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <RUB>
 A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 40.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

QY 3 ME 4
 ||
 Db 1 ME 2

RESULT 18

A21440
variant surface glycoprotein pSLc1 - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Mar-1998
C;Accession: A21440
R;Parsons, M.; Nelson, R.G.; Watkins, K.P.; Agabian, N.
Cell 38, 309-316, 1984
A;Title: Trypanosome mRNAs share a common 5' spliced leader sequence.
A;Reference number: A90853; MUID:84282716; PMID:6088073
A;Accession: A21440
A;Molecule type: mRNA
A;Residues: 1-8 <PAR>
A;Cross-references: GB:K02195; NID:g162150; PID:g162151
C;Keywords: glycoprotein

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
Db 5 EV 6

RESULT 19

G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: G33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Accession: G33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <NIC>

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
Db 7 VV 8

RESULT 20

A05169
neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C;Accession: A05169
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.I.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry
A;Reference number: A90118; MUID:85046530; PMID:6548628
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Keywords: neuropeptide

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
Db 1 EV 2

RESULT 21

PT0298
Ig heavy chain CRD3 region (clone 5-103A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0298
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0298
A;Molecule type: DNA
A;Residues: 1-8 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
Db 4 VV 5

RESULT 22

A54823
olfactory receptor 17 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C;Accession: A54823
R;Chess, A.; Simon, I.; Cedar, H.; Axel, R.
Cell 78, 823-834, 1994
A;Title: Allelic inactivation regulates olfactory receptor gene expression.
A;Reference number: A54823; MUID:94373818; PMID:8087849
A;Accession: A54823
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-8 <CHE>

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
||
Db 1 ME 2

RESULT 23

A35768
T-cell receptor alpha chain V-J region (34S-281) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 30-May-1997
C;Accession: A35768
R;Koseki, H.; Imai, K.; Nakayama, F.; Sado, T.; Moriuchi, K.; Taniguchi, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5248-5252, 1990
A;Title: Homogenous junctional sequence of the V14+ T-cell antigen receptor alpha chain
A;Reference number: A35768; MUID:90319089; PMID:2371269
A;Accession: A35768
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-8 <KOS>
A;Note: the sequence shown follows the authors' translation at position 1 of TGT
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
Db 2 VV 3

RESULT 24
B54823
Olfactory receptor I7 - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54823
R:Ches, A.; Simon, I.; Cedar, H.; Axel, R.
Cell 78, 823-834, 1994
A>Title: Allelic inactivation regulates olfactory receptor gene expression.
A:Reference number: A54823; MUID:94373818; PMID:8087849
A:Accession: B54823
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <CHE>

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
||
Db 1 ME 2

RESULT 25
I49404
prealbumin - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49404
R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A>Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: I48934; MUID:94319082; PMID:8043949
A:Accession: I49404
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: EMBL:U05689; NID:G497008; PIDN:ARB60461.1; PID:G642825

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
Db 2 VV 3

RESULT 26
I57532
gene TnIslow protein - rat (fragment)
C:Species: Rattus sp. (rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C:Accession: I57532
R:Banerjee-Basu, S.; Buonanno, A.
Mol. Cell. Biol. 13, 7019-7028, 1993
A>Title: cis-acting sequences of the rat troponin I slow gene confer tissue- and develop
A:Reference number: I57532; MUID:94019373; PMID:8413291
A:Accession: I57532
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: GB:S66172; NID:G432603
C:Genetics:
A:Gene: TnIslow

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
Db 3 EV 4

RESULT 27
B47594
aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)
C:Species: Corynebacterium flavum
C>Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 19-Dec-1997
C:Accession: B47594
R:Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinsky, A.J.
J. Bacteriol. 175, 4096-4103, 1993
A>Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd opero
A:Reference number: A47594; MUID:93308089; PMID:8100567
A:Accession: B47594
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-8 <FOL>
C:Keywords: phosphotransferase

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
||
Db 1 ME 2

RESULT 28
D24180
fibrinogen beta chain - red guenon (fragment)
N:Contains: fibrinopeptide B
C:Species: Brythrocebus patas (red guenon, hussar)
C>Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C:Accession: D24180
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A>Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey
uenons, and baboons.
A:Reference number: A91990; MUID:85289140; PMID:3928610
A:Accession: D24180
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disul

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
Db 3 EV 4

RESULT 29
PA0033
protein QA300033 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0033
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JPIID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensio
A:Reference number: PA0001
A:Accession: PA0033
A:Molecule type: protein
A:Residues: 1-9 <KAM>
A:Experimental source: leaf

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
8 VV 9

Db

RESULT 30

D48186

ATPase R1 subunit - wood tobacco (fragment)

C;Species: Nicotiana sylvestris (wood tobacco)

C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 23-Feb-1997

C;Accession: D48186

R;De Paeppe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.

Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993

A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP synthase

A;Reference number: A48186; MUID:93317598; PMID:8327463

A;Accession: D48186

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <DEI>

A;Experimental source: pollen

A;Note: sequence extracted from NCBI backbone (NCBIP:134871)

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
2 VV 3

Db

RESULT 31

S70345

amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragments)

C;Species: Aspergillus niger

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C;Accession: S70345

R;Rebort, I.; Pec, P.; Luhova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.

Biochim. Biophys. Acta 1295, 59-72, 1996

A;Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the

A;Reference number: S70344; MUID:96283794; PMID:8679675

A;Accession: S70345

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5;6-9 <FRE>

C;Keywords: oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
1 VV 2

Db

RESULT 32

AS6029

N-methylpurine DNA glycosylase - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 19-Jan-1996

C;Accession: A56029

R;Roy, R.; Brooks, C.; Mitra, S.

Biochemistry 33, 15131-15140, 1994

A;Title: Purification and biochemical characterization of recombinant N-methylpurine-DNA

A;Reference number: A56029; MUID:95092772; PMID:7999773

A;Accession: A56029

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <ROY>

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
4 EV 5

Db

RESULT 33

S39392

calpain (EC 3.4.22.17) II light chain - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 18-Feb-1994 #sequence_revision 24-Jul-1998 #text_change 29-Sep-1999

C;Accession: S39392

R;Crawford, C.; Brown, N.R.; Willis, A.C.

Biochem. J. 296, 135-142, 1993

A;Title: Studies of the active site of m-calpain and the interaction with calpastatin.

A;Reference number: S39391; MUID:94071815; PMID:8250833

A;Accession: S39392

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <CEA>

C;Superfamily: calpain small chain; calmodulin repeat homology

C;Keywords: cysteine proteinase; EF hand; hydrolase

Query Match 40.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
6 EV 7

Db

RESULT 34

JC1367

thyroliberin potentiating neuropeptide - bovine

N;Alternate names: thyrotropin-releasing hormone potentiating peptide; TRH-potentiating

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1997

C;Accession: JC1367

R;Rulant, M.; Ladram, A.; Montagne, J.J.; Delfour, A.; Nicolas, P.

Biochem. Biophys. Res. Commun. 189, 1110-1118, 1992

A;Title: Isolation and amino acid sequence of the TRH-potentiating peptide from bovine

A;Reference number: JC1367; MUID:93111999; PMID:1472021

A;Accession: JC1367

A;Molecule type: protein

A;Residues: 1-10 <BUL>

A;Experimental source: hypothalamus

C;Comment: This neuropeptide corresponds to a region of the rat thyroliberin precursor

C;Function:

A;Description: potentiates thyroliberin-induced thyrotropin secretion

C;Superfamily: thyroliberin precursor

C;Keywords: hypothalamus; neuropeptide

Query Match 40.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
||
5 ME 6

Db

RESULT 35

A47593

mercury resistance regulatory protein merR - Pseudomonas aeruginosa transposon Tn501 (f

C;Species: Pseudomonas aeruginosa

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Aug-1998

C;Accession: A47593

R;O'Halloran, T.; Walsh, C.

Science 235, 211-214, 1987

A:Title: Metalloregulatory DNA-binding protein encoded by the merR gene: isolation and d
 A:Reference number: A47593; MUID:87094195; PMID:3798107

A:Accession: A47593
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <OAH>
 C:Superfamily: transcription repressor glnr

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
 ||
 1 ME 2

RESULT 36

JQ0943
 hypothetical 1.3K protein - infectious bursal disease virus (strain 52/70)
 C:Species: Infectious bursal disease virus
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 08-Oct-1999
 A:Accession: JQ0943
 R:Bayliss, C.D.; Spies, U.; Shaw, K.; Peters, R.W.; Papageorgiou, A.; Mueller, H.; Bours
 J. Gen. Virol. 71, 1303-1312, 1990
 A:Title: A comparison of the sequences of segment A of four infectious bursal disease vi
 A:Reference number: JQ0941; MUID:90278420; PMID:2161902
 A:Accession: JQ0943
 A:Status: translation not shown
 A:Molecule type: genomic RNA
 A:Residues: 1-10 <BAY>
 A:Cross-references: GB:D00869; NID:g221038; PIDN:BAA00743.1; PID:d1001203; PID:g221039

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
 ||
 1 ME 2

RESULT 37

B39517
 probable methionine-tRNA ligase attenuator peptide - Thermus aquaticus
 C:Species: Thermus aquaticus
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 18-Jun-1993
 A:Accession: B39517
 R:Nureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, T
 J. Biol. Chem. 266, 3268-3277, 1991
 A:Title: Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus thermophilu
 esis.
 A:Reference number: A39517; MUID:91131636; PMID:1993699
 A:Accession: B39517
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-10 <NUR>
 A:Cross-references: GB:J05744

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
 ||
 1 ME 2

RESULT 38

C35389
 urease (EC 3.5.1.5) 6K chain - Morganella morganii (fragment)
 C:Species: Morganella morganii
 C:Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 23-Jun-1993

C:Accession: C35389

R:Hu, L.T.; Nicholson, E.B.; Jones, B.D.; Lynch, M.J.; Mobley, H.L.T.
 J. Bacteriol. 172, 3073-3080, 1990

A:Title: Morganella morganii urease: purification, characterization, and isolation of
 A:Reference number: A35389; MUID:90264298; PMID:2345135

A:Accession: C35389

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-10 <HUA>

C:Keywords: hydrolase

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
 ||
 7 EV 8

RESULT 39

JN0440
 peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) - sweet almond
 N:Alternate names: glycopeptidase
 C:Species: Prunus dulcis var. sativa (sweet almond)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
 A:Accession: JN0440
 R:Kaliberda, E.I.; Shemyakin, V.V.; Antonov, V.K.
 Bioorg. Khim. 16, 751-757, 1990

A:Title: Purification of sweet almond glycopeptidase and sequencing of N-terminal prot
 A:Reference number: JN0440
 A:Accession: JN0440

A:Molecule type: protein

A:Residues: 1-10 <KAL>

C:Keywords: hydrolase

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
 ||
 5 VV 6

RESULT 40

PS0209
 24K protein 4407 - rice (strain Nihonbare) (fragment)
 C:Species: Oryza sativa (rice)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
 A:Accession: PS0209
 R:Tsuigita, A.; Kamo, M.
 submitted to JIPID, April 1993

A:Reference number: PS0209

A:Accession: PS0209

A:Molecule type: protein

A:Residues: 1-10 <TSU>

A:Experimental source: callus

C:Comment: molecular weight 24K, pI 4.6.

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
 ||
 4 EV 5

RESULT 41

S19296
 16K protein - poulard wheat
 C:Species: Triticum turgidum (poulard wheat)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
 C;Accession: S19296
 R;Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.
 Biochem. J. 281, 401-405, 1992
 A;Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subunit
 A;Reference number: S19296; MUID:92143804; PMID:1736890
 A;Accession: S19296
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <SAN>

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
 Db 9 ME 10

RESULT 42
 A43977
 PMRFamide-like protein - tobacco hornworm
 C;Species: Manduca sexta (tobacco hornworm)
 C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 17-Mar-1999
 C;Accession: A43977
 R;Kingsan, T.G.; Teplow, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.;
 Peptides 11, 849-856, 1990
 A;Title: A new peptide in the PMRFamide family isolated from the CNS of the hawkmoth, Ma
 A;Reference number: A43977; MUID:91045350; PMID:2235684
 A;Accession: A43977
 A;Molecule type: protein
 A;Residues: 1-10 <KIN>
 A;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
 Db 3 VW 4

RESULT 43
 C39111
 Ig heavy chain C region - Pacific hagfish (fragment)
 C;Species: Eptatretus stoutii (Pacific hagfish)
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
 C;Accession: C39111
 R;Varner, J.; Neame, P.; Litman, G.W.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
 A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil
 A;Reference number: A39111; MUID:91156684; PMID:2000382
 A;Accession: C39111
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <VAR>
 C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
 Db 9 VW 10

RESULT 44
 B56899

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
 C;Accession: S19296
 R;Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.
 Biochem. J. 281, 401-405, 1992
 A;Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subunit
 A;Reference number: S19296; MUID:92143804; PMID:1736890
 A;Accession: S19296
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <SAN>

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
 Db 9 ME 10

RESULT 42
 A43977
 PMRFamide-like protein - tobacco hornworm
 C;Species: Manduca sexta (tobacco hornworm)
 C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 17-Mar-1999
 C;Accession: A43977
 R;Kingsan, T.G.; Teplow, D.B.; Phillips, J.M.; Riehm, J.P.; Rao, K.R.; Hildebrand, J.G.;
 Peptides 11, 849-856, 1990
 A;Title: A new peptide in the PMRFamide family isolated from the CNS of the hawkmoth, Ma
 A;Reference number: A43977; MUID:91045350; PMID:2235684
 A;Accession: A43977
 A;Molecule type: protein
 A;Residues: 1-10 <KIN>
 A;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
 Db 3 VW 4

RESULT 43
 C39111
 Ig heavy chain C region - Pacific hagfish (fragment)
 C;Species: Eptatretus stoutii (Pacific hagfish)
 C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
 C;Accession: C39111
 R;Varner, J.; Neame, P.; Litman, G.W.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
 A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil
 A;Reference number: A39111; MUID:91156684; PMID:2000382
 A;Accession: C39111
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <VAR>
 C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
 Db 9 VW 10

RESULT 44
 B56899

serum heterodimer, 24K chain - sandbar shark (fragment)
 C;Species: Carcharhinus plumbeus (sandbar shark)
 C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
 C;Accession: B56899
 R;Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.
 Comp. Biochem. Physiol. B 103, 563-569, 1992
 A;Title: Purification of a novel heterodimer from shark (Carcharhinus plumbeus) serum
 A;Reference number: A56899; MUID:93092592; PMID:1458832
 A;Accession: B56899
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <VAZ>
 C;Keywords: glycoprotein; plasma

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
 Db 1 VW 2

RESULT 45
 S77980
 Cytochrome-c oxidase (EC 1.9.3.1) chain IV - bigeye tuna (fragment)
 C;Species: Thunnus obesus (bigeye tuna)
 C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
 C;Accession: S77980
 R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
 Submitted to the Protein Sequence Database, June 1997
 A;Reference number: S77980
 A;Accession: S77980
 A;Molecule type: protein
 A;Residues: 1-10 <ARN>
 A;Experimental source: heart; liver
 C;Genetics:
 A;Genome: nuclear
 C;Function:
 A;Pathway: oxidative phosphorylation; respiratory chain
 C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
 Db 6 EV 7

RESULT 46
 B45482
 platelet activating factor acetylhydrolase - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 05-May-1995
 C;Accession: B45482
 R;Stafforini, D.M.; Rollins, E.N.; Prescott, S.M.; McIntyre, T.M.
 J. Biol. Chem. 268, 3857-3865, 1993
 A;Title: The platelet-activating factor acetylhydrolase from human erythrocytes. Purifi
 A;Reference number: A45482; MUID:93179380; PMID:8440861
 A;Accession: B45482
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-10 <STA>

Query Match 40.0%; Score 2; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
 Db 4 VW 5

RESULT 47

E49033
T-cell receptor gamma chain V-D-J region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
C:Accession: E49033; D49033
R:Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991

A:Title: Functionally distinct subsets of human gamma/delta T cells.

A:Reference number: A49033; MUID:92083926; PMID:1684157

A:Accession: E49033

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-10 <MOR>

A:Cross-references: GB:S7587; NID:G240696; PIDN:AAB20630.1; PID:G240697

A>Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)

A:Accession: D49033

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-10 <MOR2>

A:Cross-references: GB:S7587; NID:G240696; PIDN:AAB20630.1; PID:G240697

A>Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)

C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5

||

5 EV 6

RESULT 48

S71948
matrix metalloproteinase 3 precursor - bovine (fragments)
N:Alternate names: MMP-3 protein; stromelysin precursor MMP-3
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S71948
R:Arner, E.C.; Pratta, M.A.; Freimark, B.; Lischke, M.; Trzaskos, J.M.; Magolda, R.L.; W
Biochem. J. 318, 417-424, 1996
A:Title: Isothiazolones interfere with normal matrix metalloproteinase activation and in
A:Reference number: S71948; MUID:96404887; PMID:8809028

A:Accession: S71948

A:Molecule type: protein

A:Residues: 1-5; 6-10 <ARN>

C:Function:

A:Description: degrades a wide range of extracellular matrix components, including carti
A>Note: may be involved in arthritis formation

Query Match 40.0%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VM 3

||

1 VM 2

RESULT 49

S36849
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C:Accession: S36849
R:Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
A:Reference number: S25024
A:Accession: S36849

A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-10 <UAC>
C:Cross-references: EMBL:X67382; NID:G50070; PIDN:CAA47794.1; PID:es1590; PID:g1333861
C:Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2

||

6 VW 7

RESULT 50

E86128
hypothetical protein Z5903 [imported] - Escherichia coli (strain O157:H7, substrain ED)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E86128
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E86128

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-10 <STO>

A:Cross-references: GB:AE005174; NID:gl2519314; PIDN:AGS59489.1; GSPDB:GN00145; UWGP:Z

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z5903

Query Match 40.0%; Score 2; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 7.9e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2

||

7 VW 8

RESULT 51

S68392
H+-transporting two-sector ATPase (EC 3.6.3.14) chain I - Chlamydomonas reinhardtii ch
N:Alternate names: ATP synthase chain I
C:Species: chloroplast Chlamydomonas reinhardtii
C>Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 03-Jun-2002
C:Accession: S68392

R:Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.

FEBS Lett. 377, 163-166, 1995

A:Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-termina
A:Reference number: S68388; MUID:96128220; PMID:8543042

A:Accession: S68392

A:Molecule type: protein

A:Residues: 1-11 <FIE>

A:Experimental source: strain CW15

C:Genetics:

A:Genome: chloroplast

C:Superfamily: H+-transporting ATP synthase protein 6

C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; thy

Query Match 40.0%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5

||

1 EV 2

RESULT 52

A40693
transgelin - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997
C:Accession: A40693
R:Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.
J. Cell Biol. 121, 1065-1073, 1993
A:Title: Purification and properties of transgelin: a transformation and shape change sensitive protein
A:Reference number: A40693; MUID:93273790; PMID:8501116
A:Accession: A40693
A:Molecule type: protein
A:Residues: 1-11 <SHA>
A:Experimental source: aorta
C:Comment: This protein gets actin and is down regulated by transformation or loss of cell
C:Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein
C:Keywords: actin binding; cytoskeleton

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
Db 10 EV 11

RESULT 53

A57458
gene Gax protein - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999
C:Accession: A57458
R:Andres, V.; Fisher, S.; Wearsch, P.; Walsh, K.
Mol. Cell. Biol. 15, 4272-4281, 1995
A:Title: Regulation of Gax homeobox gene transcription by a combination of positive factors
A:Reference number: A57458; MUID:95349593; PMID:7623821
A:Accession: A57458
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:S79168; NID:g1050991
C:Genetics: Gax
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
||
Db 1 ME 2

RESULT 54

A55149
tetragenomycin A2 oxygenase (EC 1.-.-.-) - Streptomyces glaucescens (fragment)
N:Alternate names: tcmA2 oxygenase; tcmG
C:Species: Streptomyces glaucescens
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Mar-1996
C:Accession: A55149
R:Shen, B.; Hutchinson, C.R.
J. Biol. Chem. 269, 30726-30733, 1994
A:Title: Triple hydroxylation of tetragenomycin A2 to tetragenomycin C in Streptomyces glaucescens
A:Reference number: A55149; MUID:95074090; PMID:7982994
A:Accession: A55149
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <SHE>
C:Genetics:

A:Start codon: TTG
C:Keywords: antibiotic biosynthesis; PAD; monomer; oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
Db 5 EV 6

RESULT 55

S33519
probable secreted protein - Acholeplasma laidlawii (fragment)
C:Species: Acholeplasma laidlawii
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999
C:Accession: S33519
R:Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.
submitted to the EMBL data library, June 1993
A:Description: Sequence regions from Acholeplasma laidlawii which restore export of bet
A:Reference number: S33518
A:Accession: S33519
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <BOY>
A:Cross-references: EMBL:222875; NID:g311706; PIDN:CAA80495.1; PID:g311708

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
||
Db 6 VM 7

RESULT 56

H54346
pyruvate synthase (EC 1.2.7.1) alpha chain - Pyrococcus furiosus (fragment)
C:Species: Pyrococcus furiosus
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-May-2000
C:Accession: H54346
R:Blamey, J.M.; Adams, M.W.
Biochemistry 33, 1000-1007, 1994
A:Title: Characterization of an ancestral type of pyruvate ferredoxin oxidoreductase fr
A:Reference number: A54346; MUID:94137707; PMID:8305426
A:Accession: H54346
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <BLA>
C:Keywords: coenzyme A; oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
||
Db 2 VM 3

RESULT 57

PQ0731
unidentified 5.7/35k protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0731
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimensi
A:Reference number: PQ0696
A:Accession: PQ0731

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <KOM>

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 3 VV 4

RESULT 58

PC2173

triacylglycerol lipase (EC 3.1.1.3) II - Rhizopus niveus (strain IFO 4759) (fragments)

C:Species: Rhizopus niveus
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C:Accession: PC2173

R:Kohno, M.; Kugimiya, W.; Hashimoto, Y.; Morita, Y.

A:Title: Purification, characterization, and crystallization of two types of lipase from
A:Reference number: PC2171; MUID:94319059; PMID:7765029
A:Accession: PC2173

A:Molecule type: protein

A:Residues: 1-10;11 <KOH>

C:Comment: This enzyme catalyzes the hydrolysis of the ester bonds of triacylglycerols a
C:Comment: This enzyme is produced from lipase I by limited proteolysis due to the actio
C:Keywords: carboxylic ester hydrolase

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 6 VV 7

RESULT 59

S45698

gamma-MSH-like protein - duck leech

C:Species: Theromyzon tessulatatum (duck leech)

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C:Accession: S45698

R:Salzet, M.; Watter, C.; Bulet, P.; Malecha, J.

FEBS Lett. 348, 102-106, 1994

A:Title: Isolation and structural characterization of a novel peptide related to gamma-m
A:Reference number: S45698; MUID:94298944; PMID:8026574
A:Accession: S45698

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <SAL>

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
DB 2 VM 3

RESULT 60

I52980

glucocerebrosidase - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52980; I55971

R:Reiner, O.; Wigderson, M.; Horowitz, M.

DNA 7, 107-116, 1988

A:Title: Structural analysis of the human glucocerebrosidase genes.

A:Reference number: I52980; MUID:88195776; PMID:3359914

A:Accession: I52980

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <RES>

A:Cross-references: GB:M18916; NID:g183023; PIDN:AAA35878.1; PID:g183024

A:Accession: I55971

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-11 <RE2>

A:Cross-references: GB:M18917; NID:g183025; PIDN:AAA35879.1; PID:g183026

Query Match

40.0%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4

DB 1 ME 2

RESULT 61

S23364

T-cell receptor alpha chain J region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S23364

R:Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichm

Eur. J. Immunol. 21, 2749-2754, 1991

A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rh

A:Reference number: S23364; MUID:92037820; PMID:1657615

A:Accession: S23364

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-11 <PLU>

A:Cross-references: EMBL:X58164

C:Keywords: T-cell receptor

Query Match

40.0%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2

DB 1 VV 2

RESULT 62

S09024

carboxylesterase (EC 3.1.1.1), microsomal - golden hamster (fragment)

C:Species: Mesocricetus auratus (golden hamster)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Apr-1993
C:Accession: S09024

R:Hosokawa, M.; Maki, T.; Satoh, T.

Arch. Biochem. Biophys. 277, 219-227, 1990

A:Title: Characterization of molecular species of liver microsomal carboxylesterases o

A:Reference number: S09021; MUID:90179180; PMID:2310190

A:Accession: S09024

A:Molecule type: protein

A:Residues: 1-11 <HOS>

C:Keywords: carboxylic ester hydrolase

Query Match

40.0%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2

DB 7 VV 8

RESULT 63

PH0891

T-cell receptor beta chain V-D-J region (clone 6-1) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0891
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0891
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
10 EV 11

Db

RESULT 64
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
||
9 ME 10

Db

RESULT 65
PH0922
T-cell receptor beta chain V-D-J region (isolate 8) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0922
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0922
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
||
6 VM 7

Db

RESULT 66

I52708
ELAV-like neuronal protein 1, truncated splice form - human
N;Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: I52708
R;Skidto, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
Cancer Res. 54, 4988-4992, 1994
A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelitis
A;Reference number: I52708; MUID:94349312; PMID:8069866
A;Accession: I52708
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-11 <SEK>
A;Cross-references: GB:573887; NID:G688242; PIDN:AA14142.1; PID:94261842
C;Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726
C;Genetics:
A;Gene: GDB:ELAVL4; HUD; PNEM
A;Cross-references: GDB:I41875; OMIM:168360
A;Map position: lp36-lp36
C;Keywords: alternative splicing

Query Match 40.0%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
||
2 VM 3

Db

RESULT 67
S09082
proteasome chain 1 - rat (fragment)
N;Alternate names: multicatalytic proteinase chain 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998
C;Accession: S09082
R;Lilley, K.S.; Davison, M.D.; Rivett, A.J.
FEBS Lett. 262, 327-329, 1990
A;Title: N-terminal sequence similarities between components of the multicatalytic prot
A;Reference number: S09082; MUID:90242957; PMID:2335214
A;Accession: S09082
A;Molecule type: protein
A;Residues: 1-12 <LIL>
C;Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 40.0%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
6 VV 7

Db

RESULT 68
S26558
T-cell receptor beta chain (clone Cw3/5B8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C;Accession: S26558
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recept
A;Reference number: S26558; MUID:92364546; PMID:1380061
A;Accession: S26558
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Cross-references: EMBL:X68008
A;Experimental source: cytolytic T-lymphocyte, clone Cw3/5B8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
 ||
 Db 7 VM 8

RESULT 69
 S26559
 T-cell receptor beta chain (clone Cw3/Cas15) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C:Accession: S26559
 R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
 A:Reference number: S26512; MUID:92364546; PMID:1380061
 A:Accession: S26559
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>
 A:Cross-references: EXBL:X68009
 A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas15
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
 ||
 Db 8 EV 9

RESULT 70
 A39233
 myosin heavy chain 1, smooth muscle - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 13-Feb-1998
 C:Accession: A39233
 R:Kelley, C.A.; Adelstein, R.S.
 J. Biol. Chem. 265, 17876-17882, 1990
 A:Title: The 204-kDa smooth muscle myosin heavy chain is phosphorylated in intact cells
 A:Reference number: A39233; MUID:91009254; PMID:2170399
 A:Accession: A39233
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <REL>
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: smooth muscle

Query Match 40.0%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
 ||
 Db 11 EV 12

RESULT 71
 S65629
 protoporphyrinogen oxidase (EC 1.3.3.4) - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-May-2000
 C:Accession: S65629
 R:Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.; Ino
 Eur. J. Biochem. 230, 760-765, 1995
 A:Title: Induction of terminal enzymes for heme biosynthesis during differentiation of m
 A:Reference number: S65629; MUID:9533315; PMID:7607249

A:Accession: S65629
 A:Molecule type: protein
 A:Residues: 1-12 <TAK>
 C:Genetics:
 A:Genome: nuclear
 C:Function:
 A:Pathway: heme biosynthesis; porphyrin biosynthesis
 C:Superfamily: phytylene dehydrogenase
 C:Keywords: heme biosynthesis; mitochondrion; oxidoreductase; porphyrin biosynthesis

Query Match 40.0%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
 ||
 Db 4 VW 5

RESULT 72
 S69123
 proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
 C:Species: Rhodospirillum rubrum
 C:Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
 C:Accession: S69123
 R:Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
 Eur. J. Biochem. 228, 719-726, 1995
 A:Title: Properties of the soluble polypeptide of the proton-translocating transhydrog
 A:Reference number: S69123; MUID:9525277; PMID:7737169
 A:Accession: S69123
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <DIG>

Query Match 40.0%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
 ||
 Db 4 VW 5

RESULT 73
 S36899
 ribosomal protein S6 - Mycobacterium bovis (fragment)
 C:Species: Mycobacterium bovis
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C:Accession: S36899
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycob.
 A:Reference number: S36887; MUID:94009653; PMID:8405418
 A:Accession: S36899
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <OHA>
 C:Keywords: protein biosynthesis; ribosome

Query Match 40.0%; Score 2; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
 ||
 Db 8 VW 9

RESULT 74
 S52561
 S-enolpyruvylshikimate-3-phosphate - Euglena gracilis
 C:Species: Euglena gracilis
 C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 01-Sep-1995

C;Accession: S52561
R;Reinbothe, C.; Ortel, B.; Parthier, B.; Reinbothe, S.
Mol. Gen. Genet. 245, 616-622, 1994
A;Title: Cytosolic and plastid forms of 5-enolpyruvylshikimate-3-phosphate synthase in E
A;Reference number: S52561; MUID:95107260; PMID:7808412
A;Accession: S52561
A;Status: preliminary
A;Molecule type: Protein
A;Residues: 1-12 <RE1>

Query Match 40.0%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred.No. 9.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
||
Db 10 VV 11

RESULT 75
PA0019
acidic ribosomal P2-like protein - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 11-Apr-1995
C;Accession: PA0019
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
Submitted to JIPB, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A;Reference number: PA0001
A;Accession: PA0019
A;Molecule type: protein
A;Residues: 1-12 <KAM>
A;Experimental source: callus

Query Match 40.0%; Score 2; DB 2; Length 12;
Best Local Similarity 100.0%; Pred.No. 9.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
||
Db 3 VV 4

Search completed: November 25, 2003, 18:28:20
Job time : 5.60106 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 2.42021 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-9
Perfect score: 5
Sequence: 1 VMEV 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3	60.0	15	1	MCRA_METTE
2	3	60.0	19	1	PSBM_SYNJU
3	3	60.0	20	1	DNAX_CLOPA
4	3	60.0	20	1	DNAX_THIFE
5	2	40.0	5	1	UC22_MAIZE
6	2	40.0	6	1	ACPH_RABIT
7	2	40.0	8	1	CPD1_ENTFA
8	2	40.0	8	1	NS3_MYCTU
9	2	40.0	8	1	WPI_PBRAT
10	2	40.0	9	1	FIBB_ERYPA
11	2	40.0	9	1	UF02_MOUSE
12	2	40.0	10	1	FARP_MANSE
13	2	40.0	10	1	RT02_BOVIN
14	2	40.0	10	1	URE3_MORMO
15	2	40.0	11	1	MLG_THETS
16	2	40.0	11	1	PVK1_PERAM
17	2	40.0	12	1	HCVB_MEGCR
18	2	40.0	12	1	HS9A_RAT
19	2	40.0	12	1	NO40_SOYBN
20	2	40.0	12	1	PORD_METTM
21	2	40.0	12	1	UN39_CLOPA
22	2	40.0	12	1	UP01_CAEEL
23	2	40.0	12	1	V23K_WSSV
24	2	40.0	12	1	V2SK_WSSV
25	2	40.0	13	1	FIBB_RABIT
26	2	40.0	13	1	IDRA_CANFA
27	2	40.0	13	1	IDHP_RAT
28	2	40.0	13	1	MLA_ANOCA
29	2	40.0	13	1	MLA_CAMDR
30	2	40.0	13	1	PED1_HYDAT
31	2	40.0	13	1	UN41_CLOPA
32	2	40.0	13	1	UP71_LITWE
33	2	40.0	14	1	ADFA_TENNO

34	2	40.0	14	1	GR75_CANFA
35	2	40.0	14	1	IF2G_RAT
36	2	40.0	14	1	KLPS_SCARA
37	2	40.0	14	1	KPPI_SELMI
38	2	40.0	14	1	PKP1_PRUSE
39	2	40.0	14	1	PKK6_PPRAM
40	2	40.0	14	1	UC15_MAIZE
41	2	40.0	14	1	UN04_CLOPA
42	2	40.0	15	1	CDN2_LITGI
43	2	40.0	15	1	CDN4_LITCE
44	2	40.0	15	1	COXI_THUOB
45	2	40.0	15	1	EF1A_MICCR
46	2	40.0	15	1	ESTB_SCHGA
47	2	40.0	15	1	ESTU_MANSE
48	2	40.0	15	1	FKB7_PINPS
49	2	40.0	15	1	GR78_HORSE
50	2	40.0	15	1	KPP2_SELMI
51	2	40.0	15	1	MALT_BACTQ
52	2	40.0	15	1	MAOX_CHICK
53	2	40.0	15	1	NXSO_PSETE
54	2	40.0	15	1	PGTS_PRUSE
55	2	40.0	15	1	PH3_PRUSE
56	2	40.0	15	1	R13A_SPIOL
57	2	40.0	15	1	RKGG_CARCR
58	2	40.0	15	1	RML2_YEAST
59	2	40.0	15	1	THL_CLOPA
60	2	40.0	15	1	UBLI_MONDO
61	2	40.0	15	1	UC08_MAIZE
62	2	40.0	15	1	UC16_MAIZE
63	2	40.0	15	1	UP01_METAM
64	2	40.0	15	1	VORA_METTM
65	2	40.0	16	1	AU21_LITRA
66	2	40.0	16	1	AU22_LITAU
67	2	40.0	16	1	AU23_LITAU
68	2	40.0	16	1	AU24_LITAU
69	2	40.0	16	1	AU25_LITRA
70	2	40.0	16	1	CT12_LITCI
71	2	40.0	16	1	DHE2_THUTH
72	2	40.0	16	1	HTPG_ACICA
73	2	40.0	16	1	LE05_BIOGL
74	2	40.0	16	1	PGTL_PELAC
75	2	40.0	16	1	PH2_PRUSE
76	2	40.0	17	1	B29K_PORGI
77	2	40.0	17	1	EFG_THEAQ
78	2	40.0	17	1	FIBA_PIG
79	2	40.0	17	1	GAST_MACMU
80	2	40.0	17	1	ITHB_HIRME
81	2	40.0	17	1	LCK_RAT
82	2	40.0	17	1	LPW_AZOBR
83	2	40.0	17	1	NEP_HV1J3
84	2	40.0	17	1	PSBL_SYNJU
85	2	40.0	17	1	SP51_BACLI
86	2	40.0	17	1	UN15_CLOPA
87	2	40.0	17	1	UP31_UPEIN
88	2	40.0	17	1	UP32_UPEIN
89	2	40.0	17	1	UP33_UPEIN
90	2	40.0	17	1	UP36_UPEMJ
91	2	40.0	17	1	UP37_UPEMJ
92	2	40.0	17	1	UP41_UPEIN
93	2	40.0	17	1	YALA_TRYBB
94	2	40.0	18	1	AROF_STRBM
95	2	40.0	18	1	CT1C_LITCI
96	2	40.0	18	1	CT1D_LITCI
97	2	40.0	18	1	DRPH_PANBO
98	2	40.0	18	1	DRPH_UCAPU
99	2	40.0	18	1	FIXA_RHILE
100	2	40.0	18	1	HEX_ADECU

ALIGNMENTS

RESULT 1

```

MCRA, METTE
ID MCRA_METTE STANDARD; PRT; 15 AA.
AC P22948;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase alpha subunit (EC 2.8.4.1) (Coenzyme-B
DE sulfothioltransferase alpha) (Fragment).
OS Methanosarcina thermophila.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2210;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 1825 / TM-1;
RX MEDLINE=91193204; PubMed=2013570;
RA Jablonski P.E., Ferry J.G.;
RT "Purification and properties of methyl coenzyme M methylreductase
RT from acetate-grown Methanosarcina thermophila.";
RL J. Bacteriol. 173:2481-2487(1991).
CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
CC ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
CC to methane and an heterodisulfide.
CC -!- CATALYTIC ACTIVITY: 2-(methylthio)ethanesulfonate (methyl-CoM) +
CC N-(7-mercaptoheptanoyl)threonine 3-O-phosphate (coenzyme B) = CoM-
CC S-S-CoB + methane.
CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.
CC Coenzyme F430 is a yellow nickel porphyrinoid (By similarity).
CC -!- PATHWAY: Methanogenesis; last step.
CC -!- SUBUNIT: TRIMER OF AN ALPHA, A BETA, AND A GAMMA SUBUNIT.
CC -!- MISCELLANEOUS: THE OPTIMAL TEMPERATURE FOR ENZYME ACTIVITY IS 60
CC DEGREES CELSIUS.
CC -!- ENZYME.
KW Methanogenesis; Transferase; Nickel.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1686 MW; DS059892FCA5F63C CRC64;

Query Match 60.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 12 MEV 14

RESULT 2
PSEB_SYNVU
ID PSEB_SYNVU STANDARD; PRT; 19 AA.
AC P12312;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem II reaction center M protein (PSII-M) (Fragment).
GN PSBM.
OS Synechococcus vulcanus (Thermosynechococcus vulcanus).
OC Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
OX NCBI_TaxID=32053;
RN [1]
RP SEQUENCE.
RX MEDLINE=89338735; PubMed=2503398;
RA Ikeuchi M., Koike H., Inoue Y.;
RT "N-terminal sequencing of low-molecular-mass components in
RT cyanobacterial photosystem II core complex. Two components correspond
RT to unidentified open reading frames of plant chloroplast DNA.";
RL FEBS Lett. 253:178-182(1989).
CC -!- FUNCTION: NOT KNOWN.
CC -!- SIMILARITY: Belongs to the psbm family.
DR HAMAP; MF 00438; -; 1.
DR Pfam; PF05151; Psbm; 1.
KW Photosystem II; Transmembrane.
FT MOD_RES 1 1
MOD_RES 1 1 BLOCKED.

```

```

FT TRANSMEM 5 >19 POTENTIAL.
SQ NON_TER 19 19
SQ SEQUENCE 19 AA; 2049 MW; 339319BD8B0CFF24 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 3
DNAK_CLOPA
ID DNAK_CLOPA STANDARD; PRT; 20 AA.
AC P81341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70) (CP 2) (Fragment).
GN DNAK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HAMAP; MF 00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; PARTIAL.
KW Chaperone; ATP-binding; Heat shock.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2001 MW; 2E2E68F21E7AD48F CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db 17 VME 19

RESULT 4
DNAK_THIFE
ID DNAK_THIFE STANDARD; PRT; 20 AA.
AC P29133;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70) (Fragment).
GN DNAK.
OS Thiobacillus ferrooxidans.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE.

```



```
RC STRAIN=ATCC 19859;
RX MEDLINE=93093401; PubMed=1360930;
RA Varela P., Jerez C.A.;
RT "Identification and characterization of GroEL and DnaK homologues in
  Thiobacillus ferrooxidans.";
RL FEMS Microbiol. Lett. 77:149-153(1992).
RN [2]
RP PHOSPHORYLATION.
RX MEDLINE=96242312; PubMed=9026439;
RA Seeger M., Osorio G., Jerez C.A.;
RT "Phosphorylation of GroEL, DnaK and other proteins from Thiobacillus
  ferrooxidans grown under different conditions.";
RL FEMS Microbiol. Lett. 138:129-134(1996).
CC -!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HAMAP; MF 00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70.1; 1.
DR PROSITE; PS00329; HSP70.2; PARTIAL.
DR PROSITE; PS01036; HSP70.3; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 1985 MW; 2E2E86EC1F9AD48F CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 2 VME 4
DB 17 VME 19

RESULT 5
UC22_MAIZE
ID UC22_MAIZE STANDARD; PRT; 5 AA.
AC P80628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
  genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
  PROTEIN IS: 6.1. ITS MW IS: 30.4 kDa.
DR Maize-2DPAGE; P80628; COLEOPTILE.
DR MaizeDB; 123954; -.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 4 EV 5
```

```
RESULT 6
ACPH_RABBIT
ID ACPH_RABBIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=9222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.Q., Wolf F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
  unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
  TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
  AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
  + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol endopep ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 1 ME 2

RESULT 7
CPD1_ENTFA
ID CPD1_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPD1.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sakakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, CPD1.";
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
  BACTERIOCIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;
```

```

Query Match          40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VM 3
      ||
      3 VM 4

Db

RESULT 8
NS3_MYCTU
ID   NS3_MYCTU          STANDARD;          PRT;          8 AA.
AC   P81152;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   30 kDa non-secretory protein 3 (Fragment).
OS   Mycobacterium tuberculosis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1773;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=H37Rv;
RA   Prasad H.K., Annapurna P.S.;
RL   Submitted (DEC-1997) to the SWISS-PROT data bank.
CC   -!- CAUTION: We are unable to find this protein in the translation of
CC   the genome of strain H37Rv.
FT   NON_TER 1
FT   NON_TER 8
SQ   SEQUENCE 8 AA; 919 MW; 8D3DC40B19C0C2D2 CRC64;

Query Match          40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VW 2
      ||
      1 VW 2

Db

RESULT 9
WP1_PERAT
ID   WP1_PERAT          STANDARD;          PRT;          8 AA.
AC   P83195;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Wall protein-1 (PWP-1) (Fragment).
OS   Perkinsus atlanticus.
OC   Eukaryota; Alveolata; Perkinsea; Perkinsea; Perkinsea; Perkinsea.
OX   NCBI_TaxID=106964;
RN   [1]
RP   SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RX   MEDLINE=22044350; PubMed=12049410;
RA   Montes J.F., Duxford M., Llado A., Garcia-Valero J.;
RT   "Characterization and immunolocalization of a main proteinaceous
RT   component of the cell wall of the protozoan parasite Perkinsus
RT   atlanticus.";
RL   Parasitology 124:477-484(2002).
CC   -!- FUNCTION: Is a major protein component of the cell wall. May play
CC   a key role in the organization of the cell wall and in promoting
CC   the survival of this parasite.
CC   -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell
CC   wall components.
CC   -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental
CC   stages.
KW   Cell wall.
FT   NON_TER 8
SQ   SEQUENCE 8 AA; 765 MW; F1787DD87B1AAB16 CRC64;

Query Match          40.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches      2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EV 5
      ||
      3 EV 4

Db

RESULT 11
UF02_MOUSE
ID   UF02_MOUSE          STANDARD;          PRT;          9 AA.
AC   P38640;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   01-FEB-1995 (Rel. 31, Last annotation update)
DE   Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95009907; PubMed=7523108;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

```

RT "Separation and sequencing of familiar and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis";
 RL Electrophoresis IS:735-745(1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 32 kDa.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1102 MW; 7E73AB6D05B1AAB CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 ME 4
 Db 1 ME 2
 RESULT 12
 FARP MANSE STANDARD; PRT; 10 AA.
 AC P18523;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FWRPamide-like neuropeptide.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91045350; PubMed=2235684;
 RA Kegan T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,
 RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
 RA Hunt D.F.;
 RT "A new peptide in the FWRPamide family isolated from the CNS of the
 RT hawkmoth, Manduca sexta";
 RL Peptides 11:849-856(1990).
 CC -1- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
 CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
 CC MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
 CC FLIGHT BEHAVIOR PATTERNS.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FWRPAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CR PIR; A43977; A43977.
 CR Amidation; Neuropeptide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VV 2
 Db 3 VV 4
 RESULT 13
 RT02_BOVIN STANDARD; PRT; 10 AA.
 ID RT02_BOVIN
 AC P82923;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).
 GN MRP52.
 OS Bos taurus (Bovine).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=21276436; PubMed=11279123;
 RC TISSUE=Liver;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome;
 RT identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:19363-19374(2001).
 CC -1- SUBUNIT: Component of the mitochondrial ribosome small subunit
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR Pfam; PF00318; Ribosomal_S2; PARTIAL.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
 KW Ribosomal protein; Mitochondrion.
 FT NON TER 1 1
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 ME 4
 Db 2 ME 3
 RESULT 14
 URE3_MORMO STANDARD; PRT; 10 AA.
 ID URE3_MORMO
 AC P17339;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
 DE amidohydrolase) (Fragment).
 GN UREA.
 OS Morganella morganii (Proteus morganii).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Morganella.
 OX NCBI_TaxID=582;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90264298; PubMed=2345135;
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
 RT "Morganella morganii urease: purification, characterization, and
 RT isolation of gene sequences";
 RL J. Bacteriol. 172:3073-3080(1990).
 CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
 CC -1- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
 DR PIR; C35389; C35389.
 KW Hydrolase.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 EV 5
 Db 7 EV 8
 RESULT 15
 MLG_THETS STANDARD; PRT; 11 AA.
 ID MLG_THETS
 AC P41989;
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Theromyzon tessulatum (Leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
OX NCBI_TaxID=13286;
FN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94298944; PubMed=8026574;
RA Salzet M., Watzet C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
RT to gamma-melanocyte stimulating hormone from the brain of the leech
RT Theromyzon tessulatum.";
RL FEBS Lett. 348:102-106(1994).
CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR FIR; S45698; S45698.
KW Hormone; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACB6409C1E8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
DB 2 VM 3

RESULT 16
PVK1 PERAM
ID PVK1 PERAM STANDARD; PRT; 11 AA.
AC P41837;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Periviscerokinin-1 (Pea-PVK-1).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
FN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Abdominal perisymphathetic organs;
RX MEDLINE=95232021; PubMed=7716075;
RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
RT perisymphathetic organs of the American cockroach.";
RL Peptides 16:61-66(1995).
CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITATORY ACTIONS ON THE
CC HYPERNEURAL MUSCLE.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
DB 8 VM 9

RESULT 17
HCYB MEGCR
ID HCYB MEGCR STANDARD; PRT; 12 AA.
AC Q10584;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hemocyanin B chain (KLH-B) (Fragment).
OS Megathura crenulata (Giant keyhole limpet).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Varigastropoda; Fissurelloidea; Fissurellidae; Megathura.
OX NCBI_TaxID=55429;
FN [1]
RP SEQUENCE.
RX MEDLINE=96208935; PubMed=8829804;
RA Swerdlow R.D., Ebert R.F., Lee P., Bonaventura C., Miller K.I.;
RT "Keyhole limpet hemocyanin: structural and functional
RT characterization of two different subunits and multimers.";
RL Comp. Biochem. Physiol. 113B:537-548(1996).
CC -!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS
CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
CC ARTHROPODS.
CC -!- SUBUNIT: DODECAMERS AND EXTENDED MULTIMERS.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Hemolymph.
CC -!- BIOTECHNOLOGY: Potent immunogen used classically as a carrier
CC protein for haptens and more recently in human vaccines and for
CC immunotherapy of bladder cancer.
CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC SUBFAMILY.
DR InterPro; IPR000896; Hemocyanin.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
KW Oxygen transport; Transport; Copper; Glycoprotein;
KW Hemolymph.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1345 MW; CBFEEAA44A432412 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
DB 4 VW 5

RESULT 18
HS9A RAT
ID HS9A RAT STANDARD; PRT; 12 AA.
AC P82995;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
FN [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T., Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
RT beta isoforms from rat liver.";
RL Protoplasm 218:54-56(2001).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
DR InterPro; IPR001404; Hsp90.
DR PROSITE; PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 4 4
FT MOD_RES 4 4
FT MOD_RES 6 6
FT MOD_RES 6 6

```

FT NON TER 12 12 SIMILARITY).
SQ SEQUENCE 12 AA; 1432 MW; DB47C322CAB6C1B6 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 11 ME 12

RESULT 19
N040_SOYBN
ID_N040_SOYBN STANDARD; PRT; 12 AA.
AC P55960;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 40.
GN ENOD40.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Williams;
RX MEDLINE=94035161; PubMed=8220464;
RA Yang W.C., Katinakis P., Hendriks P., Smolders A., de Vries F.,
RA Spee J., van Kammen A., Bisseling T., Franssen H.;
RT "Characterization of GmENOD40, a gene showing novel patterns of cell-
RT specific expression during soybean nodule development.";
RL Plant J. 3:573-585(1993).
CC -!- GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
CC SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
CC DEVELOPMENT.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X69154; -; NOT_ANNOTATED_CDS.
KW Nodulation.
SQ SEQUENCE 12 AA; 1391 MW; 3C6958AE78B1A733 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 1 ME 2

RESULT 20
PORD METTM
ID_PORD_METTM STANDARD; PRT; 12 AA.
AC P80903;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit pORD (EC 1.2.7.1) (Pyruvate oxidoreductase
DE delta chain) (PORD) (Pyruvic-ferredoxin oxidoreductase delta subunit)
DE (Fragment).

```

```

GN PORD.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
CC of 80 degrees Celsius.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1241 MW; 2D54065D1BD1ADD8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 1 ME 2

RESULT 21
UN39_CLOPA
ID_UN39_CLOPA STANDARD; PRT; 12 AA.
AC P81359;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 39 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengserud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 29.5 kDa.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; 940561E66BD2CB01 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 6 EV 7

RESULT 22
UP01_CAEEL
ID_UP01_CAEEL STANDARD; PRT; 12 AA.
AC P55954;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

```

```

DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unknown protein from 2D-page (Spot 1) (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE.
RP STRAIN=Bristol N2;
RC MEDLINE=97295299; PubMed=9150941;
RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwillig R.;
RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
RT homogenates and identification of protein spots by microsequencing.";
RL Electrophoresis 18:1557-562(1997).
DR Siena-2DPAGE; P55954; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 7 ME 8

RESULT 23
V23K WSSV
ID V23K WSSV STANDARD; PRT; 12 AA.
AC P82005;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 23 kDa structural polypeptide (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
OX NCBI_TaxID=92652;
RN [1]
RN SEQUENCE.
RP STRAIN=South Carolina;
RC MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
RT virus.";
RL Arch. Virol. 145:263-274(2000).
CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1323 MW; 0C0F41E91D51A724 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 1 ME 2

RESULT 24
V25K WSSV
ID V25K WSSV STANDARD; PRT; 12 AA.
AC P82004;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 25 kDa structural polypeptide (Fragment).
OS White spot syndrome virus (WSSV).
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
OX NCBI_TaxID=92652;
RN [1]
RN SEQUENCE.
RP STRAIN=South Carolina;
RC

```

```

RX MEDLINE=20214217; PubMed=10752552;
RA Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
RT virus.";
RL Arch. Virol. 145:263-274(2000).
CC -1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1283 MW; C5409AD9ECB731A9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 9 VV 10

RESULT 25
FIBB RABIT
ID FIBB RABIT STANDARD; PRT; 13 AA.
AC P14478;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: fibrinopeptide B] (Fragment).
GN FGB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE.
RP Blomback B., Blomback M., Grondahl N.J.;
RA "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.
FT MOD_RES 4 4 SULFATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 7 EV 8

RESULT 26
IDH3A CANFA
ID IDH3A CANFA STANDARD; PRT; 13 AA.
AC P54836;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial
DE (EC 1.1.1.41) (Isocitric dehydrogenase) (NAD+-specific ICDH)
DE (Fragment).
GN IDH3A.

```

```

OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=9816340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC CC -!- CATALYTIC ACTIVITY: Isocitrate + NAD(+) = 2-oxoglutarate + CO(2) +
CC NADH.
CC -!- SUBUNIT: HETEROOLIGOMER OF SUBUNITS ALPHA, BETA, AND GAMMA IN THE
CC APPARENT RATIO OF 2:1:1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
DR HSC-2DPAGE; P54836; DOG.
DR InterPro; IPR001804; Isodh.
DR PROSITE; PS00470; IDH_IMDH; PARTIAL.
KW Oxidoreductase; NAD; Tricarboxylic acid cycle; Mitochondrion.
FT NON TER 13
FT SEQUENCE 13 AA; 1356 MW; 9ABFBC2B2A34B2D1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 EV 5
DB 3 EV 4

RESULT 27
IDHP_RAT IDHP_RAT STANDARD; PRT; 13 AA.
AC P56574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Isocitrate dehydrogenase [NADP], mitochondrial (EC 1.1.1.42)
DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP) (ICD-
DE M) (Fragment).
GN IDH2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: PLAYS A ROLE IN INTERMEDIARY METABOLISM AND ENERGY
CC PRODUCTION. IT MAY TIGHTLY ASSOCIATE OR INTERACT WITH THE PYRUVATE
CC DEHYDROGENASE COMPLEX (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
CC + NADPH.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT P8) IS: 9.0, ITS MW IS: 42 kDa.
CC -!- SIMILARITY: BELONGS TO THE ISOCITRATE AND ISOPROPYLMALATE
CC DEHYDROGENASES FAMILY.
DR InterPro; IPR001804; Isodh.
DR PROSITE; PS00470; IDH_IMDH; PARTIAL.
KW Oxidoreductase; NADP; Glyoxylate bypass; Tricarboxylic acid cycle;
KW Mitochondrion.
FT NON TER 13
FT SEQUENCE 13 AA; 1526 MW; 5FB81031723E02C3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ME 4
DB 4 ME 5

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ME 4
DB 4 ME 5

RESULT 28
MLA_ANOCA
ID_MLA_ANOCA STANDARD; PRT; 13 AA.
AC P41589;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Anolis carolinensis (Green anole) (American chameleon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=28377;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=92270473; PubMed=1667689;
RA Dorez R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;
RT "Detection of a novel sequence change in the major form of alpha-MSH
RT isolated from the intermediate pituitary of the reptile, Anolis
RT carolinensis.";
RL Peptides 12:1261-1266(1991).
CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR InterPro; IPR001941; Mcoortin_ACTH.
DR Pfam; PF00976; ACTH_domain; I.
KW Hormone; Amidation.
FT MOD RES 13
FT SEQUENCE 13 AA; 1608 MW; FF990A7358BB09C1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 ME 4
DB 4 ME 5

RESULT 29
MLA_CAMDR
ID_MLA_CAMDR STANDARD; PRT; 13 AA.
AC P01196;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin alpha (Alpha-MSH).
OS Camelus dromedarius (Dromedary) (Arabian camel), and
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX NCBI_TaxID=9838, 9796;
RN [1]
RP SEQUENCE.
RC SPECIES=C.dromedarius;
RX MEDLINE=75146434; PubMed=1125179;
RA Li C.H., Danho W.O., Chung D., Rao A.J.;
RT "Isolation, characterization, and amino acid sequence of
RT melanotropins from camel pituitary glands.";
RL Biochemistry 14:947-952(1975).
RN [2]
RP SEQUENCE.
RC SPECIES=Horse; TISSUE=Pituitary;
RX Dixon J.S., Li C.H.;
RT "The isolation and structure of alpha-melanocyte-stimulating hormone

```

```

RT from horse pituitaries.";
RL J. Am. Chem. Soc. 82:4568-4572 (1960).
CC -!- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR PIR; A01464; WTCMAD.
DR PIR; A91785; WTHOAR.
DR InterPro; IPR001941; Mcootin_ACTH.
DR Pfam; PF00976; ACTH domain; 1.
KW Hormone; Acetylation; Amidation.
FT MOD_RES 1 1 ACETYLACTION (IN ABOUT 50% OF CAMEL
FT MOD_RES 13 13 MOLECULES).
FT MOD_RES 13 13 AMIDATION.
FT SEQUENCE 13 AA; 1624 MW; FF991CA958B809C1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db 4 ME 5

RESULT 30
PEDI_HYDAT
ID_PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydrozoa; Hydra.
OC NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris.";
RL Development 122:1941-1948 (1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db 6 EV 7

RESULT 31
UN41_CLOPA
ID_UN41_CLOPA STANDARD; PRT; 13 AA.
AC P81360;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein CP 41 from 2D-page (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OC NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal

```

```

RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806 (1998).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.6, ITS MW IS: 23.5 kDa.
FT NON_TER 13 13
FT SEQUENCE 13 AA; 1402 MW; 738AECF1E66CA2CB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db 6 EV 7

RESULT 32
UP71_LITEW
ID_UP71_LITEW STANDARD; PRT; 13 AA.
AC P82050;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 7.1 [Contains: Uperin 7.1.1].
OS Litoria ewingi (Brown tree frog) (Ewing's tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OC NCBI_TaxID=104896;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=skin secretion;
RA Steinbörner S.F., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "An unusual combination of peptides from the skin glands of Ewing's
RT tree frog, Litoria ewingi. Sequence determination and antimicrobial
RT activity.";
RL Aust. J. Chem. 50:889-894 (1997).
CC -!- FUNCTION: UPERIN 7.1 SHOWS ANTIBACTERIAL ACTIVITY AGAINST L.LACTIS
CC AND S.UBERIS. UPERIN 7.1.1 IS INACTIVE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1427; METHOD=FAB; RANGE=1-13.
CC -!- MASS SPECTROMETRY: MW=1184; METHOD=FAB; RANGE=3-13.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT PEPTIDE 1 13 UPERIN 7.1.
FT PEPTIDE 3 13 AMIDATION.
FT MOD_RES 13 13
FT SEQUENCE 13 AA; 1429 MW; DE17C7204CCAB322 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db 5 VV 6

RESULT 33
ADFA_TENMO
ID_ADFA_TENMO STANDARD; PRT; 14 AA.
AC P82955;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antidiuretic factor A (ADFA) (ADF) (Antidiuretic hormone A) (ADHA).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Tenebrionidae; Tenebrio.
OC NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.

```



```

RC TISSUE=Head;
RX MEDLINE=21642653; PubMed=11756661;
RA Eisenher R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;
RT "Identification of a potent antidiuretic factor acting on beetle
RL Malpighian tubules.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).
CC -!- FUNCTION: Strong inhibitor of fluid secretion by the Malpighian
CC tubules. Uses cGMP as a second messenger and inhibits fluid
CC production by decreasing cAMP concentration.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1541.58; METHOD=MALDI.
CC -!- SIMILARITY: STRONG, TO THE C-TERMINAL OF T.MOLITOR CUTICULAR
CC PROTEIN LPCP29.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0005184; F:neuropeptide hormone activity; NAS.
DR GO: GO:0007218; P:neuropeptide signaling pathway; NAS.
KW Neuropeptide; Hormone.
SQ SEQUENCE 14 AA; 1543 MW; F49C91A3F16E43D1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db 1 VV 2

RESULT 34
GR75 CANFA STANDARD; PRT; 14 AA.
AC P99502;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Mitochondrial stress-70 protein (75 kDa glucose regulated protein)
DE (GRP 75) (Fragment).
GN HSPA9.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: IMPLICATED IN THE CONTROL OF CELL PROLIFERATION AND
CC CELLULAR AGING. MAY ALSO ACT AS A CHAPERONE.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR HSC-2DPAGE; P99502; DOG.
DR InterPro; IPR001023; Hsp70.
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; PARTIAL.
KW ATP-binding; Mitochondrion.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1438 MW; 2AAEDD1AACBAC8D8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db 9 VV 10

RESULT 35

```

```

IP2G_RAT
ID _IP2G_RAT STANDARD; PRT; 14 AA.
AC P81795;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Eukaryotic translation initiation factor 2 subunit 3 (Eukaryotic
DE translation initiation factor 2 gamma subunit) (eif-2-gamma) (pp42)
DE (Fragment).
DN EIF2S3 OR EIF2G.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96374441; PubMed=8780732;
RA Gil C., Plana M., Riera M., Itarte E.;
RT "Rat liver pp49, a protein that forms complexes with protein kinase
RT CK2, is composed of the beta and the gamma subunits of translation
RT initiation factor eif-2.";
RL Biochem. Biophys. Res. Commun. 225:1052-1057(1996).
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA. THIS
CC COMPLEX BINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY MRNA BINDING
CC TO FORM A 43S PREINITIATION COMPLEX. JUNCTION OF THE 60S RIBOSOMAL
CC SUBUNIT TO FORM THE 80S INITIATION COMPLEX IS PRECEDED BY
CC HYDROLYSIS OF THE GTP BOUND TO EIF-2 TO RELEASE OF AN EIF-2-GDP
CC BINARY COMPLEX. IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER
CC ROUND OF INITIATION, THE GDP BOUND TO EIF-2 MUST EXCHANGE WITH GTP
CC BY WAY OF A REACTION CATALYZED BY EIF-2B.
CC -!- SUBUNIT: Heterotrimer composed of an alpha, a beta, and a gamma
CC chain.
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EIF2G SUBFAMILY.
KW Initiation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1511 MW; D86EDA955ABEFA12 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
Db 6 EV 7

RESULT 36
KLPS SCARA STANDARD; PRT; 14 AA.
AC P58356;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kinin-like peptide-S (Fragment).
OS Scaptocosa raptoria (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Lycosoidea; Lycosidae; Scaptocosa.
OX NCBI_TaxID=180440;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98257639; PubMed=9604280;
RA Ferreira L.A.F., Lucas S.M., Alves E.W., Hermann V.V., Reichl A.P.,
RA Habermehl G., Zingali R.B.;
RT "Isolation, characterization and biological properties of two
RT kinin-like peptides (peptide-S and peptide-R) from Scaptocosa
RT raptoria venom.";
RL Toxicon 36:31-39(1998).
CC -!- FUNCTION: Has kinin-like biological properties. Causes contraction

```

CC on the of mammalian ileum; relaxes the duodenum and increases the
 CC capillary permeability.
 KW Vasodilator. 14 14
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1510 MW; E811E2E5D2EE27CA CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EV 5
 Db |||
 5 EV 6
 RESULT 37
 KPPI_SELMI
 ID_KPPI_SELMI STANDARD; PRT; 14 AA.
 AC P25933;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphoribulokinase, 40 kDa subunit (BC 2.7.1.19) (Phosphopentokinase)
 DE (Fragment)
 OS Selenastrum minutum.
 CC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Selenastraceae;
 CC Selenastrum.
 CC Selenastrum.
 OX NCBI_TaxID=39955;
 RN [1]
 RP SEQUENCE.
 RA Lin M., Turpin D.H.;
 RT "Purification and molecular and immunological characterization of a
 RT unique phosphoribulokinase from the green alga Selenastrum minutum.";
 RL Plant Physiol. 98:82-88(1992).
 CC -!- CATALYTIC ACTIVITY: ATP + D-ribose 5-phosphate = ADP + D-
 CC ribulose 1,5-bisphosphate.
 CC -!- PATHWAY: Calvin cycle.
 CC -!- SUBUNIT: HETERODIMER OF A 40 kDa AND A 41 kDa SUBUNIT.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
 DR InterPro; IPR006082; PRX.
 DR PROSITE; PS00567; PHOSPHORIBULOKINASE; PARTIAL.
 KW Transferase; Kinase; Calvin cycle; ATP-binding.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1379 MW; C4B1D8CD2F891062 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VV 2
 Db |||
 6 VV 7
 RESULT 38
 PHI_PRUSE
 ID_PHI_PRUSE STANDARD; PRT; 14 AA.
 AC P29263;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Prunasin beta-glucosidase I (EC 3.2.1.118) (Prunasin hydrolase
 DE isozyme I) (PH I) (Fragment).
 OS Prunus serotina (Black cherry).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC Eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 CC NCBI_TaxID=23207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Li C.P., Swain E., Poulton J.E.;
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";

RL Plant Physiol. 100:282-290(1992).
 CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
 CC glucose.
 CC -!- SUBUNIT: Monomer.
 CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
 CC EMBRYONAL TISSUES.
 CC -!- PTM: GLYCOSYLATED.
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1575 MW; FB3D7F4FB90CA9CA CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VV 2
 Db |||
 5 VV 6
 RESULT 39
 PPK6_PERAM
 ID_PPK6_PERAM STANDARD; PRT; 14 AA.
 AC P82693;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-6 (Pea-PK-6) (FXPRU-amide).
 OS Periplaneta americana (American cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 CC Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
 RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;
 RX MEDLINE=20189894; PubMed=10723010;
 RT Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach.";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.
 CC -!- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN
 CC ABDOMINAL PERISYPHATHETIC ORGANS.
 CC -!- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Amidation; Pyrokinin.
 FT MOD_RES 14 14
 SQ SEQUENCE 14 AA; 1592 MW; 396CC3FF384A998 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EV 5
 Db |||
 4 EV 5
 RESULT 40
 UC15_MAIZE
 ID_UC15_MAIZE STANDARD; PRT; 14 AA.
 AC P80621;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 245)
 DE (Fragment).
 OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Fernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.8, ITS MW IS: 35.7 kDa.
 DR Maize-2DPAGE; P80621; COLEOPTILE.
 DR Maize2DB; 123947; -.
 FT NON_TER 1 1
 FT NON_TER 14 14
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VV 2
 Db 7 VV 8
 RESULT 41
 UN04_CLOPA STANDARD; PRT; 14 AA.
 ID UN04_CLOPA
 AC P81349;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 4 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.7, ITS MW IS: 45.7 kDa.
 FT NON_TER 14 14
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1608 MW; D424A7069460EBD2 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EV 5
 Db 3 EV 4
 RESULT 42
 CDN2_LITGI STANDARD; PRT; 15 AA.
 ID CDN2_LITGI
 AC P56247;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caeridin 2.
 OS Litoria gilleni (Centralian tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=39405;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RA "Peptides from Australian frogs. The structures of the caeridins and
 RT caeridins from Litoria gilleni";
 RL J. Chem. Res. 139:937-961(1993).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
 CC glands.
 CC -1- MASS SPECTROMETRY: MW=1408; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 15 15
 FT MOD_RES 15 15
 SQ SEQUENCE 15 AA; 1410 MW; 06F1BBF272550CBF CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VV 2
 Db 5 VV 6
 RESULT 43
 CDN4_LITCE STANDARD; PRT; 15 AA.
 ID CDN4_LITCE
 AC P82076;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Caeridin 4.
 OS Litoria caerulea (Green tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=30344;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Parotoid gland;
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. Structures of the caeridins from
 RT Litoria caerulea";
 RL J. Chem. Soc. Perkin Trans. 1:573-576(1993).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
 CC glands.
 CC -1- MASS SPECTROMETRY: MW=1504; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 15 15
 FT MOD_RES 15 15
 SQ SEQUENCE 15 AA; 1506 MW; 06F1BBFBBC5195F CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VV 2
 Db 5 VV 6
 RESULT 44
 COXI_THUOB STANDARD; PRT; 15 AA.
 ID COXI_THUOB
 AC P80978;
 DT 01-NOV-1997 (Rel. 35, Created)

CC ESTER OF JH. IT IS ALSO INVOLVED IN THE TRANSPORT OF JH.
CC -1- CATALYTIC ACTIVITY: Methyl (2E,6E)-(10R,11S)-10,11-epoxy-3,7,11-
CC trimethyltrideca-2,6-dienoate + H₂O = (2E,6E)-(10R,11S)-10,11-
CC epoxy-3,7,11-trimethyltrideca-2,6-dienoate + methanol.
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR PIR; A36527; A36527.
DR InterPro; IPR002018; CarboxylesteraseB.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
KW Hydrolase; Serine esterase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1659 MW; D321EA432E58B848 CRC64;
Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 EV 5
DB ||
7 EV 8
RESULT 48
FKB7 PINPS
ID_FKB7_PINPS STANDARD; PRT; 15 AA.
AC P81104; 1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans
DE isomerase) (Cyclophilin) (PPIase) (S1205-06) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RA Plomion C., Costa P., Bahrman N., Frigerio J.-M.;
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map.";
RL Silvae Genet. 46:161-165 (1997).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108 (1999).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS DURING
CC PROTEIN SYNTHESIS. THIS PPIASE BINDS CALMODULIN (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 5.3, ITS MW IS: 72 kDa.
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR InterPro; IPR001179; FKBP_PPIASE.
DR PROSITE; PS00453; FKBP_PPIASE_1; PARTIAL.
DR PROSITE; PS00454; FKBP_PPIASE_2; PARTIAL.
DR PROSITE; PS00059; FKBP_PPIASE_3; PARTIAL.
KW Isomerase; Rotamase; Repeat; Calmodulin-binding.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1675 MW; 2B53999722277F3F CRC64;
Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 EV 5

Db ||
13 EV 14
RESULT 49
GR78 HORSE
ID_GR78_HORSE STANDARD; PRT; 15 AA.
AC P16392;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 78 kDa glucose-regulated protein (GRP 78) (Immunoglobulin heavy chain
DE binding protein) (BiP) (Fragment).
GN HSP45 OR GRP78.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RX MEDLINE=90147817; PubMed=1689156;
RA Ohlas B., Boyd N.D., Luber-Narod J., Reyes V.E., Leeman S.E.;
RT "Isolation and identification of a polypeptide in the Hsp 70 family
RT that binds substance P.";
RL Biochem. Biophys. Res. Commun. 166:978-983 (1990).
CC -1- FUNCTION: Probably plays a role in facilitating the assembly of
CC multimeric protein complexes inside the ER.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DR InterPro; IPR001023; Hsp70.
DR PROSITE; PS00297; HSP70_1; PARTIAL.
DR PROSITE; PS00329; HSP70_2; PARTIAL.
DR PROSITE; PS01036; HSP70_3; PARTIAL.
KW ATP-binding; Endoplasmic reticulum.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1647 MW; 81119D21D0EC26DB CRC64;
Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VV 2
DB ||
12 VV 13
RESULT 50
KPP2 SELMI
ID_KPP2_SELMI STANDARD; PRT; 15 AA.
AC P25934;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoribulokinase, 41 kDa subunit (EC 2.7.1.19) (Phosphopentokinase)
DE (Fragment).
OS Selenastrum minutum.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Selenastraceae;
OC Selenastrum.
OX NCBI_TaxID=39955;
RN [1]
RP SEQUENCE.
RA Lin M., Turpin D.H.;
RT "Purification and molecular and immunological characterization of a
RT unique phosphoribulokinase from the green alga Selenastrum minutum.";
RL Plant Physiol. 98:82-88 (1992).
CC -1- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-
CC ribulose 1,5-bisphosphate.
CC -1- PATHWAY: Calvin cycle.
CC -1- SUBUNIT: HETERODIMER OF A 40 kDa AND A 41 kDa SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
DR InterPro; IPR006082; PRK.
DR PROSITE; PS00567; PHOSPHORIBULOKINASE; PARTIAL.
KW Transferase; Kinase; Calvin cycle; ATP-binding.

```

FT  NON TER      15
SQ  SEQUENCE    15 AA; 1455 MW; 07A97BCD2F922C75 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 VV 2
Db  6 VV 7

RESULT 51
MALT BACTQ STANDARD; PRT; 15 AA.
ID MALT BACTQ
AC P80072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Maltase (EC 3.2.1.20) (Alpha-glucosidase I) (Fragment).
OS Bacillus thermoamyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1425;
RN [1]
RP SEQUENCE.
RC STRAIN=KPI071 / FERM P8477;
RX MEDLINE=92209510; PubMed=155585;
RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;
RT "Assignment of Bacillus thermoamyloliquefaciens KPI071
RT alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
RT similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
RT and in structural parameters calculated from the amino acid
RT composition.";
RL Eur. J. Biochem. 205:249-256(1992).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
CC linked D-glucose residues with release of D-glucose.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-ANYLASE FAMILY.
DR PIR; S21240; S21240.
KW Hydrolase; Glycosidase.
FT NON TER      15
SQ SEQUENCE    15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 VV 2
Db  10 VV 11

RESULT 52
MAOX CHICK STANDARD; PRT; 15 AA.
ID MAOX CHICK
AC Q92060;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Fragment).
GN ME1
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97056061; PubMed=8900406;
RA Hodnett D.W., Fantozzi D.A., Thurmond D.C., Klautsky S.A.,
RA Macphree K.G., Estrem S.T., Xu G., Goodridge A.G.;
RT "The chicken malic enzyme gene: structural organization and
RT identification of triiodothyronine response elements in the

```

```

RT  5'-flanking DNA.";
RL Arch. Biochem. Biophys. 334:309-324(1996).
CC -!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2) +
CC NADPH.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U49693; AAA92721.1; -
DR InterPro; IPR001891; Malic_oxred.
DR PROSITE; PS00331; MALIC_ENZYMES; PARTIAL.
KW Oxidoreductase; NADP.
FT NON TER      15
SQ SEQUENCE    15 AA; 1842 MW; CFEF180B2BA84C2B CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  4 EV 5
Db  6 EV 7

RESULT 53
NKSO PSETE STANDARD; PRT; 15 AA.
ID NKSO PSETE
AC P59073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short neurotoxin N2 (Alpha neurotoxin) (Fragment).
OS Pseudonaja textilis (Eastern brown snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophinae; Pseudonaja.
OX NCBI_TaxID=8673;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99449602; PubMed=10518793;
RA Gong N.L., Armugam A., Jeyaseelan K.;
RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
RT cloning, expression and protein characterization.";
RL Eur. J. Biochem. 265:982-989(1999).
CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
CC acetylcholine receptors (nAChR).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=6345; METHOD=Electrospray.
CC -!- MISCELLANEOUS: LD(50) is 0.80 mg/kg by intravenous injection.
CC -!- SIMILARITY: Belongs to the snake toxin family.
DR InterPro; IPR003571; Snake toxin.
DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Multigene family.
FT UNSURE      3
FT UNSURE      13
FT NON TER     15
SQ SEQUENCE    15 AA; 1727 MW; E149FD4BFD1EF0DD CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VW 2
      ||
Db      11 VW 12

RESULT 54
PGTS PELAC
ID _PGTS PELAC STANDARD; PRT; 15 AA.
AC P80564;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pyrogallol hydroxyltransferase small subunit (EC 1.9.7.1.2)
DE (Transhydroxylase) (Fragment).
OS Pelobacter acidigallici.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Pelobacteraceae; Pelobacter.
OX NCBI_TaxID=35816;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 2377 / Braunschweig;
RX MEDLINE=96215436; PubMed=8647079;
RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;
RT "One molecule of molybdopterine guanine dinucleotide is associated
RT with each subunit of the heterodimeric Mo-Fe-S protein
RT transhydroxylase of Pelobacter acidigallici as determined by SDS/PAGE
RT and mass spectrometry."
RL Eur. J. Biochem. 237:406-413(1996).
CC -|- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3-
CC trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-
CC tetrahydroxybenzene.
CC -|- COPACTOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -|- SUBUNIT: Heterodimer of a large and a small subunit.
DR PIR; S65429; S65429.
KW Oxidoreductase; Molybdenum; Iron-sulfur.
FT NON TER 15
SQ SEQUENCE 15 AA; 1843 MW; 0567BDD004C28499 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ME 4
      ||
Db      1 ME 2

RESULT 55
PH3 PRUSE
ID _PH3 PRUSE STANDARD; PRT; 15 AA.
AC P29265;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prunasin beta-glucosidase IIB (EC 3.2.1.118) (Prunasin hydrolase
DE isozyme IIB) (PH IIB) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RT Plant Physiol. 100:282-290(1992).
CC -|- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
CC glucose.
CC -|- SUBUNIT: Monomer.
CC -|- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR

```

```

CC EMBRYONAL TISSUES.
KW -|- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON TER 15
SQ SEQUENCE 15 AA; 1635 MW; 4F3D7F4FB90CFE4C CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VW 2
      ||
Db      6 VW 7

RESULT 56
R13A SPIOL
ID _R13A SPIOL STANDARD; PRT; 15 AA.
AC P82454;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 60S ribosomal protein L13a (Fragment).
GN RPL13A.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Alvaro; TISSUE=Leaf;
RA Yamaguchi K., Subramanian A.R.;
RT "N-terminal sequence of spinach cytosolic 60S ribosomal protein
RT L13a."
RL Submitted (APR-2000) to the SWISS-PROT data bank.
CC -|- SIMILARITY: BELONGS TO THE L13P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR005822; Rib_prot_L13.
DR PROSITE; PS00783; RIBOSOMAL_L13; PARTIAL.
KW Ribosomal protein.
FT NON TER 15
SQ SEQUENCE 15 AA; 1489 MW; C7B9C80F5A099EB3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VW 2
      ||
Db      11 VW 12

RESULT 57
RKGG CARCR
ID _RKGG CARCR STANDARD; PRT; 15 AA.
AC P21536;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE Rathke's gland glycoprotein (Fragment).
OS Carretta caretta (Loggerhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Chelonioidae; Cheloniidae; Carretta.
OX NCBI_TaxID=8467;
RN [1]
RP SEQUENCE.
RC TISSUE=Rathke's gland;
RX MEDLINE=90075703; PubMed=2591198;
RA Radhakrishna G., Chin C.C.Q., Wold P., Weldon P.J.;
RT "Glycoproteins in Rathke's gland secretions of loggerhead (Carretta
RT caretta) and Kemp's ridley (Leptodochelys kempi) sea turtles."
RL Comp. Biochem. Physiol. 94B:375-378(1989).
CC -|- FUNCTION: RATHKE'S GLAND SECRETIONS MAY FUNCTION AS PHEROMONES,

```

```

CC AS PREDATOR REPELLANTS, OR CONTRIBUTE TO THE MAINTENANCE OF THE
CC TURTLE SHELL.
CC -|- SIMILARITY: WITH RATHKE'S GLAND GLYCOPROTEIN FROM KEMP'S RIDLEY
CC SEA TURTLE.
CC PIR; PL0154; PL0154.
CC GLYCOPROTEIN.
CC NON TER 15 15
CC SEQUENCE 15 AA; 1477 MW; CC893BAAAAB1B5ED CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 7 VV 8

RESULT 58
RM12_YEAST
ID RM12_YEAST STANDARD; PRT; 15 AA.
AC P36522;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein l12 (Yml12) (Fragment).
GN MRPL12.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR SGD; L0002687; MRPL12.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1851 MW; 74BCD9FEDDB3900 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 8 EV 9

RESULT 59
THL_CLOPA
ID THL_CLOPA STANDARD; PRT; 15 AA.
AC P81347;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Acetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA thiolase)
DE (CP 13) (Fragment).
GN THL.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal

```

```

RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -|- CATALYTIC ACTIVITY: 2 acetyl-CoA = CoA + acetoacetyl-CoA.
CC -|- PATHWAY: JUNCTION IN THE PATHWAY LEADING TO THE PRODUCTION OF
CC EITHER ACIDS (ACETATE OR BUTYRATE) OR SOLVENTS (ACETONE, BUTANOL
CC OR ETHANOL).
CC -|- SUBUNIT: Homotrimer (By similarity).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
DR InterPro; IPR002155; Thiolase.
DR PROSITE; PS00098; THIOLASE 1; PARTIAL.
DR PROSITE; PS00737; THIOLASE 2; PARTIAL.
DR PROSITE; PS00099; THIOLASE 3; PARTIAL.
KW Transferase; Acyltransferase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1496 MW; 9735820D61BB35FC CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 3 EV 4

RESULT 60
UBL1_MONDO
ID UBL1_MONDO STANDARD; PRT; 15 AA.
AC P50103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thioesterase L1) (Neuron cytoplasmic protein 9.5)
DE (PGP 9.5) (PGP9.5) (Fragment).
GN UCHL1.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96102916; PubMed=8522974;
RA Mann D.A., Trowern A.R., Lavender F.L., Whittaker P.A.,
RA Thompson R.J.;
RT "Identification of evolutionary conserved regulatory sequences in the
RT 5' untranslated region of the neural-specific ubiquitin C-terminal
RT hydrolase (PGP9.5) gene.";
RL J. Neurochem. 66:35-46(1996).
CC -|- FUNCTION: UBIQUITIN-PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUINATED PROTEINS.
CC THIS ENZYME IS A THIOL PROTEASE THAT RECOGNIZE AND HYDROLYZE
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC -|- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U32208; AAA89059.1; -.
CC InterPro; IPR001578; UCH_1.
DR PROSITE; PS00140; UCH_1; PARTIAL.
KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family.
FT NON_TER 15 15

```


SQ SEQUENCE 15 AA; 1816 MW; 1B7A3B6E623F6E79 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
||
6 ME 7

Db

RESULT 61

UC08_MAIZE STANDARD; PRT; 15 AA.

AC P80614;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 159) (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE.

RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.4, ITS MW IS: 38.8 kDa.

CC -I- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase family.

DR Maize-2DPAGE; P80614; COLEOPTILE.

DR MaizeDB; 123934; -.

FT NON_TER 1 1

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1785 MW; 1978B1D6AB4DDF8D CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
||
10 VW 11

Db

RESULT 62

UC16_MAIZE STANDARD; PRT; 15 AA.

AC P80622;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 308) (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE.

RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pernollet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.9, ITS MW IS: 18.6 kDa.

DR Maize-2DPAGE; P80622; COLEOPTILE.

DR MaizeDB; 123948; -.

FT NON_TER 1 1

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1796 MW; D331A518F7440BE7 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
7 EV 8

Db

RESULT 63

UP01_METAN STANDARD; PRT; 15 AA.

AC P83440;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Unknown protein (fragment).

OS Metarhizium anisopliae.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocerales; Clavicipitaceae; Clavicipitaceae; Clavicipitaceae; Metarhizium.

OC mitosporic Clavicipitaceae; Metarhizium.

OX NCBI_TaxID=5530;

RN [1]

RP SEQUENCE.

RC STRAIN=54A-1b;

RX MEDLINE=22343006; PubMed=12455610;

RA Kamp A.M., Bidochka M.J.;

RT "Protein analysis in a pleomorphically deteriorated strain of the insect-pathogenic fungus Metarhizium anisopliae.";

RT Can. J. Microbiol. 48:787-792(2002).

RL Can. J. Microbiol. 48:787-792(2002).

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1651 MW; FBD76D69E1F0F4F CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 1; Length 15;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
||
5 VW 6

Db

RESULT 64

VORA_METTM STANDARD; PRT; 15 AA.

AC P80907;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ketoisovalerate oxidoreductase subunit vora (EC 1.-.-.-) (VOR) (2-oxoisovalerate oxidoreductase alpha chain) (2-oxoisovalerate-ferredoxin oxidoreductase alpha subunit) (Fragment).

GN VORA

OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).

OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.

OX NCBI_TaxID=79929;

RN [1]

RP SEQUENCE

RX MEDLINE=97261844; PubMed=9108258;

RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;

RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum.";

RL Eur. J. Biochem. 244:862-868(1997).

```

CC -!- SUBUNIT: HETROTRIMER OF THE VORA, VORB AND VORC SUBUNITS.
CC -!- MISCELLANEOUS: As a pH optimum of 9.7 and an optimal temperature
CC of 75 degrees Celsius.
KW Oxidoreductase.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1779 MW; 31320B6531CA528F CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 13 EV 14

RESULT 65
AU21_LITAU
ID AU21_LITAU STANDARD; PRT; 16 AA.
AC P82388;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aurein 2.1 [Contains: Aurein 2.1.1].
OS Litoria raniformis (Southern bell frog), and
OS Litoria aurea (Green and golden bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=116057, 8371;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC SPECIES=L.raniformis, and L.aurea;
RC TISSUE=Skin secretion;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -!- FUNCTION: AUREIN 2.1 HAS ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS,
CC L.LACTIS, L.INNOCUA, M.LUTEUS, S.EPIDERMIDIS AND S.UBERISAND.
CC PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS
CC AMPHIPATHIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation; Antibiotic.
FT PEPTIDE 1 16 AUREIN 2.1.
FT PEPTIDE 3 16 AUREIN 2.1.1.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DA4D4240F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 9 VV 10

RESULT 66
AU22_LITAU
ID AU22_LITAU STANDARD; PRT; 16 AA.
AC P82389;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aurein 2.2 [Contains: Aurein 2.2.1].
OS Litoria aurea (Green and golden bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

```

```

OC Pelodyadinae; Litoria.
OX NCBI_TaxID=8371;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Skin secretion;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC L.INNOCUA, M.LUTEUS, S.AUREUS, S.EPIDERMIDIS AND S.UBERISAND.
CC PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS
CC AMPHIPATHIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Amidation; Antibiotic.
FT PEPTIDE 1 15 AUREIN 2.2.
FT PEPTIDE 3 16 AUREIN 2.2.1.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DA354DAE2F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 9 VV 10

RESULT 67
AU23_LITAU
ID AU23_LITAU STANDARD; PRT; 16 AA.
AC P82390;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Aurein 2.3.
OS Litoria aurea (Green and golden bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=8371;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Skin secretion;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
CC L.INNOCUA, M.LUTEUS, S.AUREUS AND S.EPIDERMIDIS. PROBABLY ACTS BY
CC DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Amidation; Antibiotic.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1616 MW; 1D9A5DA424DAE2F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 9 VV 10

```

RESULT 68

AU24_LITAU STANDARD; PRT; 16 AA.
 ID AU24_LITAU STANDARD; PRT; 16 AA.
 AC P82391;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Aurein 2.4 [Contains: Aurein 1.2.1].
 OS Litoria aurea (Green and golden bell frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=8371;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20408845; PubMed=10951191;
 RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
 Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer active aurein peptides from the
 RT Australian bell frogs Litoria aurea and Litoria raniformis the
 RT solution structure of aurein 1.2.";
 RL Eur. J. Biochem. 267:5330-5341(2000).
 CC -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
 CC L.INNOCUA, M.LUTEUS, S.AUREUS, S.EPIDERMIDIS AND S.UBERIS.
 CC PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS
 CC AMPHIPATHIC STRUCTURE. SHOWS ANTICANCER ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC Amphibian defense peptide; Amidation; Antibiotic.
 FT PEPTIDE 1 16 AUREIN 2.4.
 FT PEPTIDE 3 16 AUREIN 2.4.1.
 FT MOD RES 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1630 MW; 1D87980438AAE2F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VV 2
 ||
 Db 9 VV 10

RESULT 69

AU25_LITRA STANDARD; PRT; 16 AA.
 ID AU25_LITRA STANDARD; PRT; 16 AA.
 AC P82392;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Aurein 2.5.
 OS Litoria raniformis (Southern bell frog), and
 OS Litoria aurea (Green and golden bell frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=116057, 8371;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC SPECIES=L.raniformis, and L.aurea;
 RC TISSUE=Skin secretion;
 RX MEDLINE=20408845; PubMed=10951191;
 RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
 Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer active aurein peptides from the
 RT Australian bell frogs Litoria aurea and Litoria raniformis the
 RT solution structure of aurein 1.2.";
 RL Eur. J. Biochem. 267:5330-5341(2000).
 CC -!- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
 CC L.INNOCUA, M.LUTEUS, S.AUREUS, AND S.EPIDERMIDIS. PROBABLY ACTS BY
 CC DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.

CC SHOWS ANTICANCER ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 KW Amphibian defense peptide; Amidation; Antibiotic.
 FT MOD RES 16 AMIDATION.
 SQ SEQUENCE 16 AA; 1650 MW; 1D9A5DADB4DAB2F9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VV 2
 ||
 Db 9 VV 10

RESULT 70

CT12_LITCI STANDARD; PRT; 16 AA.
 ID CT12_LITCI STANDARD; PRT; 16 AA.
 AC P81840; P81841; P81842; P81843;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Citropin 1.2 [Contains: Citropin 1.2.1; Citropin
 DE 1.2.3].
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=99435977; PubMed=10504394;
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
 Wallace J.C., Tyler M.J.;
 RT "Host defence peptides from the skin glands of the Australian blue
 RT mountains tree-frog Litoria citropa. Solution structure of the
 RT antibacterial peptide citropin 1.1.";
 RL Eur. J. Biochem. 265:627-637(1999).
 CC -!- FUNCTION: BACTERIOSTATIC ACTION FOR GRAM-POSITIVE BACTERIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: DORSAL AND SUBMENTAL SKIN GLANDS.
 KW Amphibian defense peptide; Antibiotic; Amidation.
 FT PEPTIDE 1 16 CITROPIN 1.2.
 FT PEPTIDE 3 14 CITROPIN 1.2.1.
 FT PEPTIDE 4 14 CITROPIN 1.2.2.
 FT PEPTIDE 1 11 CITROPIN 1.2.3.
 FT MOD RES 16 AMIDATION
 SQ SEQUENCE 16 AA; 1616 MW; 1D878515ABD73DE9 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VV 2
 ||
 Db 12 VV 13

RESULT 71

DHE2_THUTH STANDARD; PRT; 16 AA.
 ID DHE2_THUTH STANDARD; PRT; 16 AA.
 AC P20016;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE NAD-specific glutamate dehydrogenase (EC 1.4.1.2) (NAD-GDH
 DE (Fragment)).
 OS Thunnus thynnus (Bluefin tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

OC Scornbridae; Thunus.
 OX NCBI_TaxID=8237;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=76253947; PubMed=182270;
 RA Veronese F.M., Bevilacqua R., Bocca E., Brown D.M.;
 RT "Purification, characteristics and sequence of a peptide containing
 an essential lysine residue."
 RL Biochim. Biophys. Acta 445:1-13 (1976).
 CC -|- CATALYTIC ACTIVITY: L-glutamate + H(2)O + NAD(+) = 2-oxoglutarate
 + NH(3) + NADH.
 CC -|- SIMILARITY: BELONGS TO THE GLU/LEU/PHE/VAL DEHYDROGENASES FAMILY.
 CC PIR; A12729; A12729.
 DR InterPro; IPR006095; GLFV dehydrog.
 DR InterPro; IPR006097; GLFV dehydrog_N.
 DR Pfam; PF02812; GLFV dehydrog_N; 1.
 DR PROSITE; PS00074; GLFV DEHYDROGENASE; PARTIAL.
 KW Oxidoreductase; NAD.
 FT NON_TER 1 1
 FT ACT_SITE 12 12
 FT NON_TER 16 16
 FT SEQUENCE 16 AA; 1518 MW; FF299AA7C5F1062F CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VV 2
 DB 3 VV 4

RESULT 72
 HTPG ACICA STANDARD; PRT; 16 AA.
 ID HTPG ACICA
 AC P81876;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chaperone protein htpg (Heat shock protein htpg) (High temperature
 protein G) (Fragment).
 GN HTPG.
 OS Acinetobacter calcoaceticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=471;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=69-V;
 RX MEDLINE=99274045; PubMed=10344248;
 RA Berndorf D., Loffhagen N., Babel W.;
 RT "Induction of heat shock proteins in response to primary alcohols in
 Acinetobacter calcoaceticus."
 RL Electrophoresis 20:781-789 (1999).
 CC -|- FUNCTION: Molecular chaperone. Has ATPase activity (By
 similarity).
 CC -|- SUBUNIT: Homodimer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -|- INDUCTION: BY HEAT SHOCK AND PRIMARY ALCOHOLS.
 CC -|- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
 DR HAMAP; MF 00505; 1.
 DR InterPro; IPR001404; Hsp90.
 DR PROSITE; PS00298; HSP90; PARTIAL.
 KW Chaperone; ATP-binding; Heat shock.
 FT NON_TER 16 16
 FT SEQUENCE 16 AA; 1769 MW; 316C70D8928CB482 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EV 5

Db 13 EV 14

RESULT 73
 LE05 BIOGL STANDARD; PRT; 16 AA.
 ID LE05 BIOGL
 AC P80744;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hemolymph 65 kDa lectin BG05 (Fragment).
 GN BG05.
 OS Biophalarina glabrata (Bloodfluke planorb).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Planorbidae; Biomphalaria.
 OX NCBI_TaxID=6526;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=N-LINE; TISSUE=Hemolymph;
 RX MEDLINE=97385165; PubMed=9238039;
 RA Adema C.M., Hertel L.A., Miller R.D., Loker E.S.;
 RT "A family of fibrinogen-related proteins that precipitates parasite-
 derived molecules is produced by an invertebrate after infection."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8691-8696 (1997).
 CC -|- FUNCTION: BINDS AND PRECIPITATES ANTIGENS OF THE PARASITE
 ECHINOSTOMA PARAENSEI.
 CC -|- SUBCELLULAR LOCATION: SECRETED IN THE HEMOLYMPH.
 CC -|- INDUCTION: By infection.
 KW Lectin.
 FT NON_TER 1 1
 FT NON_TER 16 16
 FT SEQUENCE 16 AA; 1790 MW; 57489A8F2EEDAA94 CRC64;
 Query Match 40.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred.No. 7.1e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VV 2
 DB 10 VV 11

RESULT 74
 PGTL PELAC STANDARD; PRT; 16 AA.
 ID PGTL PELAC
 AC P80563;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Pyrogallol hydroxyltransferase large subunit (EC 1.97.1.2)
 DE (Transhydroxylase) (Fragment).
 OS Pelobacter acidigallici.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Pelobacteraceae; Pelobacter.
 OX NCBI_TaxID=35816;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 2377 / Braunschweig;
 RX MEDLINE=96215436; PubMed=8647079;
 RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;
 RT "One molecule of molybdopterin guanine dinucleotide is associated
 with each subunit of the heterodimeric Mo-Fe-S protein
 transhydroxylase of Pelobacter acidigallici as determined by SDS/PAGE
 and mass spectrometry."
 RL Eur. J. Biochem. 237:406-413 (1996).
 CC -|- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3-
 trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-
 tetrahydroxybenzene.
 CC -|- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
 CC -|- SUBUNIT: Heterodimer of a large and a small subunit.
 DR PIR; S65430; S65430.
 KW Oxidoreductase; Molybdenum; Iron-sulfur.

FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1620 MW; 56348D53A0AD6EE3 CRC64;
Query Match 40.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
||
Db 2 EV 3

RESULT 75

ID PH2_PRUSE STANDARD; PRT; 16 AA.
AC P29264;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Prunasin beta-glucosidase IIA (EC 3.2.1.118) (Prunasin hydrolase
isozyme IIA) (PH IIA) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosidia I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -!- CATALYTIC ACTIVITY: (R)-prunasin + H(2)O = mandelonitrile + D-
glucose.
CC -!- SUBUNIT: Homodimer.
CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH CORYLEDON
DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
EMBRYONAL TISSUES.
CC -!- PTM: GLYCOSYLATED.
KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1703 MW; FC4D7F4FB90CFE01 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 7.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
||
Db 7 VV 8

Search completed: November 25, 2003, 18:17:29
Job time : 3.42021 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 12.0479 Seconds
(without alignments)
107.095 Million cell updates/sec

Title: US-09-641-801-9
Perfect score: 5
Sequence: 1 VMEV 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 810525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23:**

1: sp_archaea:**

2: sp_bacteria:**

3: sp_fungi:**

4: sp_human:**

5: sp_invertebrate:**

6: sp_mammal:**

7: sp_mhc:**

8: sp_organelle:**

9: sp_phase:**

10: sp_plant:**

11: sp_rodent:**

12: sp_virus:**

13: sp_vertebrate:**

14: sp_unclassified:**

15: sp_rvirus:**

16: sp_bacteriap:**

17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3	60.0	9	10 Q9FXL0	Q9FXL0 lilium long
2	3	60.0	10	13 Q42355	Q42355 brachydanio
3	3	60.0	11	2 Q47606	Q47606 escherichia
4	3	60.0	14	11 Q70544	Q70544 mesocricetu
5	3	60.0	15	4 Q9Y429	Q9Y429 homo sapien
6	3	60.0	15	4 Q9UCH0	Q9UCH0 homo sapien
7	3	60.0	15	6 Q9TRP9	Q9TRP9 bos taurus
8	3	60.0	16	2 Q9RP22	Q9RP22 citrobacter
9	3	60.0	16	5 Q95Y34	Q95Y34 caenorhabdi
10	3	60.0	16	10 Q9S8L1	Q9S8L1 sorghum bic
11	3	60.0	17	12 Q85719	Q85719 reovirus (t
12	3	60.0	18	8 Q9ZY80	Q9ZY80 scellio fulg
13	3	60.0	19	10 Q94L06	Q94L06 brassica na
14	3	60.0	19	11 Q922T5	Q922T5 mus musculu
15	3	60.0	20	2 Q47614	Q47614 escherichia
16	3	60.0	20	12 Q38539	Q38539 human torov

17	3	60.0	20	12	Q72059	O72059 bovine toco
18	2	40.0	7	2	Q47029	Q47029 enterobacte
19	2	40.0	7	13	Q8J320	Q8J320 gallus gall
20	2	40.0	8	2	P72279	P72279 rhodococcus
21	2	40.0	8	2	O68485	O68485 klebsiella
22	2	40.0	8	2	Q56759	Q56759 xanthomyc
23	2	40.0	8	3	Q05403	Q05403 saccharomyc
24	2	40.0	8	4	Q16428	Q16428 homo sapien
25	2	40.0	8	4	Q9P285	Q9P285 homo sapien
26	2	40.0	8	4	Q81V87	Q81V87 homo sapien
27	2	40.0	8	5	Q9UB13	Q9UB13 albinaria h
28	2	40.0	8	5	Q94623	Q94623 manduca sex
29	2	40.0	8	5	Q94695	Q94695 physarum po
30	2	40.0	8	6	Q9MYL5	Q9MYL5 pongo pygma
31	2	40.0	8	10	Q9SB24	Q9SB24 nicotiana t
32	2	40.0	8	10	Q42507	Q42507 triticum ae
33	2	40.0	8	10	P82324	P82324 pisum sativ
34	2	40.0	8	11	Q9ET21	Q9ET21 mus musculu
35	2	40.0	8	11	Q62527	Q62527 mus spretus
36	2	40.0	8	12	Q9E8Q5	Q9E8Q5 beet soil-b
37	2	40.0	8	12	Q9E8Q2	Q9E8Q2 beet soil-b
38	2	40.0	8	12	Q9E8P9	Q9E8P9 beet soil-b
39	2	40.0	8	12	Q9E8Q3	Q9E8Q3 beet soil-b
40	2	40.0	8	12	Q9E8Q1	Q9E8Q1 beet soil-b
41	2	40.0	8	12	Q9DSN2	Q9DSN2 beet soil-b
42	2	40.0	8	12	Q9E8Q4	Q9E8Q4 beet soil-b
43	2	40.0	8	12	Q9DSN5	Q9DSN5 beet soil-b
44	2	40.0	8	12	Q9E8P7	Q9E8P7 beet soil-b
45	2	40.0	8	12	Q9DSN1	Q9DSN1 beet soil-b
46	2	40.0	8	12	Q9DSN3	Q9DSN3 beet soil-b
47	2	40.0	8	12	Q9DSN4	Q9DSN4 beet soil-b
48	2	40.0	8	12	Q9E8Q0	Q9E8Q0 beet soil-b
49	2	40.0	8	12	Q9E8Q7	Q9E8Q7 beet soil-b
50	2	40.0	8	12	Q9DSN6	Q9DSN6 beet soil-b
51	2	40.0	8	12	Q9DSN0	Q9DSN0 beet soil-b
52	2	40.0	8	12	Q9E8Q6	Q9E8Q6 beet soil-b
53	2	40.0	8	12	Q9E8P8	Q9E8P8 beet soil-b
54	2	40.0	8	13	Q9E8T5	Q9E8T5 xenopus lae
55	2	40.0	9	2	Q9R735	Q9R735 streptomyce
56	2	40.0	9	2	P82568	P82568 streptococc
57	2	40.0	9	3	Q9P8E5	Q9P8E5 kluyveromyc
58	2	40.0	9	4	Q9H4B1	Q9H4B1 homo sapien
59	2	40.0	9	4	Q9UGB4	Q9UGB4 homo sapien
60	2	40.0	9	4	Q8NHL3	Q8NHL3 homo sapien
61	2	40.0	9	5	Q27396	Q27396 babesia bov
62	2	40.0	9	6	Q9XSL0	Q9XSL0 capra hircu
63	2	40.0	9	9	Q38340	Q38340 lactococcus
64	2	40.0	9	10	Q8LPT5	Q8LPT5 zea mays (m
65	2	40.0	9	11	Q92012	Q92012 mus musculu
66	2	40.0	9	12	Q91IX6	Q91IX6 macaca neme
67	2	40.0	10	2	Q47091	Q47091 escherichia
68	2	40.0	10	2	P82588	P82588 streptococc
69	2	40.0	10	4	O00493	O00493 homo sapien
70	2	40.0	10	4	Q13318	Q13318 homo sapien
71	2	40.0	10	4	Q9UC08	Q9UC08 homo sapien
72	2	40.0	10	4	Q96QT9	Q96QT9 homo sapien
73	2	40.0	10	4	Q8WT14	Q8WT14 homo sapien
74	2	40.0	10	4	Q81ZA2	Q81ZA2 homo sapien
75	2	40.0	10	5	P82384	P82384 drosophila
76	2	40.0	10	5	P82222	P82222 bombyx mori
77	2	40.0	10	6	Q8WP04	Q8WP04 ateles belz
78	2	40.0	10	6	Q9GKI5	Q9GKI5 pan troglod
79	2	40.0	10	6	Q9GKI4	Q9GKI4 macaca arct
80	2	40.0	10	6	Q8H271	Q8H271 didelphis m
81	2	40.0	10	8	Q8WGD2	Q8WGD2 hepatus eph
82	2	40.0	10	8	Q8SL54	Q8SL54 aconium haw
83	2	40.0	10	10	Q8LPT7	Q8LPT7 zea mays (m
84	2	40.0	10	10	P83091	P83091 spinacia ol
85	2	40.0	10	12	Q39957	Q39957 hepatitis g
86	2	40.0	10	12	Q9W8B6	Q9W8B6 hepatitis g
87	2	40.0	10	12	Q39948	Q39948 hepatitis g
88	2	40.0	10	12	Q39952	Q39952 hepatitis g
89	2	40.0	10	12	Q9W910	Q9W910 hepatitis g

90 Q2625 infectious
 91 Q9wie4 hepatitis g
 92 Q90344 hepatitis g
 93 Q39949 hepatitis g
 94 Q84266 human papil
 95 Q73589 gallus gall
 96 Q54980 avian myelo
 97 Q75595 human immun
 98 Q8x4es escherichia
 99 Q9r4b1 streptococc
 100 Q93mi7 escherichia

ALIGNMENTS

RESULT 1
 Q9FXLO PRELIMINARY; PRT; 9 AA.
 AC Q9FXLO;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
 DE LIM8 protein (Fragment).
 GN LIM8
 OS Lilium longiflorum (Trumpet lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxID=4690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Hinomoto;
 RA Uefuji H., Takase H., Hiratsuka K.;
 RT "Lilium longiflorum LIM8 gene, promoter region and partial sequence."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB050987; BAB17856.1; -.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;

Query Match 60.0%; Score 3; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
 DB 1 MEV 3
 RESULT 2
 Q42355 PRELIMINARY; PRT; 10 AA.
 ID Q42355;
 AC Q42355;
 DT 01-JAN-1998 (TRENBLrel. 05, Created)
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE GATA-2 (Fragment).
 GN GATA2.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97322361; PubMed=9177206;
 RA Meng A., Tang H., Ong B.A., Farrell M.J., Lin S.;
 RT "Promoter analysis in living embryos identifies a cis-acting motif
 required for neuronal expression of GATA-2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6267-6272(1997).
 DR EMBL; AF001220; AAB61711.1; -.
 DR ZFIN; ZDB-GENE-980526-260; gata2.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1192 MW; C82A2CA6DAADDCC2 CRC64;

Query Match 60.0%; Score 3; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
 DB 1 MEV 3
 RESULT 3
 Q47606 PRELIMINARY; PRT; 11 AA.
 ID Q47606;
 AC Q47606;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE REase protein (Fragment).
 GN REase
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 modification systems."
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63622; AAA24562.1; -.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1370 MW; 68C1FF9959CB133B CRC64;

Query Match 60.0%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
 DB 1 MEV 3

RESULT 4
 O70544 PRELIMINARY; PRT; 14 AA.
 ID O70544;
 AC O70544;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Uteroglobulin/clara cell 10kDa protein (Fragment).
 GN UG/CC10.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98141958; PubMed=9473294;
 RA Gutierrez-Sagal R., Nieto A.;
 RT "Molecular cloning of the cDNA and the promoter of the hamster
 uteroglobulin/clara cell 10 kDa gene (ug/cc10): tissue-specific and
 hormonal regulation."
 RL Arch. Biochem. Biophys. 350:214-222(1998).
 DR EMBL; Y13765; CAA74098.1; -.
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1507 MW; AB8BCA79F72AF4D6 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 VWM 3
Db 9 VWM 11

RESULT 5
Q9Y4Z9 PRELIMINARY; PRT; 15 AA.
AC Q9Y4Z9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE FANCA protein (Fragment).
GN FANCA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA D'Apollito M., Ianzano L., Savino M., Rommens J., Zelante L.,
RA Savoia A.;
RA "Differential expression of FANCA and FANCC genes in human tissues and
RT alternative splicing of FANCA transcripts.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131189; CAB46099.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1590 MW; 8732D75A24DCA4F0 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3
Db 1 VWM 3

RESULT 6
Q9UCH0 PRELIMINARY; PRT; 15 AA.
AC Q9UCH0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Urinary gonadotrophin peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93229246; PubMed=8471426;
RA Kardana A., Bagshawe K.D., Coles B., Read D., Taylor M.;
RA "Characterisation of UGP and its relationship with beta-core
RT fragment.";
RL Br. J. Cancer 67:686-692(1993).
SQ SEQUENCE 15 AA; 1653 MW; CAF53561D7907FF6 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 6 MEV 8

RESULT 7
Q9TRP9 PRELIMINARY; PRT; 15 AA.
AC Q9TRP9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

Qy 1 VWM 3
Db 9 VWM 11

RESULT 8
Q9RP22 PRELIMINARY; PRT; 16 AA.
AC Q9RP22;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Int1 (Fragment).
GN INT1.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCUG42386; TRANSPOS=class I integron;
RA Norskov-Lauritsen N., Sandvang D., Hedsgaard J., Fussing V.,
RA Mortensen K.K., Sperling-Petersen H.U., Frimodt-Moller N.,
RA Schonheyder H.C.;
RT "Clonal origin of aminoglycoside-resistant Citrobacter freundii in a
RT Danish county.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF175203; AAD55062.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1830 MW; 388BB7D833A6115C CRC64;

Query Match 60.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 3 VME 5

RESULT 9
Q95Y34 PRELIMINARY; PRT; 16 AA.
AC Q95Y34;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 1.9 kDa protein.
GN Y1083AL.6.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.

```



```

OX NCBI_TaxID=6239;
RP SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Courtney L.;
RT "The sequence of C. elegans cosmid Y108G3AL.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024744; AAL13326.1; -.
DR WormPep; Y108G3AL.6; CE29605.
KW Hypothetical protein
SQ SEQUENCE 16 AA; 1904 MW; 4932099B5AA361E5 CRC64;

Query Match 60.0%; Score 3; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db |||
1 MEV 3

RESULT 10
Q9S8L1 PRELIMINARY; PRT; 16 AA.
ID Q9S8L1;
AC Q9S8L1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Cytochrome P-450 (fragment).
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE.
RX MEDLINE=95024036; PubMed=7937883;
RA Sibbesen O., Koch B., Halkier B.A., Moller B.L.;
RT "Isolation of the heme-thiolate enzyme cytochrome P-450TYR, which
RT catalyzes the committed step in the biosynthesis of the cyanogenic
RT glucoside dhurrin in Sorghum bicolor (L.) Moench.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:9740-9744(1994).
SQ SEQUENCE 16 AA; 1516 MW; D5488D84E9FD489 CRC64;

Query Match 60.0%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db |||
3 MEV 5

RESULT 11
Q85719 PRELIMINARY; PRT; 17 AA.
ID Q85719;
AC Q85719;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

```

```

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Reovirus serotype 3 S4 (Fragment).
OS Reovirus (type 3 / strain Dearing).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10886;
RN [1]
RP SEQUENCE OF 1-10 FROM N.A.
RX MEDLINE=82032340; PubMed=6270271;
RA McCrae M.A.;
RT "Terminal structure of reovirus RNAs.";
RL J. Gen. Virol. 55:393-403(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017876; PubMed=6927854;
RA Antczak J.B., Chmelo R., Pickup D.J., Joklik W.K.;
RT "Sequences at both termini of the 10 genes of reovirus serotype 3
RT (strain Dearing).";
RL Virology 121:307-319(1982).
DR EMBL; J02332; AAA47284.1; -.
DR InterPro; IPR000153; Reovirus_cap.
DR Pfam; PF00979; Reovirus_cap; 1.
FT NON TER 17
SQ SEQUENCE 17 AA; 1852 MW; A7EAB7E4649C1F0D CRC64;

Query Match 60.0%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db |||
1 MEV 3

RESULT 12
Q9ZY80 PRELIMINARY; PRT; 18 AA.
ID Q9ZY80;
AC Q9ZY80;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Scelio fulgidus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Platygastridae;
OC Scellionidae; Scelio.
OX NCBI_TaxID=32419;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF082921; AAD17781.1; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 18 AA; 2224 MW; 981713ABC608BB17 CRC64;

Query Match 60.0%; Score 3; DB 8; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db |||
2 VME 4

RESULT 13
Q94L06 PRELIMINARY; PRT; 19 AA.
ID Q94L06;
AC Q94L06;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

```

```

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DI isopropyl malate synthase (Fragment).
GN MYJ24-1-BN-7.
OS Brassica napus (Rape).
ON Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Yudal.
RA Fournann M., Froger N., Brunel D.;
RT "Amplified consensus gene markers: Tools designing for a genetic map
of Arabidopsis-known-function genes in Brassica.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258256; AAK49052.1; -.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 1989 MW; A41FC1E46CFC0E6D CRC64;

Query Match 60.0%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 9 VVM 11

RESULT 14
Q922T5 ID Q922T5 PRELIMINARY; PRT; 19 AA.
AC Q922T5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Unknown (Protein for IMAGE:3586282) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006792; AAK06792.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2143 MW; 62431F68A3580579 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 4 VME 6

RESULT 15
Q47614 ID Q47614 PRELIMINARY; PRT; 20 AA.
AC Q47614;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE URF protein.
GN URF.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91232952; PubMed=1709493;
RA Albrechtsen B., Ross B.M., Squires C., Squires C.L.;
RT "Transcriptional termination sequence at the end of the Escherichia
coli ribosomal RNA G operon: complex terminators and
antitermination.";
RL Nucleic Acids Res. 19:1845-1852(1991).
DR EMBL; X56780; CAA40098.1; -.
SQ SEQUENCE 20 AA; 2162 MW; D952ACD7417E163 CRC64;

Query Match 60.0%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

RESULT 16
O38539 ID O38539 PRELIMINARY; PRT; 20 AA.
AC O38539;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nucleocapsid protein (Fragment).
OS Human torovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Torovirus.
OX NCBI_TaxID=67605;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=38087835; PubMed=9426455;
RA Duckmanton L., Luan B., Devenish J., Tellier R., Petric M.;
RT "Characterization of torovirus from human fecal specimens.";
RL Virology 239:158-168(1997).
DR EMBL; AF024539; AAC40323.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2224 MW; CBD4007B9199F122 CRC64;

Query Match 60.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 17 VVM 19

RESULT 17
O72059 ID O72059 PRELIMINARY; PRT; 20 AA.
AC O72059;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nucleocapsid protein (Fragment).
OS Bovine torovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Torovirus.
OX NCBI_TaxID=74501;
RN [1]
RP SEQUENCE FROM N.A.
RA Duckmanton L., Carman S., Nagy E., Petric M.;
RT "Detection of Bovine Torovirus in Fecal Specimens of Calves with
Diarrhea from Ontario farms.";
RL J. Clin. Microbiol. 36:0-0(1998).
DR EMBL; AF053061; AAC15709.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2225 MW; CBD4007B8D6BF122 CRC64;

```

```

Query Match      60.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
DB 17 VVM 19

RESULT 18
Q47029 PRELIMINARY; PRT; 7 AA.
ID Q47029
AC Q47029
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Aad A1 protein (Fragment).
GN Aad A1.
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=550;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94079349; PubMed=8257126;
RA Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
RT "Analysis of the aac(3)-VIA gene encoding a novel 3'-N-
RT acetyltransferase."
RL Antimicrob. Agents Chemother. 37:2074-2079(1993).
DR EMBL; M88012; AAL16193.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;

Query Match      40.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 4 VV 5

RESULT 19
Q8JU20 PRELIMINARY; PRT; 7 AA.
ID Q8JU20
AC Q8JU20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Extracellular fatty acid binding protein (Fragment).
GN EXFABP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Wang Q., Li N., Li H.;
RT "Cloning and sequencing of 3' UTR of EXFABP gene in chicken."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF487519; AAL96665.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 780 MW; 72CBIAB2D5BEBB70 CRC64;

Query Match      40.0%; Score 2; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 6 EV 7

RESULT 20
P72279 PRELIMINARY; PRT; 8 AA.
ID P72279
AC P72279;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Biphenyl dioxygenase (Fragment).
GN BPHB.
OS Rhodococcus globerulus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=33008;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255652; PubMed=7737502;
RA Asturias J.A., Diaz E., Timmis K.N.;
RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-
RT positive bacterium Rhodococcus globerulus P6 to multicomponent
RT dioxygenases of gram-negative bacteria."
RL Gene 156:111-18(1995).
DR EMBL; X80041; CAA56350.1; -.
KW Dioxygenase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 7 VV 8

RESULT 21
O68485 PRELIMINARY; PRT; 8 AA.
ID O68485
AC O68485;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Aminoglycoside 3'-O-nucleotidyltransferase (Fragment).
GN AADA1.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=98287600; PubMed=9624504;
RA Centron D., Roy P.H.;
RT "Characterization of the 6'-N-aminoglycoside acetyltransferase gene
RT aac(6')-Iq from the integron of a natural multiresistance plasmid."
RL Antimicrob. Agents Chemother. 42:1506-1508(1998).
DR EMBL; AF047556; AAC25501.1; -.
KW Plasmid; Transferase.
FT NON_TER 8
SQ SEQUENCE 8 AA; 878 MW; EFC1B5A2CB1DD056 CRC64;

Query Match      40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
DB 4 EV 5

```

```

RESULT 22.
Q56759          PRELIMINARY;      PRT;      8 AA.
AC Q56759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Haloacid dehalogenase (Fragment).
GN DHLB.
OS Xanthobacter autotrophicus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GJ10, and CV. M50;
RX MEDLINE=95173113; PubMed=7868610;
RA Van der Ploeg J., Willemsen M., van Hall G., Janssen D.B.;
RT "Adaptation of xanthobacter autotrophicus GJ10 to bromoacetate due to
RT activation and mobilization of the haloacetate dehalogenase gene by
RT insertion element IS1247.";
RL J. Bacteriol. 177:1348-1356(1995).
DR EMBL: X84038; CAA58857.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
Db 5 WV 6

RESULT 23
Q05403          PRELIMINARY;      PRT;      8 AA.
AC Q05403;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE DNA for ORF'S from chromosome XV (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zumbstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL: X83121; CAA58183.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 40.0%; Score 2; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VW 2
Db 5 WV 6

RESULT 24
Q16428          PRELIMINARY;      PRT;      8 AA.
ID Q16428
AC Q16428
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

```

```

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GN Dystrophin protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163501; PubMed=8566960;
RA Holder E., Maeda M., Bies R.D.;
RT "Expression and regulation of the dystrophin Purkinje promoter in
RT human skeletal muscle, heart, and brain.";
RL Hum. Genet. 97:232-239(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: S81419; AAD14363.1; -.
DR EMBL: AB037493; BAA90413.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CE05B6 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EV 5
Db 3 EV 4

RESULT 25
Q9P285          PRELIMINARY;      PRT;      8 AA.
ID Q9P285
AC Q9P285;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Clotting factor VIII (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Shibata M., Shima M., Morichika S., Yoshiola A.;
RT "Human clotting factor VIII gene, junction regions of the deletion of
RT exon 4 through 7.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB040872; BAA94312.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 866 MW; 1C16987AAB05BDD3 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ME 4
Db 7 ME 8

RESULT 26
Q8IV87          PRELIMINARY;      PRT;      8 AA.
ID Q8IV87
AC Q8IV87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

```

```

DE DJ107712.2 (Serine palmitoyltransferase, long chain base subunit
GN SPTIC2L,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050320; CAD54807.1; -.
KW Transferase.
FT NON_TER
SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBEB042 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VM 3
Db ||
5 VM 6

RESULT 27
Q9UB13 PRELIMINARY; PRT; 8 AA.
ID Q9UB13;
AC Q9UB13;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Calmodulin (Fragment).
OS Albinaria hippolyti.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Clausilloidea; Clausiliidae; Alopinae; Albinaria.
OX NCBI_TaxID=69418;
RN [1]
RP SEQUENCE FROM N.A.
RA Schiltshuizen M., Hoekstra R.F., Gittenberger E.;
RT "Selective maintenance of a rare haplotype in a land snail hybrid
RT zone."
RL Proc. R. Soc. Lond., B, Biol. Sci. 266:2181-2185(1999).
DR EMBL; AF132316; AAD34386.1; -.
FT NON_TER
FT NON_TER
SQ SEQUENCE 8 AA; 906 MW; F3ADDAB2CB144056 CRC64;

Query Match 40.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
4 EV 5

RESULT 28
Q94623 PRELIMINARY; PRT; 8 AA.
ID Q94623;
AC Q94623;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE MSUSP-2 protein (Fragment).
GN USP.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Spingiodea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE=Epidermis;
RX MEDLINE=97165493; PubMed=9013254;
RA Jindra M., Huang J.Y., Malone F., Asahina M., Riddiford L.M.;
RT "Identification and mRNA developmental profiles of two ultraspiracle
RT isoforms in the epidermis and wings of Manduca sexta.";
RL Insect Mol. Biol. 6:41-53(1997).
DR EMBL; U57921; AAB64235.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 892 MW; F165BB0415A76B16 CRC64;

Query Match 40.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db ||
1 ME 2

RESULT 29
Q94695 PRELIMINARY; PRT; 8 AA.
ID Q94695;
AC Q94695;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Actin (Fragment).
GN ARDC.
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
OC Physarum.
OX NCBI_TaxID=5791;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96182101; PubMed=8622700;
RA Benard M., Lagnel C., Pallotta D., Pierron G.;
RT "Mapping of a replication origin within the promoter region of two
RT unlinked, abundantly transcribed actin genes of Physarum
RT polycephalum."
RL Mol. Cell. Biol. 16:968-976(1996).
DR EMBL; M73459; AAB03706.1; -.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; F4C6C2CAAB187B16 CRC64;

Query Match 40.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db ||
1 ME 2

RESULT 30
Q9MYL5 PRELIMINARY; PRT; 8 AA.
ID Q9MYL5;
AC Q9MYL5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Dystrophin.
OS Pongo pygmaeus (Orangutan).
OS Pan troglodytes (Chimpanzee), and
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600; 9598, 9593;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.pygmaeus, P.troglodytes, and G.gorilla;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

```

```

DR EMBL; AB037496; BAA90419.1; -.
DR EMBL; AB037494; BAA90415.1; -.
DR EMBL; AB037495; BAA90417.1; -.
SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;
Query Match
Best Local Similarity 40.0%; Score 2; DB 6; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
3 EV 4

RESULT 31
Q9SB24 PRELIMINARY; PRT; 8 AA.
AC Q9SB24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ParAt protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Niwa Y., Muranaka T., Baba A., Machida Y.;
RT "Organ-specific and auxin-inducible expression of two tobacco para-
RL DNA Res. 0:0-0(1994).
DR EMBL; D42119; BAA07700.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 905 MW; FE32D2C44455BB16 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 10; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
6 VV 7

RESULT 32
Q42507 PRELIMINARY; PRT; 8 AA.
AC Q42507;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Heat shock protein (Fragment).
GN HSP70C OR HSP70A OR HSP70B.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV MUSTANG;
RA Joshi C.P., Kumar S., Nguyen H.T.;
RX MEDLINE=96189275; PubMed=8605312;
RT "Application of modified differential display technique for cloning
and sequencing of the 3' region from three putative members of wheat
HSP70 gene family.";
RL Plant Mol. Biol. 30:641-646(1996).
DR EMBL; L41507; AAB02333.1; -.
DR EMBL; L41505; AAB02331.1; -.
DR EMBL; L41506; AAB02332.1; -.
KW Heat shock.

FT NON_TER 1
SQ SEQUENCE 8 AA; 886 MW; 71B2CB1B10532768 CRC64;
Query Match
Best Local Similarity 40.0%; Score 2; DB 10; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
6 EV 7

RESULT 33
P82324 PRELIMINARY; PRT; 8 AA.
AC P82324;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SPOT105) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=CV. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
RT targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
CC PERIPHERY.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.7, ITS MW IS: 16.8 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 839 MW; DDC68B5DDDC2D2D5 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 10; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
2 VV 3

RESULT 34
Q9ET21 PRELIMINARY; PRT; 8 AA.
AC Q9ET21;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Placenta growth factor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21182783; PubMed=11289150;
RA Green C.J., Lichtlen P., Huynh N.T., Yanovsky M., Laderoute K.R.,
RA Schaffner W., Murphy B.J.;
RT "Placenta growth factor gene expression is induced by hypoxia in
RT fibroblasts: a central role for metal transcription factor-1.";
RL Cancer Res. 61:2696-2703(2001).

```

```
DR EMBL; AF285629; AAG00527.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 982 MW; E8A9C7233682C726 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 11; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VM 3
   ||
Db 3 VM 4

RESULT 35
Q62527
ID Q62527 PRELIMINARY; PRT; 8 AA.
AC Q62527;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Transthyretin (Prealbumin) (Fragment).
GN TTR.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
EX MEDLINE=94319082; PubMed=8043949;
RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maeraki Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
CC -!- FUNCTION: THYROID HORMONE-BINDING PROTEIN. PROBABLY TRANSPORTS
CC THYROXINE FROM THE BLOODSTREAM TO THE BRAIN.
CC -!- SUBUNIT: HOMOTETRAMER.
DR EMBL; U05689; AAB60461.1; -.
DR MGD; MGI:98865; Ttr.
KW Albumin; Transport; Retinol-binding; Vitamin A; Thyroid hormone.
FT NON_TER 1
SQ SEQUENCE 8 AA; 828 MW; 9156C76455A2D2CD CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 11; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
   ||
Db 2 VV 3

RESULT 36
Q9E8Q5
ID Q9E8Q5 PRELIMINARY; PRT; 8 AA.
AC Q9E8Q5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5b;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162921; AAG21077.1; -.
FT NON_TER 1
```

```
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 12; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
   ||
Db 3 VV 4

RESULT 37
Q9E8Q2
ID Q9E8Q2 PRELIMINARY; PRT; 8 AA.
AC Q9E8Q2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=31a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162928; AAG21080.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 12; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
   ||
Db 3 VV 4

RESULT 38
Q9E8P9
ID Q9E8P9 PRELIMINARY; PRT; 8 AA.
AC Q9E8P9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=37b;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162933; AAG21083.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match
Best Local Similarity 40.0%; Score 2; DB 12; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
   ||
Db 3 VV 4
```

```
RESULT 39
Q9EBQ3 ID Q9EBQ3 PRELIMINARY; PRT; 8 AA.
AC Q9EBQ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162924; AAG21079.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db ||
3 VV 4

RESULT 40
Q9EBQ1 ID Q9EBQ1 PRELIMINARY; PRT; 8 AA.
AC Q9EBQ1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=31b;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162929; AAG21081.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db ||
3 VV 4

RESULT 41
Q9DSN2 ID Q9DSN2 PRELIMINARY; PRT; 8 AA.
AC Q9DSN2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
```

```
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=21b;
RA Koenig R., Pleij C., Huth W.;
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
RT Pomovirus - a Virus with Uncertain Pathogenic Effects.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162927; AAG43392.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db ||
3 VV 4

RESULT 42
Q9EBQ4 ID Q9EBQ4 PRELIMINARY; PRT; 8 AA.
AC Q9EBQ4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162922; AAG21078.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 935 MW; ECA40EB322D2C056 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VV 2
Db ||
3 VV 4

RESULT 43
Q9DSN5 ID Q9DSN5 PRELIMINARY; PRT; 8 AA.
AC Q9DSN5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22k protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6b;
RA Koenig R., Pleij C., Huth W.;
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
RT Pomovirus - a Virus with Uncertain Pathogenic Effects.";
```


RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162923; AAG43389.1; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 935 MW; ECA40EB322D2C056 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
 ||
 Db 3 VV 4

RESULT 44

Q9EBP7 PRELIMINARY; PRT; 8 AA.
 AC Q9EBP7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 22K protein (Fragment).
 OS Beet soil-borne virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=46436;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=41b;
 RX MEDLINE=20403266; PubMed=10948990;
 RA Koenig R., Pleij C.W., Buettner G.;
 RT "Structure and variability of the 3', end of RNA 3 of Beet soil-borne
 pomovirus--a virus with uncertain pathogenic effects.";
 RL Arch. Virol. 145:1173-1181(2000).
 DR EMBL; AF162935; AAG21085.1; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
 ||
 Db 3 VV 4

RESULT 45

Q9DSN1 PRELIMINARY; PRT; 8 AA.
 AC Q9DSN1;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 22K protein (Fragment).
 OS Beet soil-borne virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=46436;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=33a;
 RA Koenig R., Pleij C., Huth W.;
 RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
 Pomovirus - a virus with Uncertain Pathogenic Effects.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162930; AAG43393.1; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2

Db ||
 3 VV 4

RESULT 46

Q9DSN3 PRELIMINARY; PRT; 8 AA.
 AC Q9DSN3;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 22K protein (Fragment).
 OS Beet soil-borne virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=46436;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=21a;
 RA Koenig R., Pleij C., Huth W.;
 RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
 Pomovirus - a Virus with Uncertain Pathogenic Effects.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162926; AAG43391.1; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
 ||
 Db 3 VV 4

RESULT 47

Q9DSN4 PRELIMINARY; PRT; 8 AA.
 AC Q9DSN4;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 22K protein (Fragment).
 OS Beet soil-borne virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 OX NCBI_TaxID=46436;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=10b;
 RA Koenig R., Pleij C., Huth W.;
 RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
 Pomovirus - a Virus with Uncertain Pathogenic Effects.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF162925; AAG43390.1; -.
 FT NON TER 1
 SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
 ||
 Db 3 VV 4

RESULT 48

Q9EQ0 PRELIMINARY; PRT; 8 AA.
 AC Q9EQ0;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

```

DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=37a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162932; AAG21082.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

RESULT 49
Q9EBQ7 PRELIMINARY; PRT; 8 AA.
AC Q9EBQ7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162918; AAG21075.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

RESULT 50
Q9DSN6 PRELIMINARY; PRT; 8 AA.
AC Q9DSN6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5a;
RA Koenig R., Pleij C., Huth W.;
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne

```

```

RT Pomovirus - a Virus with Uncertain Pathogenic Effects.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF162920; AAG43388.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

RESULT 51
Q9DSNO PRELIMINARY; PRT; 8 AA.
AC Q9DSNO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=33b;
RA Koenig R., Pleij C., Huth W.;
RT "Structure and Variability of the 3'End of RNA 3 of Beet Soil-Borne
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF162931; AAG43394.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 977 MW; 44D40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

RESULT 52
Q9EBQ6 PRELIMINARY; PRT; 8 AA.
AC Q9EBQ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 22K protein (Fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4b;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162919; AAG21076.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db ||
3 VV 4

```

```

Qy      1 VV 2
Db      3 VV 4

RESULT 53
Q98P8P8 PRELIMINARY; PRT; 8 AA.
AC Q98P8P8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE 22k protein (fragment).
OS Beet soil-borne virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
OX NCBI_TaxID=46436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=41a;
RX MEDLINE=20403266; PubMed=10948990;
RA Koenig R., Pleij C.W., Buettner G.;
RT "Structure and variability of the 3' end of RNA 3 of Beet soil-borne
RT pomovirus--a virus with uncertain pathogenic effects.";
RL Arch. Virol. 145:1173-1181(2000).
DR EMBL; AF162934; AAG21084.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 917 MW; 58A40EB322D2C050 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VV 2
Db      3 VV 4

RESULT 54
Q98TU5 PRELIMINARY; PRT; 8 AA.
AC Q98TU5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1D transcript 2 (fragment).
GN ELRD.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21226152; PubMed=11327714;
RA Nassar F., Wegnez M.;
RT "Characterization of two promoters of the Xenopus laevis elrD gene.";
RL Biochem. Biophys. Res. Commun. 283:392-398(2001).
DR EMBL; AF329448; AAK01428.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 1008 MW; FF93372874537B16 CRC64;

Query Match 40.0%; Score 2; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 ME 4
Db      1 ME 2

RESULT 55
Q9R735 PRELIMINARY; PRT; 9 AA.
ID Q9R735

```

```

AC Q9R735;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fkba protein (fragment).
GN FKBA.
OS Streptomyces chrysomallus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1899;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94341259; PubMed=8062824;
RA Pahl A., Keller U.;
RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
RT of two FKBP-12 binding domains with its gene transcriptionally coupled
RT to the FKBP-12 gene.";
RL EMBO J. 13:3472-3480(1994).
DR EMBL; Z34523; CAA84282.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1047 MW; 9A8BCB07633B1045 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 EV 5
Db      7 EV 8

RESULT 56
P82568 PRELIMINARY; PRT; 9 AA.
ID P82568
AC P82568;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whittom M., Kilby G.W., Rogers J.,
RA VanBogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins.";
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -!- MASS SPECTROMETRY: MW=22592.04; METHOD=ELECTROSPRAY.
FT NON TER 1 1
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 EV 5
Db      5 EV 6

RESULT 57
Q9P8E5 PRELIMINARY; PRT; 9 AA.
ID Q9P8E5
AC Q9P8E5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE HIS4 protein (fragment).

```

```

GN HIS4.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL-Y1140;
RX MEDLINE=99448382; PubMed=10518937;
RA Lamas-Maceiras M., Esperanza Cerdan E., Freire-Picos M.A.;
RT "Kluyveromyces lactis HIS4 transcriptional regulation: similarities
RT and differences to Saccharomycetes cerevisiae HIS4 gene.";
RL FEBS Lett. 458:72-76(1999).
DR EMBL; AJ238494; CAB87125.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1015 MW; 5770D2D772D2D767 CRC64;

Query Match 40.0%; Score 2; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db |||
4 VV 5

RESULT 58
ID Q9H4B1 PRELIMINARY; PRT; 9 AA.
AC Q9H4B1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE IGS12 protein (Fragment).
GN P27.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Martensen P.M., Soegaard T.M., Gjermansen I.M., Buttenschoen H.N.,
RA Rossing A.B., Bonnevie-Nielsen V., Rosada C., Simonsen J.L.,
RA Justesen J.;
RT "The interferon alpha induced protein ISG12 is localized to the
RT nuclear membrane.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ294851; CAC10503.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 896 MW; 6B9CA1A72DC5BDD8 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db |||
1 ME 2

RESULT 59
ID Q9UGE4 PRELIMINARY; PRT; 9 AA.
AC Q9UGE4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE D34105.1 (Remainder of gene in sequence AL023513) (Fragment).
GN SZ6L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL078460; CAB51751.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1125 MW; 8154A2CB0B5B0411 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db |||
6 EV 7

RESULT 60
ID Q8NHL3 PRELIMINARY; PRT; 9 AA.
AC Q8NHL3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Killer-cell immunoglobulin-like receptor KIR2DL5.3 (Fragment).
GN KIR2DL5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20540100; PubMed=11086080;
RA Vilches C., Gardiner C.M., Farham P.;
RT "Gene structure and promoter variation of expressed and nonexpressed
RT variants of the KIR2DL5 gene.";
RL J. Immunol. 165:6416-6421(2000).
DR EMBL; AF260137; AAG38010.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 968 MW; 9DEF85A3D2C69735 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
Db |||
5 VV 6

RESULT 61
ID Q27396 PRELIMINARY; PRT; 9 AA.
AC Q27396;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rhopty associated protein 1.
GN RAP-1.
OS Babesia bovis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5865;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=No7;
RA Suarez C.E., Palmer G.H., Hines S.A., McElwain T.F.;
RT "The Babesia bovis rhopty associated protein-1 intergenic region
RT encodes a functional eukaryotic promoter.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; L77326; AAA96415.1; -.
DR EMBL; L77245; AAD15061.1; -.
SQ SEQUENCE 9 AA; 931 MW; 6D5BD2C865B05044 CRC64;

```

Query Match 40.0%; Score 2; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
 DB 7 VV 8

RESULT 62
 Q9XSL0 PRELIMINARY; PRT; 9 AA.
 AC Q9XSL0; (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DE Alpha s2-casein (Fragment).
 GN CSN152.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OC NCBI_TaxID=9925;
 RN [1]_TaxID=9925;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=21313038; PubMed=11419340;
 RA Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,
 RA Cosenza G., Mariani P., Pastore N., Masina P.;
 RT "An allele associated with a non detectable amount of as2 casein in
 goat milk.";
 RL Anim. Genet. 32:19-26(2001).
 DR EMBL; AJ238475; CAB44298.1; --.
 FT NON_TER 1 1
 FT VARIANT 5 5 I -> V.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1047 MW; AAA2A5A5B051EB16 CRC64;

Query Match 40.0%; Score 2; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
 DB 2 ME 3

RESULT 63
 Q38340 PRELIMINARY; PRT; 9 AA.
 AC Q38340;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Orf protein (Fragment).
 GN ORF.
 OS Lactococcus phage 936.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC psiM1-like viruses.
 OC NCBI_TaxID=39838;
 RN [1]_TaxID=39838;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96084945; PubMed=7489923;
 RA Waterfield N.R., LePage R.W., Wilson P.W., Wells J.M.;
 RA "The isolation of lactococcal promoters and their use in investigating
 bacterial luciferase synthesis in Lactococcus lactis.";
 RL Gene 165:9-15(1995).
 DR EMBL; Z48181; CAA88226.1; --.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1054 MW; 7098B2CEA6D3372B CRC64;

Query Match 40.0%; Score 2; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
 DB 1 ME 2

RESULT 64
 Q8LPT5 PRELIMINARY; PRT; 9 AA.
 AC Q8LPT5;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Beta-expansin-like protein (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OC NCBI_TaxID=4577;
 RN [1]_TaxID=4577;
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. C123;
 RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
 RA Morgante M., Rafalski J.A.;
 RT "SNP frequency, haplotype structure and linkage disequilibrium in
 elite maize inbred lines.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY094310; AAM21836.1; --.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 977 MW; 5C05B2D2CB1AAAA3 CRC64;

Query Match 40.0%; Score 2; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
 DB 6 VV 7

RESULT 65
 Q92012 PRELIMINARY; PRT; 9 AA.
 AC Q92012;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE SLC12a4 (Fragment).
 GN SLC12A4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=129S6/SvEvTac; TISSUE=Spleen;
 RA Bjoernleitt M.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF236367; AAL11037.1; --.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 1037 MW; 78305041A042CB04 CRC64;

Query Match 40.0%; Score 2; DB 11; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
 DB 3 EV 4

RESULT 66.
Q9ILX6 PRELIMINARY; PRT; 9 AA.
AC Q9ILX6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ORF 10-like protein (Fragment).
OS Macaca nemestrina rhadinovirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=123630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mne442N;
RX MEDLINE=20240083; PubMed=10775636;
RA Schultz E.R., Rankin G.W. Jr., Blanc M.P., Raden B.W., Tsai C.C.,
RA Rose T.M.;
RT "Characterization of two divergent lineages of macaque rhadinoviruses
RT related to Kaposi's sarcoma-associated herpesvirus.";
RL J. Virol. 74:4919-4928(2000).
DR EMBL; AF204167; AAF81665.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1003 MW; 41EBD5B7233AB2C7 CRC64;

Query Match 40.0%; Score 2; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VW 2
Db 8 VV 9

RESULT 67
Q47091 PRELIMINARY; PRT; 10 AA.
ID Q47091
AC Q47091;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Colicin E1 (Fragment).
OS Escherichia coli.
OG Plasmid ColE1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86094231; PubMed=3936034;
RA Waleh N.S., Johnson P.H.;
RT "Structural and functional organization of the colicin E1 operon.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:8389-8393(1985).
DR EMBL; M12543; AAA23065.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1085 MW; 88F00B32CB144041 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db 6 EV 7

RESULT 68
P82588 PRELIMINARY; PRT; 10 AA.
ID P82588
AC P82588;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA VanBogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins.";
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -1- MASS SPECTROMETRY: MW=23573.25; METHOD=ELECTROSPRAY.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1134 MW; 4D5A1DCB105695B7 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db 7 EV 8

RESULT 69
O00493 PRELIMINARY; PRT; 10 AA.
ID O00493
AC O00493;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MJD1 alt MS (Fragment).
GN MJD1 INC 45.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RA Sugawara M., Toyoshima I., Takeda S., Imota T., Kato K., Wada C.,
RA Masamune O.;
RT "Genomic DNA containing the insertion that is seen in the alternative
RT transcript of MJD1.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003802; BAA20388.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1161 MW; 9A6E507B1AB2CB05 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db 4 EV 5

RESULT 70
Q13318 PRELIMINARY; PRT; 10 AA.
ID Q13318
AC Q13318;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PU.1 (Fragment).
GN SPI-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9603882; PubMed=7478579;
RA Chen H., Ray-Galliet D., Zhang P., Hetherington C.J., Gonzalez D.A.,
RA Zhang D.E., Moreau-Gachelin F., Tenen D.G.;
RT "PU.1 (Spi-1) autoregulates its expression in myeloid cells.";
RL Oncogene 11:1549-1560 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90265606; PubMed=1693183;
RA Ray D., Culine S., Ravitain A., Moreau-Gachelin F.;
RT "The human homologue of the putative proto-oncogene Spi-1:
RT characterization and expression in tumors [published erratum appears
RT in Oncogene 1990 Oct;5(10):1611-2].";
RL Oncogene 5:663-668 (1990).
DR EMBL; U34046; AAC50247.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1157 MW; C2EB4216933EBDC6 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db ||
7 ME 8

RESULT 71
Q9UCQ8 PRELIMINARY; PRT; 10 AA.
AC Q9UCQ8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein.";
RL J. Biol. Chem. 267:2524-2529 (1992).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1171 MW; 736F44577AF1B2CB CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
3 EV 4

RESULT 72
Q96QT9 PRELIMINARY; PRT; 10 AA.
AC Q96QT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protein tyrosine phosphatase 1B (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21326081; PubMed=11316810;
RA Fukada T., Tonks N.K.;
RT "The Reciprocal Role of Egr-1 and Sp Family Proteins in Regulation of
RT the PPIB Promoter in Response to the p210 Bcr-Abl Oncoprotein-
RT tyrosine Kinase.";
RL J. Biol. Chem. 276:25512-25519 (2001).
DR EMBL; AY029236; AAK31734.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1314 MW; AC08E219CB133B16 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
Db ||
1 ME 2

RESULT 73
Q8WTT4 PRELIMINARY; PRT; 10 AA.
AC Q8WTT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dystrophin (Fragment).
GN DYSTROPHIN OR DMD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ditta S.D., Klamt H.J., Ray P.N., Morton R.G.;
RT "The role of matrix attachment regions in transcriptional regulation
RT from the muscle-specific promoter in the dystrophin gene.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Beggs A.H., Koenig M., Kunkel L.M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA den Dunnen J.T.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF276053; AAL35752.1; -.
DR EMBL; AF213401; AAL61549.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1339 MW; 2B999202CB1B0363 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EV 5
Db ||
6 EV 7

RESULT 74
Q81ZA2 PRELIMINARY; PRT; 10 AA.
AC Q81ZA2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cardiac troponin T (Fragment).
GN TNNT2.

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Bahl A., Kubo T., Steffensen U., Steffensen M., McKenna W.J.,
RA Mogensen J.;
RT "Homo sapiens Troponin T (TNNT2) introns 6 and 7 and exon 7.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AV160215; AAN71650.1; -
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1099 MW; AB24EC6325BB1B16 CRC64;

Query Match 40.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred.No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ME 4
DB 3 ME 4

RESULT 75
P82384
ID P82384 PRELIMINARY; PRT; 10 AA.
AC P82384;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE Larval cuticle Lcp9 protein (Fragment).
GN LCP9.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE.
RC STRAIN=OREGON-R; TISSUE=Larva;
RA Chihara C.J.;
RT "Third instar cuticle proteins.";
RL DIS 83:0-0(2000).
CC -!- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
DR FlyBase; FBgn0025578; Lcp9.
DR InterPro; IPR000618; Insect cuticle.
DR PROSITE; PS00233; CUTICLE; PARTIAL.
KW Cuticle; Structural protein.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1105 MW; 7EF84522D2CAADB CRC64;

Query Match 40.0%; Score 2; DB 5; Length 10;
Best Local Similarity 100.0%; Pred.No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VV 2
DB 6 VV 7

```

Search completed: November 25, 2003, 18:25:28
 Job time : 15.0979 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 16.1968 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-9
Perfect score: 5
Sequence: 1 VNEV 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A Geneseq 19Jun03:*

1:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	5	100.0	5	22 AAB72254	Colostrinin derive
2	5	100.0	5	22 AAB72508	Colostrinin peptid
3	5	100.0	5	22 AAB72540	Colostrinin peptid
4	5	100.0	5	22 AAB59321	Ewe colostrinin pe
5	5	100.0	5	23 AA20236	Colostrinin consti
6	5	100.0	5	23 AA20236	Colostrinin consti
7	5	100.0	5	23 AA014585	Neural cell regula
8	5	100.0	5	22 AAB59351	Ewe colostrinin pe
9	4	80.0	9	22 AAY46069	Immunogenic peptid

10	4	80.0	9	15 AAY38335	MAGE-derived HLA-b
11	4	80.0	9	15 AAR73833	Antigen fragment 1
12	4	80.0	9	16 AAR65122	MAGE 1 immunogenic
13	4	80.0	9	20 AAY45916	Immunogenic peptid
14	4	80.0	9	20 AAY46133	Immunogenic peptid
15	4	80.0	9	20 AAY46358	Immunogenic peptid
16	4	80.0	9	20 AAY47189	Immunogenic peptid
17	4	80.0	9	20 AAY47274	Immunogenic peptid
18	4	80.0	9	20 AAY47275	Immunogenic peptid
19	4	80.0	10	15 AAY38327	MAGE-derived HLA-b
20	4	80.0	10	15 AAR47332	HLA-A1 MAGE 1 anti
21	4	80.0	10	20 AAY45908	Immunogenic peptid
22	4	80.0	10	20 AAY46049	Immunogenic peptid
23	4	80.0	10	20 AAY46105	Immunogenic peptid
24	4	80.0	10	20 AAY46106	Immunogenic peptid
25	4	80.0	11	20 AAY46073	Immunogenic peptid
26	4	80.0	11	20 AAY47431	Immunogenic peptid
27	4	80.0	11	20 AAY47558	Immunogenic peptid
28	4	80.0	11	21 AAB12653	Immunogenic peptid
29	4	80.0	16	16 AAR83269	Protein kinase pep
30	3	60.0	4	12 AAR15779	HIV principal neut
31	3	60.0	4	12 AAR15650	Farnesyl-protein t
32	3	60.0	4	15 AAR49744	Ras protein inhibi
33	3	60.0	4	16 AAR77806	Farnesyltransferas
34	3	60.0	4	17 AAW04436	Farnesyl transfera
35	3	60.0	4	20 AAY18380	N-Ras geranylgeran
36	3	60.0	4	20 AAY18367	N-Ras geranylgeran
37	3	60.0	4	20 AAY18350	N-Ras geranylgeran
38	3	60.0	4	20 AAY18337	N-Ras geranylgeran
39	3	60.0	4	20 AAY18324	N-Ras geranylgeran
40	3	60.0	4	20 AAY13426	Human N-Ras peptid
41	3	60.0	4	20 AAY17051	Human N-Ras peptid
42	3	60.0	4	20 AAY02235	"CAAXG" motif from
43	3	60.0	4	20 AAW99755	CAAX-G motif pepi
44	3	60.0	4	20 AAW99740	CAAX-G motif pepi
45	3	60.0	4	21 AAB03979	N-Ras C-terminal p
46	3	60.0	4	21 AAY92850	CAAX-F motif from
47	3	60.0	4	22 AAB34980	Chimpanzee erythro
48	3	60.0	4	23 AAE29301	Chimpanzee erythro
49	3	60.0	5	16 AAR62999	M. prolifera fucos
50	3	60.0	5	16 AAR69999	High affinity Ige
51	3	60.0	5	16 AAR70276	VIM-containing pep
52	3	60.0	5	16 AAR70277	VIM-containing pep
53	3	60.0	5	16 AAR70275	Thrombospondin 1 (
54	3	60.0	5	17 AAW05024	Thrombospondin-der
55	3	60.0	5	19 AAW87390	Peptide determined
56	3	60.0	5	23 AAB59311	Peptide #56 for us
57	3	60.0	5	24 ABUS7836	Thrombospondin 1 r
58	3	60.0	5	24 ABUS7837	Thrombospondin 1 c
59	3	60.0	5	24 ABUS7838	Thrombospondin 1 c
60	3	60.0	6	16 AAR70272	Thrombospondin 1 (
61	3	60.0	6	17 AAR77518	Cytochrome-P450-lp
62	3	60.0	6	17 AAW05018	Thrombospondin-der
63	3	60.0	6	17 AAW05022	Thrombospondin-der
64	3	60.0	6	17 AAW05023	Thrombospondin-der
65	3	60.0	6	18 AAW1047	6Pl staurosporine
66	3	60.0	6	22 AAB45986	Transdominant effe
67	3	60.0	6	23 AAE22870	Carrot red leaf lu
68	3	60.0	6	23 ABB55686	Mutated protein Pe
69	3	60.0	6	24 ABUS7569	HIV polypeptide ex
70	3	60.0	6	24 ABUS7834	Thrombospondin 1 c
71	3	60.0	7	14 AAR35098	Transdominant effe
72	3	60.0	7	14 AAR35098	B. thuringiensis l
73	3	60.0	7	15 AAR52638	Myrotrophin trypti
74	3	60.0	7	16 AAR82905	X.luminescens flav
75	3	60.0	7	16 AAR78214	B. thuringiensis e
76	3	60.0	7	17 AAW05011	Thrombospondin-der
77	3	60.0	7	17 AAW05012	Thrombospondin-der
78	3	60.0	7	17 AAW05015	Thrombospondin-der
79	3	60.0	7	17 AAW05016	Thrombospondin-der
80	3	60.0	7	17 AAW05017	Thrombospondin-der
81	3	60.0	7	20 AAY50318	Neutrophil-activat
82	3	60.0	7	20 AAW67462	Human delta-sarcog

83 E. coli DP3B prote
84 S. typhimurium DP3
85 Protein fragment D
86 Protein fragment D
87 Human delta melano
88 Human Breast cance
89 Human cell death p
90 Rabbit delta-sarco
91 Protein sequence b
92 Human MAGE-A2 clas
93 Hepatitis C virus
94 Enterokinase recog
95 Mutated protein Fe
96 G-protein coupled
97 G-protein coupled
98 Proteome analysis
99 C-terminal prenyl
100 Subpeptide 4N1-1 o

3 60.0 7 21 AAW90753
3 60.0 7 21 AAW90754
3 60.0 7 21 AAW90755
3 60.0 7 21 AAW90756
3 60.0 7 21 AAY80505
3 60.0 7 22 AAU68305
3 60.0 7 22 AAG98675
3 60.0 7 22 AAE00528
3 60.0 7 22 AAB20127
3 60.0 7 23 ABG79014
3 60.0 7 23 ABB07088
3 60.0 7 23 AAU81667
3 60.0 7 23 ABB55662
3 60.0 7 24 ABJ37357
3 60.0 7 24 ABJ37437
3 60.0 7 24 ABP74813
3 60.0 8 15 AAR63218
3 60.0 8 16 AAR70288

ALIGNMENTS

RESULT 1
AAB72254
ID AAB72254 standard; peptide; 5 AA.

AC AAB72254;
DT 14-MAY-2001 (first entry)

DE Colostrinin derived cytokine inducing peptide SEQ ID 9.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.

OS Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REGE-) REGEN THERAPEUTICS PLC.

PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

DR WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
PT treating central nervous system diseases and bacterial and viral
PT infections, comprises administering colostrinin as an immunological
PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
CC a proline rich polypeptide aggregate contained in colostrum. The
CC peptides have immune response modulatory activity, and are capable of
CC inducing cytokines. Colostrinin and its derived peptides are useful for
CC inducing cytokine production, for modulating an immunological response
CC and for inducing blood cell proliferation. The peptides are useful in the
CC treatment of disorders of the central nervous system, neurological
CC disorders, mental disorders, dementia, neurodegenerative diseases,
CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
CC disorders of the immune system, bacterial and viral infections and
CC acquired immunological deficiencies.

XX SQ Sequence 5 AA;
Query Match 100.0%; Score 5; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVMEV 5

Db 1 VVMEV 5

RESULT 2

AAB72508

ID AAB72508 standard; Peptide; 5 AA.

XX AC AAB72508;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #9.

XX KW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;

XX DR WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the
PT cell with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations -

XX Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 5; DB 22; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVMEV 5

Db 1 VVMEV 5

RESULT 3

AAB72540

ID AAB72540 standard; Peptide; 5 AA.

XX AC AAB72540;

XX DT 09-MAY-2001 (first entry)

XX

```

DE Colostrinin peptide #9.
KW Neuroprotective; neural cell differentiation regulator; colostrinin;
KW colostrum.
XX
XX Unidentified.
XX OS
XX WO200112651-A2.
XX PN
XX 22-FEB-2001.
XX PD
XX PF 17-AUG-2000; 2000WO-US22774.
XX PR
XX 17-AUG-1999; 99US-0149633.
XX PR
XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA
XX Boldogh I;
XX PI
XX WPI; 2001-226545/23.
XX DR
XX Use of colostrinin, its constituent peptide or analog as a neural cell
XX regulator, for promoting neural cell differentiation and treating
XX damaged neural cells in a patient
XX PT
XX Claim 6; Page 21; 35pp; English.
XX PS
XX The present invention relates to a method for promoting neural cell
XX differentiation and treating damaged neural cells, using colostrinin and
XX colostrinin constituent peptides (e.g. the present peptide) as a neural
XX cell regulator. Colostrinin is a polypeptide complex found in colostrum.
XX CC
XX Query Match 100.0%; Score 5; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 VVMEV 5
XX Db 1 VVMEV 5
XX
XX RESULT 4
XX AAB59321
XX ID AAB59321 standard; Peptide; 5 AA.
XX AC
XX AAB59321;
XX XX
XX DT 21-MAR-2001 (first entry)
XX DE
XX Ewe colostrinin peptide fragment B-6.
XX DE
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
XX KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX KW
XX Ovis sp.
XX OS
XX WO200075173-A2.
XX PN
XX 14-DEC-2000.
XX PD
XX 02-JUN-2000; 2000WO-GB02128.
XX PF
XX 02-JUN-1999; 99GB-0012852.
XX PR
XX (REGE-) REGEN THERAPEUTICS PLC.
XX PA
XX Georgiades JA;
XX PI
XX WPI; 2001-071058/08.
XX DR
XX Peptides having an N-terminal amino acid sequence isolated from
XX PT

colostrinin for treating e.g. disorders of the central nervous system
and immune system, viral and bacterial infections, and diseases
characterized by amyloid plaques -
Claim 7; Page 27; 63pp; English.
The present invention provides the sequences of a number of peptides
found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
fragment of colostrum. These peptides can be used in the treatment of
central nervous system disorders such as senile dementia, Parkinson's
disease, Alzheimer's disease, psychosis and neurosis, immune system
disorders such as bacterial and viral infections, to improve the
development of a child's immune system, as a dietary supplement, and to
promote the dissolution of beta-amyloid plaques.
Sequence 5 AA;
Query Match 100.0%; Score 5; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VVMEV 5
Db 1 VVMEV 5
RESULT 5
AAB20236
ID AAB20236 standard; peptide; 5 AA.
AC AAB20236;
XX
XX 18-JUN-2002 (first entry)
XX DT
XX Colostrinin constituent peptide #9.
XX DE
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
XX KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
XX KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
XX KW transplantation; implantation; dermatological; vulnerary.
XX KW
XX Unidentified.
XX OS
XX Key, Location/Qualifiers
XX FH Modified-site 5
XX FT /note= "Optionally C-terminal amide"
XX FT
XX WO200213850-A1.
XX PN
XX 21-FEB-2002.
XX PD
XX 17-AUG-2000; 2000WO-US22776.
XX PF
XX 17-AUG-2000; 2000WO-US22776.
XX PR
XX (TEXA ) UNIV TEXAS SYSTEM.
XX PA
XX Stanton GU, Hughes TK, Boldogh I;
XX PI
XX WPI; 2002-269151/31.
XX DR
XX Composition useful for the modulation of blood cell proliferation in a
XX PT patient comprises a blood cell regulator selected from colostrinin, its
XX PT constituent peptide and/or analog
XX PT
XX Claim 6; Page 25; 51pp; English.
XX PS
XX The invention relates to a composition which comprises a blood cell
XX CC regulator selected from colostrinin, its constituent peptide and/or
XX CC analogue. The invention is used for modulating the oxidative stress
XX CC level in a cell e.g. mammalian or human cell present in a cell culture,
XX CC tissue, organ, or organism; or for treating oxidative damage to the skin
XX CC of a patient e.g. animal or human; to modulate oxidative stress during/

```

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 VVMEV 5
 |||||
 Db 1 VVMEV 5

RESULT 6

AA051044
 ID AAM51044 standard; Peptide; 5 AA.

XX AC AAM51044;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide.

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 5 /note= "Optional C-terminal amidation"

XX WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX (TEXA) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. The peptide is
 CC classified as having a beta-casein homologue precursor. Methods
 CC are claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions

CC effective to induce a cytokine; modulating an immune response in a
 CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 5; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 1 VVMEV 5
 |||||
 Db 1 VVMEV 5

RESULT 7

AA014585

ID AAO14585 standard; peptide; 5 AA.

XX AC AAO14585;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 9.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 5 /note= "Optional C-terminal amide"

XX WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog -

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in

DT 29-SEP-1999 (first entry)
 XX MAGE-derived HLA-binding peptide.
 XX Immunogen; HLA; human leukocyte antigen; binding motif; antiviral;
 KW MHC; major histocompatibility complex; viral infection; anticancer;
 KW prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
 XX Homo sapiens.
 OS WO9403205-A1.
 XX 17-FEB-1994.
 XX 06-AUG-1993; 93WO-US07421.
 XX 05-MAR-1993; 93US-0027746.
 PR 07-AUG-1992; 92US-0926666.
 XX (CYTE-) CYTEL CORP.
 FA Celis E, Grey HM, Kubo RT, Sette A;
 XX WPI; 1994-065403/08.
 XX Peptide which specifically binds selected MHC allele - used to
 PT induce an immune response for treatment or prevention of viral
 PT infection or cancer, or for diagnosis
 XX Disclosure; Page 112; 150pp; English.
 XX The sequence is a specific example of a group of new immunogenic
 CC peptides having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding
 CC motif. For example, the peptides having an HLA-A3.2 binding motif
 CC each have 9-10 residues and contain, from the N-terminus to the
 CC C-terminus, (a) a first conserved residue selected from L, M, I,
 CC V, S, A, T, F, C, G, D and E and (b) a second conserved residue of
 CC K, R, Y, H or F, where the first and second conserved residues are
 CC separated by 6-7 residues. The peptides are capable of binding
 CC selected MHC molecules and inducing an immune response. They can be
 CC used to treat and/or prevent viral infection and cancer, e.g. prostate
 CC cancer, lymphoma, hepatitis or AIDS. They can also be used to produce
 CC antibodies for use as diagnostic or therapeutic agents. The peptides
 CC can also be used as diagnostic agents.
 XX SQ Sequence 9 AA;
 Query Match 80.0%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VMEV 5
 DB ||||
 2 VMEV 5
 RESULT 11
 AAR73833
 ID AAR73833 standard; peptide; 9 AA.
 XX AC AAR73833;
 XX 25-MAR-2003 (updated)
 DT 22-JUN-1995 (first entry)
 XX Antigen fragment 149, from MAGE1(a) has binding affinity for HLA-2.1.
 DE antigen; epitope; immunogenic target protein; PSA; HBVc; EBV;
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;
 KW diagnostic; MHC class I molecule; major histocompatibility complex;

KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PIP; 8mer;
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;
 KW herpes simplex virus; influenza A; M1; LCMV.
 XX Homo sapiens.
 OS WO9420127-A1.
 XX 15-SEP-1994.
 XX 04-MAR-1994; 94WO-US02353.
 XX 05-MAR-1993; 93US-0027146.
 PR 04-JUN-1993; 93US-0073205.
 PR 29-NOV-1993; 93US-0159184.
 XX (CYTE-) CYTEL CORP.
 XX Grey HM, Kast WM, Sette A, Sidney J;
 XX WPI; 1994-302678/37.
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX Disclosure; Page 85; 138pp; English.
 XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 1%
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from MAGE1(a) has a
 CC binding value of 0.0410. The peptides of the invention can induce
 CC cytotoxic T lymphocytes which can react with target cells. They can
 CC be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 9 AA;
 Query Match 80.0%; Score 4; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VMEV 5
 DB ||||
 6 VMEV 9
 RESULT 12
 AAR65122
 ID AAR65122 standard; peptide; 9 AA.
 XX AC AAR65122;
 XX 25-MAR-2003 (updated)
 DT 09-OCT-1995 (first entry)
 XX MAGE 1 immunogenic peptide 219-227.
 DE MAGE 1; immunogenic peptide 219-227; cytotoxic C cells;
 KW in vitro activation; cancer; AIDS; bacterial infections; malaria;
 KW fungal infections; tuberculosis; hepatitis.
 XX Homo sapiens.
 OS WO9504817-A1.
 XX 16-FEB-1995.
 XX 01-AUG-1994; 94WO-US08672.
 PF

CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 9 AA;
 Query Match 80.0%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VMEV 5
 Db 5 VMEV 8
 |||||
 |||||
 RESULT 15
 AAY46358
 ID AAY46358 standard; Peptide; 9 AA.
 AC AAY46358;
 XX
 XX 01-DEC-1999 (first entry)
 XX
 XX Immunogenic peptide having a human leukocyte antigen binding motif #969.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 KW
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9945954-A1.
 PN
 XX 16-SEP-1999.
 PD
 XX 13-MAR-1998; 98WO-US05039.
 PF
 XX 13-MAR-1998; 98WO-US05039.
 PR
 XX (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 XX
 XX New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 PT
 XX Claim 1; Page 68; 150pp; English.
 PS
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell

CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 9 AA;
 Query Match 80.0%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VMEV 5
 Db 2 VMEV 5
 |||||
 |||||
 RESULT 16
 AAY47189
 ID AAY47189 standard; Peptide; 9 AA.
 AC AAY47189;
 XX
 XX 01-DEC-1999 (first entry)
 XX
 XX Immunogenic peptide having a human leukocyte antigen binding motif #1800.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 KW
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9945954-A1.
 PN
 XX 16-SEP-1999.
 PD
 XX 13-MAR-1998; 98WO-US05039.
 PF
 XX 13-MAR-1998; 98WO-US05039.
 PR
 XX (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 XX
 XX New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 PT
 XX Claim 1; Page 97; 150pp; English.
 PS
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell

CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 XX
 SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMEV 5
 Db 4 VMEV 7
 |||||

RESULT 17
 AAY47274

ID AAY47274 standard; Peptide; 9 AA.
 XX
 AC AAY47274;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #1885.

XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 XX immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98WO-US05039.
 XX
 PR 13-MAR-1998; 98WO-US05039.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX WPI; 1999-551214/46.
 DR
 XX
 PT New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 XX
 PS Claim 1; Page 101; 150pp; English.
 XX
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and

CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 XX
 SQ Sequence 9 AA;

Query Match 80.0%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMEV 5
 Db 6 VMEV 9
 |||||

RESULT 18
 AAY47275

ID AAY47275 standard; Peptide; 9 AA.
 XX
 AC AAY47275;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #1885.

XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 XX immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98WO-US05039.
 XX
 PR 13-MAR-1998; 98WO-US05039.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX WPI; 1999-551214/46.
 DR
 XX
 PT New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 XX
 PS Claim 1; Page 101; 150pp; English.
 XX
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and

CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.

SQ Sequence 9 AA;
 Query Match 80.0%; Score 4; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VMEV 5
 ||||
 Db 6 VMEV 9

RESULT 19

AAV38327
 ID AAV38327 standard; Peptide; 10 AA.

XX AAV38327;

DT 29-SEP-1999 (first entry)

DE MAGE-derived HLA-binding peptide.

KW Immunogen; HLA; human leukocyte antigen; binding motif; antiviral;
 KW MHC; major histocompatibility complex; viral infection; anticancer;
 KW prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.

OS Homo sapiens.

XX WO9403205-A1.

PN 17-FEB-1994.

PF 06-AUG-1993; 93WO-US07421.

PR 05-MAR-1993; 93US-0027746.

PR 07-AUG-1992; 92US-0926666.

XX (CYTE-) CYTEL CORP.

PI Celis E, Grey HM, Kubo RT, Sette A;

XX WPI; 1994-065403/08.

PT Peptide which specifically binds selected MHC allele - used to
 PT induce an immune response for treatment or prevention of viral
 PT infection or cancer, or for diagnosis

XX Disclosure; Page 112; 150pp; English.

XX The sequence is a specific example of a group of new immunogenic
 CC peptides having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding
 CC motif. For example, the peptides having an HLA-A3.2 binding motif
 CC each have 9-10 residues and contain, from the N-terminus to the
 CC C-terminus, (a) a first conserved residue selected from L, M, I,
 CC V, S, A, T, F, C, G, D and E and (b) a second conserved residue of
 CC K, R, Y, H or F, where the first and second conserved residues are
 CC separated by 6-7 residues. The peptides are capable of binding
 CC selected MHC molecules and inducing an immune response. They can be
 CC used to treat and/or prevent viral infection and cancer, e.g. prostate
 CC cancer, lymphoma, hepatitis or AIDS. They can also be used to produce
 CC antibodies for use as diagnostic or therapeutic agents. The peptides

CC can also be used as diagnostic agents.

SQ Sequence 10 AA;

Query Match 80.0%; Score 4; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VMEV 5
 ||||
 Db 3 VMEV 6

RESULT 20

AAV47332
 ID AAV47332 standard; Protein; 10 AA.

XX AAV47332;

DT 14-MAY-2003 (updated)

DT 25-MAR-2003 (updated)

DT 31-AUG-1994 (first entry)

XX HLA-A1 MAGE 1 antigen peptide fragment 215-224.

XX Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;
 KW immune response; viral infection; cancer; prostate cancer; lymphoma;
 KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.

OS Synthetic.

XX WO9403205-A1.

PD 17-FEB-1994.

XX 06-AUG-1993; 93WO-US07421.

XX 07-AUG-1992; 92US-0926666.

PR 05-MAR-1993; 93US-0027746.

XX (CYTE-) CYTEL CORP.

XX Celis E, Grey HM, Kubo RT, Sette A;

XX WPI; 1994-065403/08.

PT Peptide which specifically binds selected MHC allele - used to
 PT induce an immune response for treatment or prevention of viral
 PT infection or cancer, or for diagnosis

XX Example 8; Page 52; 150pp; English.

XX The sequences given in AAR47304-33 and AAR49201-44 are immunogenic
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif.
 CC These peptides may be used in the composition of the invention.
 CC These peptides are capable of binding selected MHC molecules and
 CC inducing an immune response. They can be used to treat and/or
 CC prevent viral infection and cancer, eg. prostate cancer, lymphoma,
 CC hepatitis or AIDS. They can also be used to produce antibodies for
 CC use as diagnostic or therapeutic agents. The peptides can also be
 CC used as diagnostic agents.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 14-MAY-2003 to correct PS field.)

XX Sequence 10 AA;

Query Match 80.0%; Score 4; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VMEV 5
 ||||
 Db 6 VMEV 9

```

RESULT 21
AAV45908
ID AAY45908 standard; Peptide; 10 AA.
XX AC
XX AAY45908;
XX DT
XX 01-DEC-1999 (first entry)
XX DE
XX Immunogenic peptide having a human leukocyte antigen binding motif #519.
XX KW
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX OS
XX Synthetic.
XX OS
XX Homo sapiens.
XX PN
XX WO9945954-A1.
XX XX
XX 16-SEP-1999.
XX PD
XX 13-MAR-1998; 98WO-US05039.
XX PF
XX 13-MAR-1998; 98WO-US05039.
XX PR
XX 13-MAR-1998; 98WO-US05039.
XX PA
XX (EPIM-) EPIIMUNE INC.
XX PI
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX DR
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX PT
XX and diagnosis of cancers and viral diseases -
XX PS
XX Claim 1; Page 46; 150pp; English.
XX CC
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX SQ
XX Sequence 10 AA;
XX
XX Query Match 80.0%; Score 4; DB 20; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 VMEV 5
XX ||||
XX 3 VMEV 6
XX Db

RESULT 22
AAV46049
ID AAY46049 standard; Peptide; 10 AA.
XX AC
XX AAY46049;
XX DT
XX 01-DEC-1999 (first entry)
XX DE
XX Immunogenic peptide having a human leukocyte antigen binding motif #660.
XX KW
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX OS
XX Synthetic.
XX OS
XX Homo sapiens.
XX PN
XX WO9945954-A1.
XX XX
XX 16-SEP-1999.
XX PD
XX 13-MAR-1998; 98WO-US05039.
XX PF
XX 13-MAR-1998; 98WO-US05039.
XX PR
XX 13-MAR-1998; 98WO-US05039.
XX PA
XX (EPIM-) EPIIMUNE INC.
XX PI
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX DR
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX PT
XX and diagnosis of cancers and viral diseases -
XX PS
XX Claim 1; Page 54; 150pp; English.
XX CC
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX SQ
XX Sequence 10 AA;
XX
XX Query Match 80.0%; Score 4; DB 20; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 VMEV 5
XX ||||
XX 6 VMEV 9
XX Db

RESULT 23
AAV46105

```

ID AAY46105 standard; Peptide; 10 AA.
 AC AAY46105;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #716.
 XX
 DE Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 XX immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9945954-A1.
 PN
 XX 16-SEP-1999.
 PD
 XX 13-MAR-1998; 98WO-US05039.
 PF
 XX 13-MAR-1998; 98WO-US05039.
 PR
 XX (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 XX
 DR New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 PT
 XX Claim 1; Page 56; 150pp; English.
 PS
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 4; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VMEV 5
 Db |||||
 3 VMEV 6
 RESULT 24
 AAY46106
 ID AAY46106 standard; Peptide; 10 AA.
 XX

AC AAY46106;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #717.
 XX
 DE Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9945954-A1.
 PN
 XX 16-SEP-1999.
 PD
 XX 13-MAR-1998; 98WO-US05039.
 PF
 XX 13-MAR-1998; 98WO-US05039.
 PR
 XX (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 XX
 DR New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 PT
 XX Claim 1; Page 56; 150pp; English.
 PS
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 10 AA;
 Query Match 80.0%; Score 4; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VMEV 5
 Db |||||
 1 VMEV 4
 RESULT 25
 AAY46073
 ID AAY46073 standard; Peptide; 11 AA.
 XX
 AC AAY46073;
 XX

DT 01-DEC-1999 (first entry)
 DE Immunogenic peptide having a human leukocyte antigen binding motif #684.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 XX immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 KW Synthetic.
 OS Homo sapiens.
 XX WO9945954-A1.
 PN 16-SEP-1999.
 XX 13-MAR-1998; 98WO-US05039.
 PF 13-MAR-1998; 98WO-US05039.
 XX 13-MAR-1998; 98WO-US05039.
 PR (EPIM-) EPIMMUNE INC.
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 DR New immunogenic peptides with HLA binding motif, useful in treatment
 XX and diagnosis of cancers and viral diseases -
 PT Claim 1; Page 55; 150pp; English.
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 11 AA;
 Query Match 80.0%; Score 4; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VMEV 5
 Db 7 VMEV 10
 RESULT 26
 AAY47431
 ID AAY47431 standard; Peptide; 11 AA.
 XX AAY47431;
 XX 01-DEC-1999 (first entry)
 DT Immunogenic peptide having a human leukocyte antigen binding motif #2169.
 XX

DE Immunogenic peptide having a human leukocyte antigen binding motif #2042.
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 KW Synthetic.
 OS Homo sapiens.
 XX WO9945954-A1.
 PN 16-SEP-1999.
 XX 13-MAR-1998; 98WO-US05039.
 PF 13-MAR-1998; 98WO-US05039.
 XX 13-MAR-1998; 98WO-US05039.
 PR (EPIM-) EPIMMUNE INC.
 XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 DR New immunogenic peptides with HLA binding motif, useful in treatment
 XX and diagnosis of cancers and viral diseases -
 PT Claim 1; Page 108; 150pp; English.
 XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 11 AA;
 Query Match 80.0%; Score 4; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VMEV 5
 Db 8 VMEV 11
 RESULT 27
 AAY47558
 ID AAY47558 standard; Peptide; 11 AA.
 XX AAY47558;
 XX 01-DEC-1999 (first entry)
 DT Immunogenic peptide having a human leukocyte antigen binding motif #2169.
 XX

KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.

XX Synthetic.

OS Homo sapiens.

XX Homo sapiens.

XX WO9945954-A1.

XX 16-SEP-1999.

XX 13-MAR-1998; 98WO-US05039.

XX 13-MAR-1998; 98WO-US05039.

XX (EPIM-) EPIMUNE INC.

PA Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;

XX WPI; 1999-551214/46.

XX New immunogenic peptides with HLA binding motif, useful in treatment

PT and diagnosis of cancers and viral diseases -

XX Claim 1; Page 114; 150pp; English.

XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides

CC having a human major histocompatibility complex (MHC) Class I (also

CC known as human leukocyte antigen (HLA) binding motif. The immunogenic

CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes

CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell

CC response against the antigen from which the peptide is derived.

CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are

CC normally induced by an antigen in the form of a peptide fragment bound

CC to a HLA molecule, rather than the intact foreign antigen itself, and

CC are particularly important in tumour rejection and in fighting viral

CC infections. The peptides are therefore useful therapeutically to treat

CC or prevent viral infections and cancers in mammals (especially humans)

CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.

CC They can be administered as vaccines to elicit an immune response in

CC individuals susceptible or otherwise at risk of viral infection or

CC cancer, or used to treat chronic or acute conditions. They are also

CC useful diagnostically, and can be used to induce a cytotoxic T cell

CC response, by contacting a cytotoxic T cell with the peptide e.g. to

CC produce CTLs ex vivo for infusion back into a patient. The

CC polynucleotides encoding the immunogenic peptides are also useful

CC therapeutically and for immunisation as above.

XX SQ Sequence 11 AA;

Query Match 80.0%; Score 4; DB 20; Length 11;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VMEV 5

DB 8 VMEV 11

RESULT 28

AAB12653

ID AAB12653 standard; peptide; 11 AA.

XX AAB12653;

XX 13-NOV-2000 (first entry)

DT Protein kinase peptide INSR human.

XX Protein kinase; P38-gamma; crystallised P38 complex; structure;

XX Protein co-ordinate data; inhibitor; identification.

KW

XX Homo sapiens.
 OS WO200036096-A1.
 XX 22-JUN-2000.

XX 08-DEC-1999; 99WO-US29096.

XX 16-DEC-1998; 98US-0112354.

XX 03-NOV-1999; 99US-0163373.

XX (VERT-) VERTEX PHARM INC.

XX Bellon S, Bemis G, Wilson K, Fitzgibbon M;

XX WPI; 2000-548618/50.

XX Crystallized protein-kinase ligand complexes and their structural

PT coordinates useful for designing and identifying protein kinase

PT inhibitors -

XX Claim 5; Page 33; 179pp; English.

XX The present invention describes crystallised protein-kinase ligand

CC complexes (especially P38-ligand complexes) and their structure

CC coordinates (SCs). The key structural features of the proteins,

CC especially the shape of the substrate binding site, are useful in

CC methods for designing and/or identifying selective inhibitors of

CC protein kinases and in solving the structures of other proteins with

CC similar features. The SCs may be displayed on a computer for graphical

CC 3 dimensional representation of the structure and for computer aided

CC molecular design of new inhibitors. The SCs are based on the structure

CC of the phosphorylated P38-gamma complex which has been solved and which

CC reveals new structural information useful for understanding the

CC activated states of other, related kinase proteins. The present sequence

CC represents a protein kinase peptide sequence which is used in the

CC exemplification of the present invention.

XX SQ Sequence 11 AA;

Query Match 80.0%; Score 4; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVME 4

DB 5 VVME 8

RESULT 29

AAR83269

ID AAR83269 standard; peptide; 16 AA.

XX AAR83269;

XX 18-APR-1996 (first entry)

DT HIV principal neutralisation epitope binding to 447 antibody.

DE SPNE; selected principal neutralisation epitope; vaccine; HIV;

XX outer membrane proteosome; Neisseria; OMPC; AIDS; 447 antibody.

XX Synthetic.

XX GB2282378-A.

XX 05-APR-1995.

PD 23-SEP-1994; 94GB-0019253.

XX 30-SEP-1993; 93US-0130111.

XX

```

PA (MERI ) MERCK & CO INC.
XX
XX Arnold BA, Conley AJ, Keller PM, Shaw AR;
XX WPI; 1995-125265/17.
XX
XX New antigenic conjugate useful as vaccine for AIDS - comprising HIV
XX principal neutralisation epitope covalently linked to outer membrane
XX proteosome of Neisseria
XX
XX Claim 14; Page 8; 73pp; English.
XX
XX An antigenic conjugate, useful as a vaccine for AIDS, has the formula
XX (SPNE)n-(OMPC), where SPNE is a selected principal neutralisation
XX epitope of HIV, which is one of 27 specified polypeptides (including the
XX present sequence) or their fragments containing at least 5 amino acids
XX and including the GPCR loop region or its homologue; OMPC is purified
XX outer membrane proteosome of Neisseria (pref. N. meningitidis); and n
XX is 1-200, indicating the number of SPNE moieties covalently linked to
XX the OMPC. The conjugates may be substituted by anions, and conjugation
XX may be via a biogenic spacer. The SPNE polypeptides bind an HIV broadly
XX neutralising monoclonal antibody (447 antibody) in a competition assay
XX in the presence of natural HIV antigen such as gp120, and were
XX originally identified in the screening of phage epitope libraries having
XX randomly or semi-randomly generated epitope polypeptides accessible to
XX the antibody. The sequences of these polypeptides were deduced from
XX their corresponding DNA sequence, in turn determined by PCR.
XX
XX Sequence 16 AA;
XX
XX Query Match 80.0%; Score 4; DB 16; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 VMEV 5
XX ||||
XX 11 VMEV 14
XX
XX
XX
XX RESULT 30
XX AAR15779
XX ID AAR15779 standard; Protein; 4 AA.
XX
XX AC AAR15779;
XX
XX DT 25-MAR-2003 (updated)
XX DT 09-JAN-2003 (updated)
XX DT 29-JAN-1992 (first entry)
XX
XX DE Farnesyl-protein transferase inhibitor (32).
XX
XX KW Farnesyl; transferase; FT; inhibitor; p21ras; rat.
XX
XX OS Synthetic.
XX
XX FN WO9116340-A.
XX
XX PD 31-OCT-1991.
XX
XX PF 18-APR-1991; 91WO-02650.
XX
XX PR 20-NOV-1990; 90US-0615715.
XX PR 18-APR-1990; 90US-0510706.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Brown MS, Goldstein JL, Reiss Y;
XX
XX WPI; 1991-339750/46.
XX
XX Compsn. comprising purified farnesyl-protein transferase - used
XX to inhibit attachment of farnesyl moiety to RAS protein in
XX malignant cells and to treat cancer
XX
XX Claim 25; Page 68; 87pp; English.
XX
XX This peptide or the peptides represented in AAR15751-81, AAR14723 and
XX AAR14711 inhibit the rat FTs represented in AAR14712-22. They show FT
XX inhibition at an IC50 of 0.01-10 microm. The most potent inhibitors are
XX ones in which phenylalanine occurs at the third position of a
XX tetrapeptide whose N-terminus is cysteine. The inhibitors have a
XX farnesyl acceptor or inhibitor sequence within its structure and are
XX capable of inhibiting the farnesylation of p21ras by FT.
XX See also AAR14711-23 and AAQ14541-47.
XX (Updated on 09-JAN-2003 to add missing OS field.)
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 4 AA;
XX
XX Query Match 60.0%; Score 3; DB 12; Length 4;
XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 VVM 3
XX |||
XX 2 VVM 4
XX
XX
XX RESULT 31
XX AAR15650
XX ID AAR15650 standard; Protein; 4 AA.
XX
XX AC AAR15650;
XX
XX DT 25-MAR-2003 (updated)
XX DT 17-MAR-1992 (first entry)
XX
XX DE Ras protein inhibitor tetrapeptide.
XX
XX KW Plasma membrane; cancer; transformation.
XX
XX OS Synthetic.
XX
XX FN EP461869-A.
XX
XX PD 18-DEC-1991.
XX
XX PF 12-JUN-1991; 91EP-0305283.
XX
XX PR 17-MAY-1991; 91US-0700232.
XX PR 12-JUN-1990; 90US-0536840.
XX
XX PA (MERI ) MERCK & CO INC.
XX PA (GIBB/) GIBBS J B.
XX
XX PI Gibbs JB, Dixon RAF, Garsky VM, Schrabar MD;
XX
XX WPI; 1991-370840/51.
XX
XX New tetrapeptide inhibitors of Ras protein farnesylation -
XX prevent the transformation of normal cells into cancer cells
XX
XX Claim 5; Page 7; 7pp; English.
XX
XX The amino acid sequence is that of a tetrapeptide which inhibits
XX plasma membrane localisation and prevents transformation of normal
XX cells into cancer cells. It can also be used for inhibiting
XX farnesylation of Ras protein and is an inhibitor of farnesyl-protein
XX transferase. Admin. of the peptide not only decreases the amt. of
XX Ras in the membrane but also generates a cytosolic pool of Ras.
XX See also AAR15648 and AAR15649.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 4 AA;
XX
XX Query Match 60.0%; Score 3; DB 12; Length 4;

```

```
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 2 VWM 4

RESULT 32
AAR49744
ID AAR49744 standard; Peptide; 4 AA.
XX
AC AAR49744;
XX
DT 25-MAR-2003 (updated)
DT 08-AUG-1994 (first entry)
XX
DE Farnesyltransferase-inhibitor.
XX
KW Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;
KW ras protein; farnesylation; cancer therapy.
XX
OS Synthetic.
XX
PN WO9404561-AL.
XX
PD 03-MAR-1994.
XX
PF 24-AUG-1993; 93WO-US08062.
XX
PR 24-AUG-1992; 92US-0935087.
XX
PA (GETH ) GENENTECH INC.
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Brown MS, Goldstein JL, Marsters JC, Reiss Y;
XX WPI; 1994-083105/10.
XX
PT New farnesyl-transferase inhibitors - used for inhibiting
PT attachment of a farnesyl moiety to a p21ras protein in malignant
PT cells
XX
PS Disclosure; Page 33; 183pp; English.
XX
CC Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which
CC include a family of tetrapeptides based on the recognition site
CC (AAR49776) of farnesyltransferase (FT), are potential anticancer agents
CC that inhibit FT, thereby preventing expression of p21ras.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 4 AA;
Query Match 60.0%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 2 VWM 4

RESULT 33
AAR77806
ID AAR77806 standard; Protein; 4 AA.
XX
AC AAR77806;
XX
DT 25-MAR-2003 (updated)
DT 23-JAN-1996 (first entry)
XX
DE Farnesyl transferase inhibitor tetrapeptide, CVWM.
XX

Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 2 VWM 4

RESULT 34
AAW04436
ID AAW04436 standard; peptide; 4 AA.
XX
AC AAW04436;
XX
DT 30-JUL-1997 (first entry)
XX
DE Farnesyl transferase peptide inhibitor used in cancer treatment.
XX
KW Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;
KW ras protein; K-ras B; malignant; detection; identification.
XX
OS Synthetic.
XX
PN WO9634113-A2.
XX
PD 31-OCT-1996.
XX
PF 29-APR-1996; 96WO-US05969.
XX
PR 27-APR-1995; 95US-0429964.
XX

Farnesyl transferase; inhibitor; cancer; ras; p21.
Synthetic.
US5420245-A.
30-MAY-1995.
03-APR-1992; 92US-0863169.
16-JAN-1992; 92US-0822011.
18-APR-1990; 90US-0510706.
20-NOV-1990; 90US-0615715.
03-APR-1992; 92US-0863169.
(TEXA ) UNIV TEXAS.
Brown MS, Goldstein JL, Reiss Y;
WPI; 1995-206308/27.
New farnesyl transferase inhibitor peptide(s) - based on farnesyl
acceptor substrate carboxy terminal sequences, used for the
treatment of cancer
Claim 2; Column 61; 55pp; English.
AAR77800, AAR77805-R77838 are tetrapeptide inhibitors of farnesyl
transferase. They all obey a generic formula for the C-terminal
sequence of 4-10 amino acid inhibitory peptides; the formula is
-CAAX, where C= cysteine, A= any aliphatic, aromatic or hydroxy
amino acid and X= any normal amino acid. Farnesyl transferase is
involved in the farnesylation of various cellular proteins
including the cancer related ras proteins. The transforming
activity of ras is dependent on the localisation of the protein
to membranes, a property which is thought to be dependent upon
the addition of farnesyl groups. The peptide inhibitors are
useful for treating cancers and ras-related cancers in particular.
(Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 4 AA;
Query Match 60.0%; Score 3; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 2 VWM 4
```


XX (TEXA) UNIV TEXAS SYSTEM.
 XX PA Brown MS, Goldstein JL, James GL;
 XX DR WPI; 1996-497642/49.
 XX PT Assay for farnesyl transferase activity - by determining ability to
 PT transfer farnesyl moiety to K-Ras B protein, partic. useful for
 PT identifying inhibitors
 XX PS Example 1; Page 33; 257pp; English.
 XX CC AA04433-W04465 are peptide inhibitors of farnesyl transferase (FT)
 CC activity. The peptides block the attachment of prenyl groups to ras
 CC proteins in malignant cells of patients suffering from cancer or a
 CC precancerous state and as such are used to treat cancer. The peptides
 CC were identified by determining the ability of candidate substances to
 CC inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety
 CC to a K-RasB protein.
 XX SQ Sequence 4 AA;
 Query Match 60.0%; Score 3; DB 17; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VVM 3
 Db |||
 2 VVM 4
 RESULT 35
 AAY18380
 ID AAY18380 standard; peptide; 4 AA.
 XX AC AAY18380;
 XX DT 20-AUG-1999 (first entry)
 XX DE N-Ras geranylgeranylated CAAAX motif.
 XX KW CAAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;
 KW cancer; proliferative disorder; restenosis; hepatitis delta virus;
 KW neurofibromin benign proliferative disorder; polycystic kidney disease;
 KW fused azacyclic ring system; therapy; infection.
 XX OS Synthetic.
 XX PN WO9927928-A1.
 XX PD 10-JUN-1999.
 XX PF 30-NOV-1998; 98WO-US25325.
 XX PR 06-APR-1998; 98GB-0007364.
 XX PR 04-DEC-1997; 97US-0067552.
 XX PA (MERI) MERCK & CO INC.
 XX PI Ciccarone TM, Desolms SJ;
 XX DR WPI; 1999-394825/33.
 XX PT New bicyclic pyridine derivative peptide and peptidomimetic farnesyl
 PT protein transferase inhibitors, used for treating cancer and other
 PT proliferative disorders
 XX PS Disclosure; Page 62; 131pp; English.
 XX CC This sequence represents a CAAAX motif.
 CC The invention relates to peptides and peptidomimetics (I), containing a
 CC bicyclic pyridine derivative ring system. The peptides and peptidomimetics (I), containing a

CC peptidomimetics can be used for treating cancer. (I) are also useful for
 CC the treatment of other proliferative disorders, including neurofibromin
 CC benign proliferative disorder, blindness related to retinal
 CC vascularisation, infections by hepatitis delta and related viruses,
 CC restenosis and polycystic kidney disease. They may also be useful in
 CC treatment of fungal infections; and in qualitative and quantitative
 CC assays for farnesyl protein transferase. (I) are selective, non-thiol,
 CC farnesyl protein transferase inhibitors.
 XX SQ Sequence 4 AA;
 Query Match 60.0%; Score 3; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VVM 3
 Db |||
 2 VVM 4
 RESULT 36
 AAY18367
 ID AAY18367 standard; peptide; 4 AA.
 XX AC AAY18367;
 XX DT 20-AUG-1999 (first entry)
 XX DE N-Ras geranylgeranylated CAAAX motif.
 XX KW CAAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;
 KW cancer; proliferative disorder; restenosis; hepatitis delta virus;
 KW neurofibromin benign proliferative disorder; polycystic kidney disease;
 KW fused azacyclic ring system; therapy; infection.
 XX OS Synthetic.
 XX PN WO9927929-A1.
 XX PD 10-JUN-1999.
 XX PF 30-NOV-1998; 98WO-US25324.
 XX PR 04-DEC-1997; 97US-0984732.
 XX PA (MERI) MERCK & CO INC.
 XX PI Halczenko W, Stump CA;
 XX DR WPI; 1999-394826/33.
 XX PT New fused aza-cyclic peptide and peptidomimetic compound farnesyl
 PT protein transferase inhibitors, used for treating cancer and other
 PT proliferative disorders
 XX PS Disclosure; Page 72; 141pp; English.
 XX CC This sequence represents a CAAAX motif.
 CC The invention relates to peptides and peptidomimetics (I), containing a
 CC fused azacyclic ring system. The peptides and peptidomimetics can be used
 CC for treating cancer. (I) are also useful for the treatment of other
 CC proliferative disorders, including neurofibromin benign proliferative
 CC disorder, blindness related to retinal vascularisation, infections by
 CC hepatitis delta and related viruses, restenosis and polycystic kidney
 CC disease. They may also be useful in treatment of fungal infections; and
 CC in qualitative and quantitative assays for farnesyl protein transferase.
 CC (I) are selective, non-thiol, farnesyl protein transferase inhibitors.
 XX SQ Sequence 4 AA;
 Query Match 60.0%; Score 3; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
 Db |||
 2 VVM 4

RESULT 37
 AAY18350
 ID AAY18350 standard; peptide; 4 AA.
 AC AAY18350;
 XX
 DT 19-AUG-1999 (first entry)
 XX
 DE N-Ras geranylgeranylated CAAX motif.
 XX
 KW CAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;
 KW piperidine ring; homopiperidine ring; cancer; proliferative disorder;
 KW neurofibromin benign proliferative disorder; hepatitis delta virus;
 KW infection; polycystic kidney disease; restenosis; therapy.
 OS Synthetic.
 XX
 PN WO9927933-A1.
 XX
 PD 10-JUN-1999.
 XX
 PF 30-NOV-1998; 98WO-US25348.
 XX
 PR 04-DEC-1997; 97US-0985124.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Desolms SJ;
 XX
 DR WPI; 1999-385315/32.
 XX
 XX New piperidine or homopiperidine derivative peptide or
 PT peptidomimetic compound farnesyl protein transferase inhibitors,
 PT used for treating cancer and other proliferative disorders
 XX
 PS Disclosure; Page 79; 145pp; English.
 XX
 CC This sequence represents a CAAX motif.
 CC The invention relates to peptides and peptidomimetics (I), containing a
 CC piperidine or homopiperidine ring. The peptides and peptidomimetics can
 CC be used for treating cancer. (I) are also useful for the treatment of
 CC other proliferative disorders, including neurofibromin benign
 CC proliferative disorder, blindness related to retinal vascularisation,
 CC infections by hepatitis delta and related viruses, restenosis and
 CC polycystic kidney disease. They may also be useful in treatment of fungal
 CC infections; and in qualitative and quantitative assays for farnesyl
 CC protein transferase.
 XX
 SQ Sequence 4 AA;

Query Match 60.0%; Score 3; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
 Db |||
 2 VVM 4

RESULT 38
 AAY18337
 ID AAY18337 standard; peptide; 4 AA.
 AC AAY18337;
 XX
 DT 19-AUG-1999 (first entry)
 XX

DE N-Ras geranylgeranylated CAAX motif.
 XX
 KW CAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;
 KW cancer; proliferative disorder; restenosis; hepatitis delta virus;
 KW neurofibromin benign proliferative disorder; polycystic kidney disease;
 KW tetrahydrobenzazepine ring system; therapy; tetrahydroisoquinoline;
 KW infection.
 XX
 OS Synthetic.
 XX
 PN WO9928314-A1.
 XX
 PD 10-JUN-1999.
 XX
 PF 30-NOV-1998; 98WO-US25383.
 XX
 PR 04-DEC-1997; 97US-0985337.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Ciccarone TM, Desolms SJ;
 XX
 DR WPI; 1999-385349/32.
 XX
 XX New benzo-heterocyclic peptide and peptidomimetic compound farnesyl
 PT protein transferase inhibitors, used for treating cancer and other
 PT proliferative disorders
 XX
 PS Disclosure; Page 92; 184pp; English.
 XX
 CC This sequence represents a CAAX motif.
 CC The invention relates to peptides and peptidomimetics (I), linked to a
 CC tetrahydroisoquinoline or tetrahydrobenzazepine ring system. The peptides
 CC and peptidomimetics can be used for treating cancer. (I) are also useful
 CC for the treatment of other proliferative disorders, including
 CC neurofibromin benign proliferative disorder, blindness related to retinal
 CC vascularisation, infections by hepatitis delta and related viruses,
 CC restenosis and polycystic kidney disease. They may also be useful in
 CC treatment of fungal infections; and in qualitative and quantitative
 CC assays for farnesyl protein transferase.
 XX
 SQ Sequence 4 AA;

Query Match 60.0%; Score 3; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
 Db |||
 2 VVM 4

RESULT 39
 AAY18324
 ID AAY18324 standard; peptide; 4 AA.
 XX
 AC AAY18324;
 XX
 DT 19-AUG-1999 (first entry)
 XX
 DE N-Ras geranylgeranylated CAAX motif.
 XX
 KW CAAX motif; farnesyl-protein transferase; inhibitor; fungal infection;
 KW fused aza-bicyclic system; cancer; proliferative disorder; restenosis;
 KW neurofibromin benign proliferative disorder; hepatitis delta virus;
 KW infection; polycystic kidney disease; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9928313-A1.
 XX
 PD 10-JUN-1999.
 XX

```

PF 30-NOV-1998; 98WO-US25352.
XX
PR 04-DEC-1997; 97US-0985320.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Ciccarone TM, Haiczenko W, Hutchinson JH, Lumma WC;
PI Stokker GE, Stump CA, Williams TM;
XX
DR WPI; 1999-385348/32.
XX
XX New aza-bicyclic peptide and peptidomimetic compound farnesyl
PT protein transferase inhibitors, used for treating cancer or other
PT proliferative disorders
XX
PS Disclosure; Page 85; 201pp; English.
XX
XX This sequence represents a CAAX motif.
CC
CC The invention relates to peptides and peptidomimetics (I), containing a
CC fused aza-bicyclic system. The peptides and peptidomimetics can be used
CC for treating cancer. (I) are also useful for the treatment of other
CC proliferative disorders, including neurofibromin benign proliferative
CC disorder, blindness related to retinal vascularisation, infections by
CC hepatitis delta and related viruses, restenosis and polycystic kidney
CC disease. They may also be useful in treatment of fungal infections; and
CC in qualitative and quantitative assays for farnesyl protein transferase.
XX
SQ Sequence 4 AA;
Query Match 60.0%; Score 3; DB 20; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VWM 3
Db |||
2 VWM 4
RESULT 41
AAV17051
ID AAY17051 standard; peptide; 4 AA.
XX
AC AAY17051;
XX
XX 20-JUL-1999 (first entry)
DT
XX
DE Human N-Ras peptide used in farnesyl-protein transferase assays.
XX
KW Bicyclic compound; inhibitor; prenyl-protein transferase; prenylation;
KW oncogene; Ras; tumour angiogenesis; vision deficit; oncogenic mutation;
KW retinal vascularisation; proliferative disease; viral; fungal; infection;
KW hepatitis infection; restenosis; polycystic kidney disease; assay;
KW arteriosclerosis; diabetic vascular pathology.
XX
OS Homo sapiens.
XX
PN WO9918096-A1.
XX
PD 15-APR-1999.
XX
PF 01-OCT-1998; 98WO-US20525.
XX
PR 14-APR-1998; 98GB-0007948.
PR 02-OCT-1997; 97US-0060871.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Desolms SJ, Lumma WC, Shaw AW, Sisko JT, Tucker TJ;
XX
DR WPI; 1999-312433/26.
XX
XX Novel chemotherapeutic bicyclic compounds
PT
PS Examples; Page 85; 178pp; English.
XX
CC The invention relates to novel bicyclic compounds that inhibit prenyl-
CC protein transferase and the prenylation of the oncogene protein Ras.
CC The bicyclic compounds may also inhibit tumour angiogenesis, thereby
CC affecting the growth of tumours. They may also be useful in the treatment
CC of certain forms of vision deficit related to retinal vascularisation.
CC The compounds are also useful for inhibiting other proliferative
CC diseases, both benign and malignant, in which Ras proteins are aberrantly
CC activated as a result of oncogenic mutation in other genes. They may also
CC be used in the treatment of certain viral infections, in particular in
CC the treatment of hepatitis delta and related viruses. The compounds are
CC useful in the prevention of restenosis after percutaneous transluminal
CC coronary angioplasty by inhibiting neointimal formation. They may also be
CC used in the treatment and prevention of polycystic kidney disease, fungal
CC infections, arteriosclerosis and diabetic vascular pathologies.
XX

```

SQ Sequence 4 AA;

Query Match 60.0%; Score 3; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
 |||
 Db 2 VWM 4

RESULT 42

AAV02235
 ID AAV02235 standard; peptide; 4 AA.
 XX AC AAV02235;
 XX DT 07-JUL-1999 (first entry)
 XX DE "CAAXG" motif from human N-Ras protein.
 XX KW CAAXG motif; prenyl-protein transferase; farnesylation;
 KW oncogene protein Ras; tumour angiogenesis; tumour growth;
 KW vision deficit; retinal vascularisation; proliferative disease;
 KW oncogene mutation; viral infection; hepatitis delta; restenosis;
 KW percutaneous transluminal coronary angioplasty; neointimal formation;
 KW polycystic kidney disease; fungal infection; arteriosclerosis;
 KW diabetic vascular pathology.
 XX OS Homo sapiens.
 XX FN WO991777-A1.
 XX PD 15-APR-1999.
 XX PF 07-OCT-1998; 98WO-US21063.
 XX PR 08-OCT-1997; 97US-0062660.
 XX PA (MERI) MERCK & CO INC.
 XX PI Ciccarone TM, Desolms SJ, Graham SL, Hutchinson JH;
 PI Shaw AW;
 XX DR WPI; 1999-277200/23.
 XX PT New small molecule phenyl-containing compounds
 XX PS Disclosure; Page 71; 200pp; English.
 XX CC AAV02233-43 represent "CAAXG" motif from various human proteins. The
 CC specification describes small molecule phenyl-containing compounds
 CC which inhibit a prenyl-protein transferase and the farnesylation of
 CC the oncogene protein Ras. The compounds inhibit tumour angiogenesis,
 CC thereby affecting the growth of tumours. They may therefore be useful
 CC in the treatment of certain forms of vision deficit related to
 CC retinal vascularisation. The compounds are also useful for inhibiting
 CC other proliferative diseases, both benign and malignant, in which Ras
 CC proteins are aberrantly activated as a result of oncogenic mutation in
 CC other genes, and for the treatment of certain viral infections,
 CC particularly hepatitis delta and related viruses. The compounds are
 CC also useful in the prevention of restenosis after percutaneous
 CC transluminal coronary angioplasty by inhibiting neointimal formation.
 CC The compounds may also be useful in the treatment and prevention of
 CC polycystic kidney disease, fungal infections, arteriosclerosis and
 CC diabetic vascular pathologies.

SQ Sequence 4 AA;

Query Match 60.0%; Score 3; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
 |||
 Db 2 VWM 4

RESULT 43

AAW99755
 ID AAW99755 standard; peptide; 4 AA.
 XX AC AAW99755;
 XX DT 03-JUN-1999 (first entry)
 XX DE CAAX-G motif peptide N-Ras.
 XX KW Cancer; prenyl-protein transferase inhibitor; GGTase-I; Ras protein;
 KW geranylgeranyl-protein transferase type I; farnesyl-protein transferase;
 KW proliferative disorder; benign; malignant; oncogenic mutation;
 KW neurofibromatosis; restenosis; polycystic kidney disease; angiogenesis;
 KW retinal vascularisation; arteriosclerosis; fungal infection;
 KW diabetic vascular pathology.
 XX OS Synthetic.
 XX FN WO9910524-A1.
 XX PD 04-MAR-1999.
 XX PF 26-AUG-1998; 98WO-US17698.
 XX PR 06-APR-1998; 98GB-0007361.
 XX DR 27-AUG-1997; 97US-0057228.
 XX PA (MERI) MERCK & CO INC.
 XX PI Burkhardt AL, Buser-Doepner CA, Huang PS, Kobian KS;
 PI Kohl NE, Lobell RB;
 XX DR WPI; 1999-204676/17.
 XX PT Inhibition of prenyl-protein transferases, e.g. for cancer therapy
 PT - using a compound which inhibits cellular processing of a protein
 PT substrate of one or both of geranylgeranyl-protein transferase and
 PT farnesyl-protein transferase
 XX PS Disclosure; Page 9; 177pp; English.
 XX CC A method has been developed for inhibiting prenyl-protein transferases,
 CC for cancer therapy. The method uses a compound which inhibits cellular
 CC processing of a protein substrate of one or both of geranylgeranyl-
 CC protein transferase and farnesyl-protein transferase. Methods and
 CC products from the present invention can be used for identifying
 CC compounds for treating cancer and other proliferative disorders, both
 CC benign and malignant, in which Ras proteins are aberrantly activated as a
 CC result of oncogenic mutation in other genes. They can be used for e.g.
 CC treating neurofibromatosis, preventing restenosis after percutaneous
 CC transluminal coronary angioplasty by inhibiting neointimal formation,
 CC preventing polycystic kidney disease, for inhibiting for inhibiting
 CC angiogenesis in the treatment of certain forms of vision deficit related
 CC to retinal vascularisation, in the treatment of hepatitis delta and
 CC related viruses, in the prevention and therapy of arteriosclerosis and
 CC diabetic vascular pathologies, and fungal infections. The dual FTP and
 CC GPT-1 inhibitors can inhibit the growth of cancer cells at
 CC concentrations that do not cause mechanism based toxicity in rapidly
 CC proliferating tissues, e.g. bone marrow. The present sequence represents
 CC a CAAX-G motif peptide for use in the method of the invention.

SQ Sequence 4 AA;

Query Match 60.0%; Score 3; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VVM	3
Db	2	VVM	4
RESULT 44			
AAW99740			
ID	AAW99740	standard; peptide; 4 AA.	
XX	AC		
XX	AAW99740;		
XX	AC		
XX	DT	03-JUN-1999 (first entry)	
XX	DE		
XX	DE	CAAX-G motif peptide N-Ras.	
XX	KW	Cancer; prenyl-protein transferase inhibitor; GGTase-I; Ras protein; geranylgeranyl-protein transferase type I; farnesyl-protein transferase; proliferative disorder; benign; malignant; oncogenic mutation; neurofibromatosis; restenosis; polycystic kidney disease; angiogenesis; retinal vascularisation; arteriosclerosis; fungal infection; diabetic vascular pathology.	
XX	OS	Synthetic.	
XX	PN	WO9910523-A1.	
XX	PD	04-MAR-1999.	
XX	PF	26-AUG-1998; 98WO-US17697.	
XX	PR	18-NOV-1997; 97GB-0024331.	
XX	PR	27-AUG-1997; 97US-0057340.	
XX	PA	(MERI) MERCK & CO INC.	
XX	PI	Barnett SF, Heimbrook DC, Huber HE, Patrick DR;	
XX	DR	WPI; 1998-204675/17.	
XX	PT	Inhibition of prenyl-protein transferases, e.g. for cancer therapy	
XX	PT	- using a compound which is a dual inhibitor of farnesyl-protein transferase and geranylgeranyl-protein transferase	
XX	PS	Claim 11; Page 152; 180pp; English.	
XX	CC	A method has been developed for inhibiting prenyl-protein transferases (PPTs) and treating cancer comprises a compound that is a dual inhibitor of farnesyl-protein transferase (FTP) and geranylgeranyl-protein transferase type I (GPT-1). The compounds identified as inhibitor of PPTs can be used for treating cancer and other proliferative disorders, both benign and malignant, in which Ras proteins are aberrantly activated as a result of oncogenic mutation in other genes. They can be used for e.g. treating neurofibromatosis, preventing restenosis after percutaneous transluminal coronary angioplasty by inhibiting neointimal formation, preventing polycystic kidney disease, for inhibiting angiogenesis in the treatment of certain forms of vision deficit related to retinal vascularisation, in the treatment of hepatitis delta and related viruses, in the prevention and therapy of arteriosclerosis and diabetic vascular pathologies, and fungal infections. The dual FTP and GPT-1 inhibitors can inhibit the growth of cancer cells at concentrations that do not cause mechanism based toxicity in rapidly proliferating tissues, e.g. bone marrow. The present sequence represents a specifically claimed CAAX-G motif peptide for use in the method of the invention.	
XX	Sequence	4 AA;	
XX	Query Match	60.0%; Score 3; DB 20; Length 4;	
XX	Best Local Similarity	100.0%; Pred. No. 9.2e+05;	
XX	Matches	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	VVM	3
	2	VVM	4
Db	2	VVM	4
RESULT 45			
AAW99740			
ID	AAW99740	standard; peptide; 4 AA.	
XX	AC		
XX	AAW99740;		
XX	AC		
XX	DT	26-FEB-2001 (first entry)	
XX	DE		
XX	DE	N-Ras C-terminal peptide.	
XX	KW	Prostate cancer; prostate specific antigen; PSA; sperm; semenogelin; fibronectin; prenyl protein transferase; insulin like growth factor binding protein; farnesyl protein transferase; gernal geranyl protein transferase; FIPase; GPTase; Rab GPTase; isoprenoid; tumour; treatment; human.	
XX	OS	Homo sapiens.	
XX	PN	WO200059930-A1.	
XX	PD	12-OCT-2000.	
XX	PF	31-MAR-2000; 2000WO-US08762.	
XX	PR	05-APR-1999; 99US-0127746.	
XX	PA	(MERI) MERCK & CO INC.	
XX	PI	DeFeo-jones D, Jones RE, Oliff AI;	
XX	XX	WPI; 2000-679354/66.	
XX	XX	Treating cancer, especially cancer associated with cells that produce prostate specific antigen (PSA), particularly prostate cancer, comprises administering prenyl-protein transferase inhibitor(s) and PSA conjugate(s)	
XX	PS	Disclosure; Page 515; 546pp; English.	
XX	CC	Prostate specific antigen (PSA) is a single chain 33kDa glycoprotein that is produced almost exclusively by the human prostate epithelium. PSA is mainly responsible for the dissolution of the gel structure formed at ejaculation by proteolysis of the major proteins in the sperm entrapping gel, semenogelin I and semenogelin II and fibronectin. However, PSA may proteolytically degrade insulin-like growth factor binding protein 3 (IGFBP-3) allowing IGF to stimulate specifically the growth of PSA secreting cells. Prostate metastases are known to secrete immunologically reactive PSA, therefore a cytotoxic compound that could be activated by the proteolytic activity of PSA should be prostate cell specific as well as specific for PSA secreting metastases. Conjugates which comprise an oligopeptide which can be selectively cleaved by enzymatically active PSA attached via a linker to a cytotoxic compound are useful in the treatment of prostate cancer. However, new methods of treating cancer, particularly cancer associated with cells that produce prostate specific antigen (PSA) are described which comprise administering at least one inhibitor of a prenyl-protein transferase and at least one PSA conjugate as described. Prenylation of proteins by intermediates of the isoprenoid biosynthetic pathway represents a class of post-translational modification. This modification is typically required for the membrane localisation and function of proteins and prenylated proteins characteristically share C-terminal sequences of CAAX, XXCC or XXCC (where C is Cys and X is any other amino acid. Three post-translational processing steps have been described for proteins having a C-terminal CAAX sequence: addition of either a 15 carbon (farnesyl) or 20 carbon (geranylgeranyl) isoprenoid to the Cys residue, proteolytic cleavage of the last 3 amino acids and methylation of the new C-terminal carboxylate. Three enzymes have been described that catalys protein prenylation: farnesyl-protein	

XX	SQ	Sequence	4 AA;
	Query Match	60.0%; Score 3; DB 21; Length 4;	
	Best Local Similarity	100.0%; Pred.No.9.2e+05;	
	Matches	3; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
	Qy	1 VWM 3	
	Db	2 VWM 4	
	RESULT 47		
	AAB34980		
	ID AAB34980 standard; Peptide; 4 AA.		
	AC AAB34980;		
	XX XX	27-MAR-2001 (first entry)	
	XX XX	Chimpanzee erythropoietin fragment SEQ ID NO: 6.	
	XX KW	Chimpanzee; erythropoietin; EPO; hybridisation probe; gene therapy;	
	XX XW	mapping; therapeutic agent.	
	XX OS	Pan sp.	
	XX PN	WO2000068376-A1.	
	XX PD	16-NOV-2000.	
	XX PF	05-MAY-2000; 2000WO-US12370.	
	XX PR	07-MAY-1999; 99US-0307307.	
	XX PS	28-MAR-2000; 2000US-0307307.	
	XX PA	(GETH) GENENTECH INC.	
	XX PI	Desauvage F, Henner DJ;	
	XX DR	WPI; 2001-007393/01.	
	XX PT	Nucleic acids encoding chimpanzee erythropoietin, useful for treatment	
	XX PP	of e.g. anemia, also derived proteins, antibodies and modulators -	
	XX PS	Disclosure; Page 7; 109pp; English.	
	XX CC	The present invention provides the coding and protein sequences of	
	XX CC	chimpanzee erythropoietin (EPO). These sequences can be used in gene	
	XX CC	therapy, to block the activity of EPO, as hybridisation probes, in	
	XX CC	genetic and chromosome mapping and as therapeutic agents.	
	SQ	Sequence	4 AA;
	Query Match	60.0%; Score 3; DB 22; Length 4;	
	Best Local Similarity	100.0%; Pred.No.9.2e+05;	
	Matches	3; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
	Qy	3 MEV 5	
	Db	1 MEV 3	
	RESULT 48		
	AAE29301		
	ID AAE29301 standard; peptide; 4 AA.		
	XX AC	AAE29301;	
	XX DT	27-JAN-2003 (first entry)	
	XX DE	Chimpanzee erythropoietin (CHEPO) peptide #1.	
	XX XX		

KW Chimpanzee; erythropoietin; gene therapy; blood disorder; immunoadhesin;
 KW chromosome identification; tissue typing; antianaemic; CHEPO.
 XX
 XX Pan troglodytes.
 XX WO200274807-A2.
 XX PD 26-SEP-2002.
 XX PF 14-FEB-2002; 2002WO-US04773.
 XX PR 20-MAR-2001; 2001US-0813775.
 XX (GETH) GENENTECH INC.
 XX PA Desauvage F, Henner DJ;
 XX WIPI; 2002-759880/82.
 XX New immunoadhesin comprising a chimpanzee erythropoietin (CHEPO)
 PT polypeptide, useful for the treatment of blood disorders with low or
 PT defective red blood cell production -
 XX Disclosure; Page 100; 120pp; English.
 XX The invention relates to immunoadhesins comprising chimpanzee
 CC erythropoietin (CHEPO) polypeptide. The invention further relates to
 CC methods using and compositions comprising CHEPO immunoadhesins. The
 CC methods and compositions of the present invention are useful for the
 CC treatment of blood disorders characterised by low or defective red
 CC blood cell production. The CHEPO polypeptides may also be used as
 CC molecular weight markers, tissue typing and chromosome identification.
 CC CHEPO DNA is used in gene therapy. The present sequence is chimpanzee
 CC erythropoietin peptide.
 XX
 SQ Sequence 4 AA;
 Query Match 60.0%; Score 3; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 MEV 5
 DB 1 MEV 3
 RESULT 49
 AAR82999
 ID AAR82999 standard; peptide; 5 AA.
 AC AAR82999;
 XX 02-MAY-1996 (first entry)
 XX M. prolifera fucose contg. proteoglycan trypsin digest peptide.
 DE
 XX Proteoglycan; trypsin digest; marine sponge; fucose;
 KW immunostimulants; cancer; viral infection; natural killer; cells;
 KW gamma/delta-T; metastases; retro-viral; immunosuppressants.
 XX Microciconia prolifera.
 OS
 XX WO9525745-A1.
 PN 28-SEP-1995.
 XX 24-MAR-1995; 95WO-IB00208.
 PF 24-MAR-1994; 94GB-0005846.
 PR (MISE/) MISEVIC G.
 PA Misevic G;
 XX

XX WIPI; 1995-344588/44.
 DR Fucose contg proteoglycan and acidic glycan cpds - with
 XX immunostimulating activity, partic for treating cancer and viral
 PT infections, includes new cpds isolated from sponges and sea
 PT urchin(e)
 XX Example 1; Page 8; 27pp; English.
 PS M. prolifera (a marine sponge) derived fucose contg. proteoglycans
 XX (PGs) have the trypsin digest protein backbone peptides AAR82999-03.
 CC The PGs stimulate the proliferation of natural killer (NK) and/or
 CC gamma/delta-T cells, useful in the treatment of cancer, esp.
 CC metastases and (retroviral) infections, they may also be used to
 CC screen for immunosuppressant cpds.. Monovalent forms of the PGs
 CC inhibit the activation of NK and gamma/delta-T cells, and are
 CC therefore useful as immunosuppressants.
 XX
 SQ Sequence 5 AA;
 Query Match 60.0%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVM 3
 DB 2 VVM 4
 RESULT 50
 AAR69999
 ID AAR69999 standard; Protein; 5 AA.
 XX AAR69999;
 XX 25-MAR-2003 (updated)
 DT 21-OCT-1995 (first entry)
 XX High affinity IGE receptor beta-subunit variant.
 DE
 XX IGE receptor; mutation; polymorphism; atopy diagnosis.
 KW Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "Ile-181 in wt"
 FT
 XX WO9505481-A1.
 PN 23-FEB-1995.
 XX 17-AUG-1994; 94WO-GB01801.
 PF 18-AUG-1993; 93GB-0017185.
 PR 27-MAY-1994; 94GB-0010669.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX Cookson WOCM, Hopkin JM, Shirakawa T;
 XX WIPI; 1995-098778/13.
 DR N-PSDB; AAQ80599.
 XX Diagnostic method for atopy - comprises detecting presence of
 PT mutation or polymorphism in gene encoding beta-subunit of high
 PT affinity Igs receptor.
 XX Claim 4; Page 33; 48pp; English.
 PS The sequence corresponds to mutant high affinity IgE receptor
 XX (180-184). The mutation at AA 181 arises from mutations
 CC

CC in exon 6 of the gene found on chromosome-11q. The mutations
 CC can be detected in a method for the diagnosis of atopy or
 CC predisposition to atopy.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
 ||||
 Db 3 VVM 5

RESULT 51

AAR70276
 ID AAR70276 standard; peptide; 5 AA.

XX AAR70276;

DT 14-NOV-1995 (first entry)

DE VVM-containing peptide, non-thrombospondin binding.

XX Thrombospondin 1; TSI; receptor; inactive; cell-adhesion.

XX Synthetic.

PN US5399667-A.

XX 21-MAR-1995.

PF 05-MAR-1993; 93US-0029333.

PR 05-MAR-1993; 93US-0029333.

XX (UNIW) UNIV WASHINGTON.

PI Frazier WA, Kosfeld MD;

DR WPI; 1995-130736/17.

PT Thrombospondin receptor binding peptide(s) - comprise tri:peptide
 PT sequence Val-Val-Met (VVM)

XX Example 1; Column 8; 25pp; English.

CC AAR70276-78 are synthetic peptides containing the tri-peptide VVM which
 CC are incapable of binding to the thrombospondin 1 (TS1) receptor cell-
 CC binding domain (CBD).

XX SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
 ||||
 Db 3 VVM 5

RESULT 52

AAR70277
 ID AAR70277 standard; peptide; 5 AA.

XX AAR70277;

DT 14-NOV-1995 (first entry)

DE VVM-containing peptide, non-thrombospondin binding.

XX Thrombospondin 1; TSI; receptor; inactive; cell-adhesion.
 XX Synthetic.
 XX US5399667-A.
 XX 21-MAR-1995.
 XX 05-MAR-1993; 93US-0029333.
 XX 05-MAR-1993; 93US-0029333.
 XX (UNIW) UNIV WASHINGTON.
 XX Frazier WA, Kosfeld MD;
 XX WPI; 1995-130736/17.
 XX Thrombospondin receptor binding peptide(s) - comprise tri:peptide
 XX sequence Val-Val-Met (VVM)
 XX Example 1; Column 8; 25pp; English.
 XX AAR70276-78 are synthetic peptides containing the tri-peptide VVM which
 CC are incapable of binding to the thrombospondin 1 (TS1) receptor cell-
 CC binding domain (CBD).
 XX SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
 ||||
 Db 3 VVM 5

RESULT 53

AAR70275
 ID AAR70275 standard; peptide; 5 AA.

XX AAR70275;

DT 14-NOV-1995 (first entry)

XX Thrombospondin 1 (TS1) receptor binding peptide.

XX Thrombospondin 1; TSI; receptor; inhibition; cell-adhesion.

XX Synthetic.

PN US5399667-A.

XX 21-MAR-1995.

PF 05-MAR-1993; 93US-0029333.

PR 05-MAR-1993; 93US-0029333.

XX (UNIW) UNIV WASHINGTON.

PI Frazier WA, Kosfeld MD;

DR WPI; 1995-130736/17.

XX Thrombospondin receptor binding peptide(s) - comprise tri:peptide
 XX sequence Val-Val-Met (VVM)

PS Claim 1; Column 29; 25pp; English.

XX AAR70271-75 are synthetic peptides containing the tri-peptide VVM which

CC are capable of binding to the thrombospondin 1 (TSP1) receptor cell-
 CC binding domain (CBD). These peptides are useful in preventing cell-
 CC adhesion of several normal and transformed cell lines.

XX SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
 |||
 Db 3 VVM 5

RESULT 54
 AAW05024
 ID AAW05024 standard; peptide; 5 AA.
 XX AC
 XX AC AAW05024;
 XX DT 03-DEC-1996 (first entry)
 XX DE Thrombospondin-derived, homotypic platelet aggregation inducer #17.
 XX KW Thrombospondin; TSP; platelet aggregation; induction; activation;
 XX KW antagonist; RGD peptide; thrombus formation; receptor binding.
 XX OS Synthetic.
 XX PN WO9611942-A1.
 XX PD 25-APR-1996.
 XX PF 17-OCT-1995; 95WO-AU00683.
 XX PR 18-OCT-1994; 94AU-0008858.
 XX RA (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
 XX PI Burns GF;
 XX DR WPI; 1996-221937/22.
 XX PT Identifying platelet aggregation antagonists - using
 PT thrombospondin-derived octa-peptide or its mutants, derivatives or
 PT modified forms, some of which are new
 XX PS Claim 4; Page 24; 38pp; English.
 XX CC A peptide derived from the region of thrombospondin (TSP) which
 CC binds to the carboxy terminal receptor on platelets and which induces
 CC homotypic platelet aggregation even in the presence of RGD peptides
 CC or their mimetics has been identified previously. The peptide has
 CC the sequence RYVVMWK and was disclosed by Kosfeld and Frazier in
 CC J.Biol.Chem.268:8808-8814 (1993) where it was designated "peptide
 CC 4N1-1". Peptides able to induce homotypic platelet aggregation and
 CC which differ by at least 1 amino acid from the sequence of peptide
 CC 4N1-1 are claimed. The present peptide is a preferred example.

XX SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
 |||
 Db 1 VVM 3

RESULT 55
 AAW87390
 ID AAW87390 standard; peptide; 5 AA.
 XX AC
 XX AC AAW87390;
 XX DT 09-FEB-1999 (first entry)
 XX DE Peptide determined by the method of the invention.
 XX KW Amino acid determination; molecular mass; fragmentation spectrum;
 XX KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.
 XX OS Synthetic.
 XX PN GB2325465-A.
 XX PD 25-NOV-1998.
 XX PF 22-MAY-1998; 98GB-0011196.
 XX PR 22-MAY-1997; 97GB-0010582.
 XX RA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Parekh RB, Prime SB, Townsend RR, Wedd NS;
 XX DR WPI; 1998-571195/49.
 XX PT Peptide sequence determination used in e.g. DNA cloning - by
 PT comparing mass spectra of the unknown peptide with a library of
 PT linear chain known peptide sequences
 XX PS Example 3; Page 24; 40pp; English.
 XX CC The invention relates to a method for determination of the amino acid
 CC sequence of an unknown peptide. The method comprises (a) determining
 CC the molecular mass and an experimental fragmentation spectrum for the
 CC peptide; (b) comparing the experimental fragmentation spectrum of the
 CC unknown peptide with a theoretical fragmentation spectra calculated for
 CC a peptide library composed of all possible linear sequences of amino
 CC acids having a total mass that corresponds to the molecular mass of the
 CC unknown peptide; and (c) identifying a peptide in the library with a
 CC theoretical fragmentation spectrum that most closely matches the
 CC fragmentation spectrum of the unknown peptide. The method is useful in
 CC DNA cloning, anti-body production, identification of recombinant
 CC products, and the study of post-translational modifications. It allows
 CC the sequence of unknown peptides or proteins with no sub-sequences
 CC identity, to be characterised using mass spectrometry. Sequences
 CC AAW87377 to AAW87444 represent linear peptides constructed to exemplify
 CC the method.

KW cell culture media; rapid identification of biologically active compound;
 KW peptide library; concatamer-based recombinant expression method;
 XX large-scale recombinant production method; antibacterial.
 OS Synthetic.
 XX WO200202591-A2.
 PN 10-JAN-2002.
 XX 04-JUN-2001; 2001WO-US17943.
 XX 30-JUN-2000; 2000US-0608892.
 XX (BECT) BECTON DICKINSON & CO.
 XX Haaland PD, Sherman DB, Campbell RL, Stewart WW, Lloyd SA;
 PI Erickson BW;
 XX WPI; 2002-195744/25.
 DR Novel synthetic peptides which include cell-growth affecting peptides
 PT and peptides which enhance or inhibit cellular protein production,
 PT useful for enhancing or inhibiting cell growth or cellular protein
 PT production -
 XX Claim 1; Page 9; 4lpp; English.
 PS The present invention relates to synthetic peptides which include
 CC cell-growth affecting peptides and peptides which enhance or inhibit
 CC cellular protein production. The peptides of the invention are useful
 CC for enhancing or inhibiting cell growth of bacteria, particularly
 CC Clostridium perfringens, or cellular protein production of beta-toxins,
 CC in cell culture. They are also useful in a peptide library for the rapid
 CC identification of biologically active compounds which affect the
 CC properties of cells in culture media. The peptide can be used in
 CC concatamer-based recombinant expression methods or in large-scale,
 CC economical recombinant production methods. The peptides reduce the
 CC number and quantity of undefined components in culture media, reduce
 CC the need for animal-derived components, improve media consistency and
 CC quality control, and provide a method for precisely controlling and
 CC adjusting the performance of the cell culture.
 CC AAU85876-AAU85969 represent the synthetic peptides of the invention.
 XX SQ Sequence 5 AA;
 Query Match 60.0%; Score 3; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VME 4
 Db |||
 2 VME 4
 RESULT 57
 ABUS7836
 ID ABUS7836 standard; Peptide; 5 AA.
 AC
 XX ABUS7836;
 XX 10-APR-2003 (first entry)
 XX Thrombospondin 1 receptor cell binding domain peptide C7.
 DE Thrombospondin-1; mouse; rat; human; chicken; tumour cell migration;
 KW cell adhesion; platelet aggregation; wound healing; laminin; TS-1.
 XX Homo sapiens.
 OS Mus sp.
 XX US6469138-B1.
 PN

PD 22-OCT-2002.
 XX 21-FEB-1995; 95US-0391820.
 XX 05-MAR-1993; 93US-0029333.
 XX (UNIW) UNIV WASHINGTON.
 XX Frazier WA, Kosfeld MD;
 XX WPI; 2003-196751/19.
 XX Novel peptide that binds to thrombospondin 1 receptor, useful as probe
 PT sequence in computer search of all available databases -
 XX Examples; Column 7; 25pp; English.
 XX This invention relates to a novel peptide that binds to the
 CC thrombospondin 1 (TS-1) receptor. Thrombospondin 1 is a protein which
 CC acts to promote cell adhesion and is involved in platelet aggregation,
 CC wound healing and tumour cell migration. Also disclosed in the
 CC invention is Laminin peptides which have been shown to be able to
 CC substitute for TS-1 peptides. Preferably the peptides of
 CC the invention share a tripeptide motif VVM and are useful as probe
 CC sequences in a computer search of all available databases for
 CC similar receptor binding motif peptides. The present sequence
 CC represents a thrombospondin-1 (TS-1) or Laminin cell binding domain
 CC peptide of the invention.
 XX SQ Sequence 5 AA;
 Query Match 60.0%; Score 3; DB 24; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VVM 3
 Db |||
 3 VVM 5
 RESULT 58
 ABUS7837
 ID ABUS7837 standard; Peptide; 5 AA.
 AC
 XX ABUS7837;
 XX 10-APR-2003 (first entry)
 XX Thrombospondin 1 cell binding domain peptide #1.
 DE Thrombospondin-1; mouse; rat; human; chicken; tumour cell migration;
 KW cell adhesion; platelet aggregation; wound healing; laminin; TS-1.
 XX Synthetic.
 OS
 XX US6469138-B1.
 XX 22-OCT-2002.
 XX 21-FEB-1995; 95US-0391820.
 XX 05-MAR-1993; 93US-0029333.
 XX (UNIW) UNIV WASHINGTON.
 XX Frazier WA, Kosfeld MD;
 XX WPI; 2003-196751/19.
 XX Novel peptide that binds to thrombospondin 1 receptor, useful as probe
 PT sequence in computer search of all available databases -
 XX Examples; Column 8; 25pp; English.
 PS

XX This invention relates to a novel peptide that binds to the
CC thrombospondin 1 (TS-1) receptor. Thrombospondin 1 is a protein which
CC acts to promote cell adhesion and is involved in platelet aggregation,
CC wound healing and tumour cell migration. Also disclosed in the
CC invention is laminin peptides which have been shown to be able to
CC substitute for TS-1 peptides. Preferably the peptides of
CC the invention share a tripeptide motif VVM and are useful as probe
CC sequences in a computer search of all available databases for
CC similar receptor binding motif peptides. The present sequence
CC represents a thrombospondin-1 (TS-1) or Laminin cell binding domain
CC peptide of the invention.
XX Sequence 5 AA;
SQ

Query Match 60.0%; Score 3; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VVM 3
Db 3 VVM 5

RESULT 59
ABU57838
ID ABU57838 standard; Peptide; 5 AA.
AC ABU57838;
XX
XX
DT 10-APR-2003 (first entry)
XX
DE Thrombospondin 1 cell binding domain peptide 7N3-1.
XX
KW Thrombospondin-1; mouse; rat; human; chicken; tumour cell migration;
KW cell adhesion; platelet aggregation; wound healing; laminin; TS-1.
XX
OS Synthetic.
XX
XX US6469138-B1.
XX
XX 22-OCT-2002.
XX
XX 21-FEB-1995; 95US-0391820.
XX
XX 05-MAR-1993; 93US-0029333.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Frazier WA, Kosfeld MD;
XX
XX WPI; 2003-196751/19.
XX
XX Novel peptide that binds to thrombospondin 1 receptor, useful as probe
XX sequence in computer search of all available databases -
XX
XX Examples; Column 8; 25pp; English.
XX

This invention relates to a novel peptide that binds to the
CC thrombospondin 1 (TS-1) receptor. Thrombospondin 1 is a protein which
CC acts to promote cell adhesion and is involved in platelet aggregation,
CC wound healing and tumour cell migration. Also disclosed in the
CC invention is laminin peptides which have been shown to be able to
CC substitute for TS-1 peptides. Preferably the peptides of
CC the invention share a tripeptide motif VVM and are useful as probe
CC sequences in a computer search of all available databases for
CC similar receptor binding motif peptides. The present sequence
CC represents a thrombospondin-1 (TS-1) or Laminin cell binding domain
CC peptide of the invention.
XX Sequence 5 AA;
SQ

Query Match 60.0%; Score 3; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VVM 3
Db 3 VVM 5

RESULT 61
AAR77518
ID AAR77518 standard; Peptide; 6 AA.
XX
XX AAR77518;
XX
XX 27-MAR-1996 (first entry)
XX
XX Cytochrome-P450-lpr N-terminal peptide.
XX
XX Cytochrome P450-lpr; P450-monoxygenase; insecticide;
XX biological control; pesticide degradation; bioremediation;
XX transgenic plant; crop improvement; insect resistance; housefly;
XX PCR; primer; polymerase chain reaction.
XX
XX Musca domestica Learn-PyR.
XX

Query Match 60.0%; Score 3; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VVM 3
Db 4 VVM 6

RESULT 60
AAR70272
ID AAR70272 standard; peptide; 6 AA.
XX
XX AAR70272;
XX
XX 14-NOV-1995 (first entry)
XX
XX Thrombospondin 1 (TS1) receptor binding peptide.
XX
XX Thrombospondin 1; TS1; receptor; inhibition; cell-adhesion.
XX
XX Synthetic.
XX
XX US5399667-A.
XX
XX 21-MAR-1995.
XX
XX 05-MAR-1993; 93US-0029333.
XX
XX 05-MAR-1993; 93US-0029333.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Frazier WA, Kosfeld MD;
XX
XX WPI; 1995-130736/17.
XX
XX Thrombospondin receptor binding peptide(s) - comprise tri:peptide
XX sequence Val-Val-Met (VVM)
XX
XX Claim 1; Column 29; 25pp; English.
XX
XX AAR70271-75 are synthetic peptides containing the tri-peptide VVM which
XX are capable of binding to the thrombospondin 1 (TS1) receptor cell-
XX binding domain (CBD). These peptides are useful in preventing cell-
XX adhesion of several normal and transformed cell lines.
XX
XX Sequence 6 AA;
SQ

Query Match 60.0%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VVM 3
Db 4 VVM 6

RESULT 61
AAR77518
ID AAR77518 standard; Peptide; 6 AA.
XX
XX AAR77518;
XX
XX 27-MAR-1996 (first entry)
XX
XX Cytochrome-P450-lpr N-terminal peptide.
XX
XX Cytochrome P450-lpr; P450-monoxygenase; insecticide;
XX biological control; pesticide degradation; bioremediation;
XX transgenic plant; crop improvement; insect resistance; housefly;
XX PCR; primer; polymerase chain reaction.
XX
XX Musca domestica Learn-PyR.
XX

XX WO9530745-A1.
 XX 16-NOV-1995.
 XX 08-MAY-1995; 95WO-US05758.
 XX 10-MAY-1994; 94US-0241388.
 XX (CORR) CORNELL RES FOUND INC.
 XX
 XX Scott JG, Tomita T;
 XX WPI; 1995-404112/51.
 XX N-PSDB; AAT05519.
 XX
 XX DNA encoding cytochrome P450-lpr - used for insect control,
 XX bioremediation of insecticides or reducing crop sensitivity to
 XX pesticides
 XX
 XX Example 8; Page 30; 87pp; English.
 XX
 XX A peptide (AAR77518) corresponding to a fragment of housefly cytochrome
 XX P450-lpr was used to design degenerate primer AS3 (AAT05519), used for
 XX the PCR amplification of internal sequences of P450-lpr cDNA.
 XX
 XX Sequence 6 AA;
 XX
 XX Query Match 60.0%; Score 3; DB 16; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VME 4
 DB 2 VME 4
 XX
 XX
 XX RESULT 62
 XX AAW05018
 XX ID AAW05018 standard; peptide; 6 AA.
 XX AC AAW05018;
 XX DT 03-DEC-1996 (first entry)
 XX
 XX Thrombospondin-derived, homotypic platelet aggregation inducer #9.
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;
 XX antagonist; RGD peptide; thrombus formation; receptor binding.
 XX Synthetic.
 XX WO9611942-A1.
 XX 25-APR-1996.
 XX 17-OCT-1995; 95WO-AU00683.
 XX 18-OCT-1994; 94AU-0008858.
 XX (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
 XX Burns GF;
 XX WPI; 1996-221937/22.
 XX Identifying platelet aggregation antagonists - using
 XX thrombospondin-derived octa-peptide or its mutants, derivatives or
 XX modified forms, some of which are new
 XX Claim 3; Page 24; 38pp; English.
 XX A peptide derived from the region of thrombospondin (TSP) which
 XX binds to the carboxy terminal receptor on platelets and which induces
 XX homotypic platelet aggregation even in the presence of RGD peptides
 XX or their mimetics has been identified previously. The peptide has
 XX the sequence RPYVVMWK and was disclosed by Kosfeld and Frazier in
 XX J Biol.Chem.268:8808-8814 (1993) where it was designated "peptide
 XX 4N1-1". Peptides able to induce homotypic platelet aggregation and
 XX which differ by at least 1 amino acid from the sequence of peptide
 XX 4N1-1 are claimed. The present peptide is a preferred example.
 XX Sequence 6 AA;
 XX Query Match 60.0%; Score 3; DB 17; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVM 3
 DB 4 VVM 6
 XX
 XX RESULT 63
 XX AAW05022
 XX ID AAW05022 standard; peptide; 6 AA.
 XX AC AAW05022;
 XX DT 03-DEC-1996 (first entry)
 XX
 XX Thrombospondin-derived, homotypic platelet aggregation inducer #13.
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;
 XX antagonist; RGD peptide; thrombus formation; receptor binding.
 XX Synthetic.
 XX WO9611942-A1.
 XX 25-APR-1996.
 XX 17-OCT-1995; 95WO-AU00683.
 XX 18-OCT-1994; 94AU-0008858.
 XX (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
 XX Burns GF;
 XX WPI; 1996-221937/22.
 XX Identifying platelet aggregation antagonists - using
 XX thrombospondin-derived octa-peptide or its mutants, derivatives or
 XX modified forms, some of which are new
 XX Claim 3; Page 24; 38pp; English.
 XX A peptide derived from the region of thrombospondin (TSP) which
 XX binds to the carboxy terminal receptor on platelets and which induces
 XX homotypic platelet aggregation even in the presence of RGD peptides
 XX or their mimetics has been identified previously. The peptide has
 XX the sequence RPYVVMWK and was disclosed by Kosfeld and Frazier in
 XX J Biol.Chem.268:8808-8814 (1993) where it was designated "peptide
 XX 4N1-1". Peptides able to induce homotypic platelet aggregation and
 XX which differ by at least 1 amino acid from the sequence of peptide
 XX 4N1-1 are claimed. The present peptide is a preferred example.
 XX Sequence 6 AA;
 XX Query Match 60.0%; Score 3; DB 17; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVM 3
 DB 4 VVM 6
 XX
 XX RESULT 64
 XX AAW05018
 XX ID AAW05018 standard; peptide; 6 AA.
 XX AC AAW05018;
 XX DT 03-DEC-1996 (first entry)
 XX
 XX Thrombospondin-derived, homotypic platelet aggregation inducer #9.
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;
 XX antagonist; RGD peptide; thrombus formation; receptor binding.
 XX Synthetic.
 XX WO9611942-A1.
 XX 25-APR-1996.
 XX 17-OCT-1995; 95WO-AU00683.
 XX 18-OCT-1994; 94AU-0008858.
 XX (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
 XX Burns GF;
 XX WPI; 1996-221937/22.
 XX Identifying platelet aggregation antagonists - using
 XX thrombospondin-derived octa-peptide or its mutants, derivatives or
 XX modified forms, some of which are new
 XX Claim 3; Page 24; 38pp; English.
 XX A peptide derived from the region of thrombospondin (TSP) which

CC binds to the carboxy terminal receptor on platelets and which induces
 CC homotypic platelet aggregation even in the presence of RGD peptides
 CC or their mimetics has been identified previously. The peptide has
 CC the sequence RPYVVMWK and was disclosed by Kosfeld and Frazier in
 CC J Biol.Chem.268:8808-8814 (1993) where it was designated "peptide
 CC 4N1-1". Peptides able to induce homotypic platelet aggregation and
 CC which differ by at least 1 amino acid from the sequence of peptide
 CC 4N1-1 are claimed. The present peptide is a preferred example.
 XX Sequence 6 AA;
 XX Query Match 60.0%; Score 3; DB 17; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVM 3
 DB 4 VVM 6
 XX
 XX RESULT 63
 XX AAW05022
 XX ID AAW05022 standard; peptide; 6 AA.
 XX AC AAW05022;
 XX DT 03-DEC-1996 (first entry)
 XX
 XX Thrombospondin-derived, homotypic platelet aggregation inducer #13.
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;
 XX antagonist; RGD peptide; thrombus formation; receptor binding.
 XX Synthetic.
 XX WO9611942-A1.
 XX 25-APR-1996.
 XX 17-OCT-1995; 95WO-AU00683.
 XX 18-OCT-1994; 94AU-0008858.
 XX (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
 XX Burns GF;
 XX WPI; 1996-221937/22.
 XX Identifying platelet aggregation antagonists - using
 XX thrombospondin-derived octa-peptide or its mutants, derivatives or
 XX modified forms, some of which are new
 XX Claim 3; Page 24; 38pp; English.
 XX A peptide derived from the region of thrombospondin (TSP) which
 XX binds to the carboxy terminal receptor on platelets and which induces
 XX homotypic platelet aggregation even in the presence of RGD peptides
 XX or their mimetics has been identified previously. The peptide has
 XX the sequence RPYVVMWK and was disclosed by Kosfeld and Frazier in
 XX J Biol.Chem.268:8808-8814 (1993) where it was designated "peptide
 XX 4N1-1". Peptides able to induce homotypic platelet aggregation and
 XX which differ by at least 1 amino acid from the sequence of peptide
 XX 4N1-1 are claimed. The present peptide is a preferred example.
 XX Sequence 6 AA;
 XX Query Match 60.0%; Score 3; DB 17; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVM 3
 DB 4 VVM 6
 XX
 XX RESULT 64
 XX AAW05018
 XX ID AAW05018 standard; peptide; 6 AA.
 XX AC AAW05018;
 XX DT 03-DEC-1996 (first entry)
 XX
 XX Thrombospondin-derived, homotypic platelet aggregation inducer #9.
 XX Thrombospondin; TSP; platelet aggregation; induction; activation;
 XX antagonist; RGD peptide; thrombus formation; receptor binding.
 XX Synthetic.
 XX WO9611942-A1.
 XX 25-APR-1996.
 XX 17-OCT-1995; 95WO-AU00683.
 XX 18-OCT-1994; 94AU-0008858.
 XX (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
 XX Burns GF;
 XX WPI; 1996-221937/22.
 XX Identifying platelet aggregation antagonists - using
 XX thrombospondin-derived octa-peptide or its mutants, derivatives or
 XX modified forms, some of which are new
 XX Claim 3; Page 24; 38pp; English.
 XX A peptide derived from the region of thrombospondin (TSP) which

```

Db      .      2 VVM 4

RESULT 64
AAW05023
ID AAW05023 standard; peptide; 6 AA.
XX
AC AAW05023;
XX
DT 03-DEC-1996 (first entry)
XX
DE Thrombospondin-derived, homotypic platelet aggregation inducer #14.
XX
KW Thrombospondin; TSP; platelet aggregation; induction; activation;
KW antagonist; RGD peptide; thrombus formation; receptor binding.
XX
OS Synthetic.
XX
PN WO9611942-A1.
XX
PD 25-APR-1996.
XX
PF 17-OCT-1995; 95WO-AU00683.
XX
PR 18-OCT-1994; 94AU-0008858.
XX
PA (UYNE-) UNIV NEWCASTLE RES ASSOC LTD.
XX
PI Burns GF;
XX
DR WPI; 1996-221937/22.
XX
PT Identifying platelet aggregation antagonists - using
PT thrombospondin-derived octa-peptide or its mutants, derivatives or
PT modified forms, some of which are new
XX
PS Claim 3; Page 24; 38pp; English.
XX
CC A peptide derived from the region of thrombospondin (TSP) which
CC binds to the carboxy terminal receptor on platelets and which induces
CC homotypic platelet aggregation even in the presence of RGD peptides
CC or their mimetics has been identified previously. The peptide has
CC the sequence RFYVNMK and was disclosed by Kosfeld and Frazier in
CC J.Biol.Chem.268:8808-8814 (1993) where it was designated "peptide
CC 4N1-1". Peptides able to induce homotypic platelet aggregation and
CC which differ by at least 1 amino acid from the sequence of peptide
CC 4N1-1 are claimed. The present peptide is a preferred example.
XX
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
   |||
   2 VVM 4
Db

RESULT 65
AAW41047
ID AAW41047 standard; Protein; 6 AA.
XX
AC AAW41047;
XX
DT 12-MAY-1998 (first entry)
XX
DE 6P1 staurosporine selected clone.
XX
KW Transdominant bioactive agent; phenotype alteration; signalling pathway;
KW antitumour agent; cardiovascular disease; angiogenesis; atherosclerosis;
KW obesity; neurodegeneration; bone disease; infection; allergy; therapy;
KW staurosporine selected clone.

XX OS Synthetic.
XX PN WO9727213-A1.
XX PD 31-JUL-1997.
XX PF 23-JAN-1997; 97WO-US01048.
XX PR 23-JAN-1996; 96US-0589911.
XX PR 23-JAN-1996; 96US-0589109.
XX PA (STRD ) UNIV LELAND STANFORD JUNIOR.
XX PI Noaln GP, Rothenberg SM;
XX DR WPI; 1997-393612/36.
XX DR N-PSDB; AAV03821.
XX PT Screening for trans-dominant active agents able to alter cell
XX PT phenotype - useful to identify potential drugs with e. g.
XX PT anti-tumour activity
XX PS Example 3; Page 72; 91pp; English.
XX
CC This sequence is a staurosporine selected clone identified using the
CC method of the invention. The method is for screening for transdominant
CC bioactive agents (A) able to alter the phenotype of a cell comprises:
CC (a) introducing a library of different randomised nucleic acids (I) into
CC cells; and (b) screening the cells for altered phenotype due to presence
CC of (A). (A) are potential pharmaceuticals, from their effect on
CC signalling pathways. A particular application is to identify peptides,
CC encoded by (I), that have antitumour activity or are able to increase
CC sensitivity to, or reduce toxicity of, known antitumour agents. More
CC generally the method can identify agents for treatment of many other
CC conditions, e.g. cardiovascular diseases, angiogenesis, atherosclerosis,
CC obesity, neurodegeneration, bone disease, viral and other infections,
CC allergy etc.
XX
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
   |||
   1 MEV 3
Db

RESULT 66
AAB45986
ID AAB45986 standard; Peptide; 6 AA.
XX
AC AAB45986;
XX
DT 02-APR-2001 (first entry)
XX
DE Transdominant effector peptide associated screening peptide #65.
XX
KW Intracellular transdominant bioactive agent; screening; cell phenotype;
KW effector peptide.
XX
OS Unidentified.
XX
PN US6153380-A.
XX
PD 28-NOV-2000.
XX
PR 23-JAN-1997; 97US-0789333.
XX
PR 23-JAN-1996; 96US-0589108.
PR 23-JAN-1996; 96US-0589911.

```

XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (RIGE-) RIGEL PHARM INC.
 XX
 XX Rothenberg SM, Nolan GP;
 XX WPI; 2001-060084/07.
 DR
 XX Methods for screening intracellular transdominant effector peptides and
 PT RNA molecules comprise delivering random oligonucleotides to cells,
 PT which are then screened for an altered phenotype -
 XX
 PS Example 3; Column 97-98; 57pp; English.
 XX
 CC This invention describes novel in vitro screening methods (I) for a
 CC transdominant intracellular bioactive agent capable of altering the
 CC phenotype of a cell. (I) comprises: (a) introducing a molecular library
 CC of randomized candidate nucleic acids into several cells; and (b)
 CC screening the cells for a cell exhibiting an altered phenotype, where the
 CC altered phenotype is due to the presence of a transdominant bioactive
 CC agent. The methods are particularly useful for screening intracellular
 CC transdominant effector peptides and RNA molecules selected inside living
 CC cells from randomized pools. (I) is also useful for introducing random
 CC libraries into cells to screen for bioactive compounds. The methods allow
 CC rapid and highly efficient screening of large numbers of random
 CC oligonucleotides and their corresponding expression products in a single
 CC step. In addition, the methods allow screening in the absence of
 CC significant prior characterization of the cellular defect.
 XX
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 MEV 5
 DB 1 MEV 3

RESULT 67
 AAE22870
 ID AAE22870 standard; peptide; 6 AA.
 AC AAE22870;
 DT 09-AUG-2002 (first entry)
 XX Carrot red leaf luteovirus (CRLV) peptide motif #3.
 DE
 XX Carrot red leaf luteovirus; CRLV; potato leaf roll polerovirus; PLRV;
 KW barley yellow dwarf virus; BYDV; beet Western yellow virus; BWYV;
 KW luteovirus detection.
 XX Carrot red leaf luteovirus.
 OS
 XX WO200222868-A2.
 PN
 XX 21-MAR-2002.
 PD
 XX 10-SEP-2001; 2001WO-GE04053.
 PF
 XX 14-SEP-2000; 2000GB-0022505.
 PR
 XX (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
 PA
 XX Cooper JI, Naylor M;
 PI WPI; 2002-393973/42.
 DR
 XX Primer useful in diagnosing the presence of luteovirus sequences in
 PT plant tissue, is capable of hybridizing to conserved regions of nucleic
 PT acid for e.g. carrot red leaf luteovirus and barley yellow dwarf virus

PT
 XX Claim 7; Page 17; 29pp; English.
 PS
 XX The invention relates to a method for detecting luteoviruses and primers
 CC capable of hybridizing to conserved regions of nucleic acids of
 CC carrot red leaf luteovirus (CRLV), potato leaf roll polerovirus (PLRV),
 CC barley yellow dwarf virus (BYDV) and beet Western yellow virus (BWYV).
 CC These primers are useful for diagnosing the presence of a luteovirus
 CC sequence in a plant tissue nucleic acid sample. The method comprises
 CC treating the nucleic acid with a first polymerase chain reaction (PCR)
 CC primer, preferably CL2, to obtain a DNA product, treating the DNA
 CC product with one or more second PCR primers, preferably a mixture of
 CC CL1 and CL2 to obtain a PCR product, and comparing the nucleotide
 CC sequence or corresponding amino acid sequence of the PCR product with
 CC a known nucleotide sequence or corresponding amino acid sequence
 CC characteristics of the luteovirus. The primers of the invention are
 CC also useful for diagnosing the presence of CRLV or PLRV sequences in
 CC a plant tissue, where the second PCR primers used are CL1 and CL3.
 CC The present sequence is CRLV peptide motif.
 XX
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 MEV 5
 DB 4 MEV 6

RESULT 68
 ABB55686
 ID ABB55686 standard; Peptide; 6 AA.
 XX ABB55686;
 AC ABB55686;
 DT 20-FEB-2002 (first entry)
 XX Mutated protein Fes fragment #5.
 DE
 XX Enzyme inhibitor; wild-type enzyme; mutant; muten; cytostatic;
 KW osteopathic; immunomodulatory; antiallergic; protein kinase; cancer;
 KW allergy; transplant rejection; osteoporosis.
 XX Unidentified.
 OS Synthetic.
 XX WO200188530-A2.
 PN
 XX 22-NOV-2001.
 PD
 XX 17-MAY-2001; 2001WO-EP05661.
 PF
 XX 17-MAY-2000; 2000DE-1024174.
 PR
 XX (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
 PA Warmuth M, Mathes R, Hallek M;
 XX WPI; 2002-055716/07.
 DR
 XX Selecting enzyme inhibitors active against wild type, but not mutant
 PT enzyme, useful for treating or preventing diseases such as cancer,
 PT allergy and osteoporosis -
 XX Disclosure; Fig 7; 56pp; German.
 PS
 XX The present invention relates to a method of selecting inhibitors which
 CC are active against wild-type enzymes but not against mutant enzymes.
 CC These inhibitors can be used particularly to inhibit disease-associated
 CC enzymes, especially protein kinases, and are useful in the treatment of

CC cancer, allergies, transplant rejection and osteoporosis. The present
CC sequence is a peptide fragment described in the exemplification of the
CC invention.

XX
XX
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
|||
Db 3 VME 5

RESULT 69
ABU57569
ID ABU57569 standard; Peptide; 6 AA.
XX
AC ABU57569;
XX
XX 09-APR-2003 (first entry)
XX HIV polypeptide expression related polypeptide.
XX
XX Immunoassay; human immunodeficiency virus; HIV; antibody;
KW gag antigen; acquired immunodeficiency syndrome; AIDS; HIV infection;
KW vaccine; gene therapy; protein expression system.
XX
XX Synthetic.
XX
XX US6458527-B1.
XX
XX 01-OCT-2002.
XX
XX 28-JUN-1993; 93US-0083391.
XX
XX 24-DEC-1987; 87US-0138894.
XX 17-AUG-1992; 92US-0931191.
XX 31-OCT-1984; 84US-0667501.
XX 30-JAN-1985; 85US-0696534.
XX 06-SEP-1985; 85US-0773447.
XX
XX (CHIR) CHIRON CORP.
XX
XX Luciw PA, Dina D, Steimer K, Pescador RS, George-Nascimento C;
XX Parkes D, Hallelwell R, Barr PJ, Truett M;
XX
XX WPI; 2003-182063/18.
XX N-PSDB; ABX77347.
XX
XX Immunoassay for detecting the presence of antibodies to a human
PT immunodeficiency virus (HIV) for diagnosing, treating or preventing HIV
PT infection, comprises contacting the sample with an HIV gag antigen -
XX
XX Disclosure; Column 55; 101pp; English.

XX The invention describes an immunoassay for detecting the presence of
CC antibodies to a human immunodeficiency virus (HIV) in a sample by:
CC contacting the sample with an HIV gag antigen that binds anti-HIV
CC antibodies in an acquired immunodeficiency syndrome (AIDS) patient sera;
CC and determining binding, where the improvement comprises employing as
CC the gag antigen either a synthetic polypeptide or a recombinant
CC polypeptide. The method is used for detecting the presence of antibodies
CC to a human immunodeficiency virus (HIV) in a human sample. The
CC method is used in the preparation of a medicament for diagnosing,
CC treating or preventing HIV infection e.g. a vaccine or for gene
CC therapy. This is the amino acid sequence of a peptide associated with
CC the creation of systems to express proteins encoded by HIV.

XX
XX
XX Sequence 6 AA;

Query Match 60.0%; Score 3; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
|||
Db 1 MEV 3

RESULT 70
ABU57834
ID ABU57834 standard; Peptide; 6 AA.
XX
XX AC ABU57834;
XX
XX 10-APR-2003 (first entry)
XX Thrombospondin 1 cell binding domain peptide fragment.
XX
XX Thrombospondin-1; mouse; rat; human; chicken; tumour cell migration;
KW cell adhesion; platelet aggregation; wound healing; laminin; TS-1.
XX
XX Synthetic.
XX OS
XX US6469138-B1.
XX PN
XX 22-OCT-2002.
XX PD
XX 21-FEB-1995; 95US-0391820.
XX PF
XX 05-MAR-1993; 93US-0029333.
XX PR
XX (UNIW) UNIV WASHINGTON.
XX PA
XX Frazier WA, Kosfeld MD;
XX PI
XX WPI; 2003-196751/19.
XX DR
XX Novel peptide that binds to thrombospondin 1 receptor, useful as probe
PT sequence in computer search of all available databases -
XX
XX Disclosure; Column 2; 25pp; English.

XX This invention relates to a novel peptide that binds to the
CC thrombospondin 1 (TS-1) receptor. Thrombospondin 1 is a protein which
CC acts to promote cell adhesion and is involved in platelet aggregation,
CC wound healing and tumour cell migration. Also disclosed in the
CC invention is Laminin peptides which have been shown to be able to
CC substitute for TS-1 peptides. Preferably the peptides of
CC the invention share a tripeptide motif VVM and are useful as probe
CC sequences in a computer search of all available databases for
CC similar receptor binding motif peptides. The present sequence
CC represents a thrombospondin-1 (TS-1) or Laminin cell binding domain
CC peptide of the invention.

XX
XX
XX SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
|||
Db 4 VVM 6

RESULT 71
ABU14070
ID ABU14070 standard; Peptide; 6 AA.
XX
XX AC ABU14070;
XX
XX 27-FEB-2003 (first entry)
XX DT
XX

DE Transdominant effector peptide screening related peptide #15.
 XX Transdominant effector peptide; screening; cell phenotype;
 KW transdominant bioactive agent; disease pathogenesis; drug discovery;
 KW signal system regulation.
 XX Synthetic.
 OS US6455247-B1.
 XX PN
 XX PD 24-SEP-2002.
 XX PF 23-JAN-1997; 97US-0787738.
 XX PR 23-JAN-1996; 96US-0589109.
 XX PR 23-JAN-1996; 96US-0589311.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (RIGB-) RIGEL PHARM INC.
 XX Nolan GP, Rothenberg SM;
 XX WPI; 2003-110187/10.
 DR N-PSDB; ABX64339.
 XX Screening for a transdominant bioactive agent that alters the phenotype
 PT of a cell by introducing a molecular library of randomized candidate
 PT nucleic acids each operably linked to a nucleic acid encoding a
 PT secretion signal into first cells -
 XX Example 3; Column 50; 56pp; English.
 XX The invention describes a method of screening for a transdominant
 CC bioactive agent that alters the phenotype of a cell. The method is
 CC useful for screening for transdominant effector peptides and RNA
 CC molecules. These peptides and RNA molecules are useful in disease
 CC pathogenesis, and discovering chemical drugs that regulate signal
 CC systems. This sequence represents a peptide associated with the method
 CC of identifying transdominant effector peptides described in the
 CC invention.
 XX Sequence 6 AA;
 SQ Query Match 60.0%; Score 3; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 MEV 5
 DB |||
 1 MEV 3
 RESULT 72
 AAR35098
 ID AAR35098 standard; Protein; 7 AA.
 XX AAR35098;
 XX 25-MAR-2003 (updated)
 DT 05-AUG-1993 (first entry)
 XX B. thuringiensis lepidopteran toxin probe (i) design peptide.
 DE Probe; Bacillus thuringiensis; Bt; insecticidal; active; endotoxin;
 KW lepidoptera; diptera; coleoptera.
 XX Synthetic.
 OS US5204237-A.
 XX PN
 XX PD 20-APR-1993.
 XX PF 26-JUL-1991; 91US-0737569.

XX 25-OCT-1989; 89US-0427068.
 PR 26-JUL-1991; 91US-0737569.
 XX (MYCO) MYCOGEN CORP.
 XX Gaertner FH, Schwab GE, Sick AJ;
 PI WPI; 1993-143952/17.
 XX Gene probe for identifying endotoxin sequences in Bacillus
 PT thuringiensis - are universal, type specific or gene specific,
 PT for rapid detection and characterisation of insecticidal activity
 XX Disclosure; Column 2; 5pp; English.
 CC The sequences given in AAR35090-100 and AAR34628-32 are peptides which
 CC were used to design the probes given in AAQ0219-34. These probes can
 CC be used to identify Bacillus thuringiensis (Bt) DNA which encodes
 CC insecticidally active endotoxin. Probe (a) identifies genes encoding
 CC a toxin effective against any sort of insect. Sequences (b) and (e)-
 CC (1) are specific for toxins against lepidoptera; sequences (c), (m)
 CC and (n) for toxins active against diptera and sequence (d), (o) and
 CC (p) for toxins active against coleoptera.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 7 AA;
 SQ Query Match 60.0%; Score 3; DB 14; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.2e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VME 4
 DB |||
 2 VME 4
 RESULT 73
 AAR52638
 ID AAR52638 standard; peptide; 7 AA.
 XX AAR52638;
 XX 11-JUL-1994 (first entry)
 DT Myrotrophin tryptic peptide.
 DE Myrotrophin tryptic peptide.
 XX Myrotrophin; tryptic peptide; soluble protein factor;
 KW myocardial hypertrophy; hypertension.
 XX Rattus sp.
 OS US5284932-A.
 XX PN 08-FEB-1994.
 PD 07-SEP-1990; 90US-0578935.
 XX 07-SEP-1990; 90US-0578935.
 XX (CLEV-) CLEVELAND CLINIC FOUND.
 PA Sen S;
 XX WPI; 1994-056404/07.
 DR Myotrophin partially characterised soluble protein factor -
 PT purified from hypertrophied heart, regulates myocardial
 PT hypertrophy in hypertension
 XX Disclosure; Page 12; 21pp; English.
 XX Rat hypertrophied heart myrotrophin peptides (AAR52637-42) were

CC obtained by carboxymethylation of purified myrotrophin, followed by
CC trypsin digestion. Purification of myrotrophin peptides may lead to
CC the development of peptide analogs and/or antagonists for use in
CC the control of cardiac hypertrophy.

XX
XX
SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
|||
Db 5 MEV 7

RESULT 74
AAR82905
ID AAR82905 standard; Protein; 7 AA.
XX
AC AAR82905;
XX
DT 13-DEC-1995 (first entry)
XX
DE x.luminescens flavin reductase peptide for primer synthesis.
XX
KW Flavin reductase; Vibrio fischeri; primer; PCR; amplification; probe;
KW Xenorhabdus luminescens; expression plasmid; FMN reducing activity;
KW E.coli; ss.
XX
OS Synthetic.
XX
PN JP07079783-A.
XX
PD 28-MAR-1995.
XX
PF 28-JUN-1993; 93JP-0181850.
XX
PR 28-JUN-1993; 93JP-0181850.
XX
PA (CHCC) CHISSO CORP.
XX
DR WPI; 1995-157853/21.
DR N-PSDB; AAT01084.
XX
PT Flavin reductase gene from Vibrio fischeri - useful for production
PT of enzyme with FMN reducing activity
XX
PS Example 1; Fig 1; 10pp; Japanese.
XX
CC The sequence of a peptide from the Xenorhabdus luminescens flavin
CC reductase protein which was used to generate the primer AAT01084. The
CC primers AAT01084-5 were used to amplify the gene encoding flavin
CC reductase (fre) from Vibrio fischeri strain ATCC-7744 (see AAQ88282-4).
CC The resultant fragment was cloned into pUC8 and used as a probe to obtain
CC the full length gene sequence (AAQ88284) of the V.fischeri fire gene from
CC a lambda phage library. The gene was inserted into the expression plasmid
CC pUC13 and transformed into E.coli D1210. The resultant transformant
CC E.coli D1210/pfPR1 was used for the IPTG-inducible expression of the fre
CC gene. The gene encodes a protein with FMN reducing activity.

XX
SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
|||
Db 5 VVM 7

RESULT 75

AAR78214
ID AAR78214 standard; Peptide; 7 AA.
XX
AC AAR78214;
XX
DT 25-MAR-2003 (updated)
DT 22-FEB-1996 (first entry)
XX
DE B. thuringiensis endotoxin derived peptide.
XX
KW Endotoxin; probe; microbes; peptide; detection; lepidopteran.
XX
OS Bacillus thuringiensis.
XX
PN US5430137-A.
XX
PD 04-JUL-1995.
XX
PF 30-OCT-1992; 92US-0968781.
XX
PR 30-OCT-1992; 92US-0968781.
PR 25-OCT-1989; 89US-0427068.
PR 26-JUL-1991; 91US-0737569.
XX
PA (MYCO) MYCOGEN CORP.
XX
PI Gaertner FH, Narva KE, Schnepf HE, Schwab GE, Sick AJ;
PI Thompson M;
XX
DR WPI; 1995-245777/32.
XX
PT Nucleotide sequence used as probes to identify Bacillus
PT thuringiensis - are derived from the B.thuringiensis endotoxin
PT genes, for identifying microbes which encode toxins
XX
PS Example 2; Columns 43-44; 30pp; English.
XX
CC The nucleotide sequences which encode AAR78210-R78217, B.
CC thuringiensis (B.t.) endotoxin derived peptides, specify the probes
CC AAQ94859-Q94866 respectively. The probes can be used for the detection
CC of endotoxin producing B.t. microbes. The probes aid in the search
CC for useful microbes hosting toxin encoding genes, specifically from
CC lepidopteran species.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
|||
Db 2 VME 4

Search completed: November 25, 2003, 18:15:51
Job time : 18.1968 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 9.94681 Seconds
(without alignments)
92.715 Million cell updates/sec

Title: US-09-641-801-9

Perfect score: 5

Sequence: 1 VNEV 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA.*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5	100.0	5	15	US-10-281-652-9
2	5	100.0	12	11	US-09-994-595-121
3	4	80.0	8	12	US-10-137-867-350
4	3	60.0	3	12	US-10-137-867-540
5	3	60.0	4	11	US-09-813-775C-6
6	3	60.0	5	11	US-09-731-092-4
7	3	60.0	6	10	US-09-916-940-91
8	3	60.0	6	12	US-10-096-550-91
9	3	60.0	7	10	US-09-922-261-140
10	3	60.0	7	10	US-09-884-767A-134
11	3	60.0	8	9	US-09-110-716-4
12	3	60.0	8	12	US-10-022-066-238
13	3	60.0	8	14	US-10-042-991-5
14	3	60.0	8	15	US-10-046-801-18
15	3	60.0	9	12	US-10-022-066-190
16	3	60.0	9	12	US-10-239-313A-294
17	3	60.0	9	12	US-10-119-536A-76
18	3	60.0	9	12	US-10-136-145-24
19	3	60.0	9	14	US-10-026-001-5
20	3	60.0	9	14	US-10-114-091-5
21	3	60.0	9	15	US-10-195-117-26
22	3	60.0	10	7	US-08-344-824-54
23	3	60.0	10	7	US-08-344-824-55
24	3	60.0	10	7	US-08-344-824-56
25	3	60.0	10	7	US-08-344-824-58
26	3	60.0	10	7	US-08-344-824-59
27	3	60.0	10	7	US-08-344-824-60
28	3	60.0	10	9	US-09-012-135A-13
29	3	60.0	10	10	US-09-923-831-8
30	3	60.0	10	10	US-09-071-838-269
31	3	60.0	10	10	US-09-766-889A-20
32	3	60.0	10	10	US-09-766-889A-59
33	3	60.0	10	11	US-09-983-802-315
34	3	60.0	10	12	US-10-022-066-607
35	3	60.0	10	12	US-10-170-832-49
36	3	60.0	10	12	US-10-233-580-42
37	3	60.0	10	12	US-10-332-282-2
38	3	60.0	10	12	US-10-239-313A-295
39	3	60.0	10	15	US-10-192-869-7
40	3	60.0	10	15	US-10-201-386-14
41	3	60.0	10	15	US-10-161-097-5
42	3	60.0	10	15	US-10-128-711-83
43	3	60.0	10	15	US-10-213-512-269
44	3	60.0	10	15	US-10-060-019-1
45	3	60.0	11	15	US-09-954-385-400
46	3	60.0	12	12	US-10-119-528-104
47	3	60.0	13	9	US-09-012-135A-25
48	3	60.0	13	10	US-09-813-333-30
49	3	60.0	13	12	US-10-137-867-268
50	3	60.0	13	14	US-10-044-703-30
51	3	60.0	14	11	US-03-229-173-35
52	3	60.0	14	12	US-10-176-416-19
53	3	60.0	14	15	US-10-192-806-19
54	3	60.0	14	15	US-10-120-604-124
55	3	60.0	14	15	US-10-207-655-300
56	3	60.0	14	15	US-10-286-134-12
57	3	60.0	14	15	US-09-759-143-808
58	3	60.0	15	9	US-09-780-683-808
59	3	60.0	15	9	US-09-822-827-808
60	3	60.0	15	9	US-09-791-171-84
61	3	60.0	15	10	US-09-945-249-88
62	3	60.0	15	10	US-09-895-793-808
63	3	60.0	15	10	US-09-895-814-808
64	3	60.0	15	11	US-09-918-873-20
65	3	60.0	15	12	US-09-804-960-84
66	3	60.0	15	12	US-10-144-678A-808
67	3	60.0	15	12	US-10-199-820-273
68	3	60.0	15	12	US-10-294-025-808
69	3	60.0	15	14	US-10-012-896-808
70	3	60.0	15	15	US-10-060-019-2
71	3	60.0	15	15	US-10-233-822-13
72	3	60.0	16	8	US-08-424-550B-181
73	3	60.0	16	10	US-09-813-333-20
74	3	60.0	16	10	US-09-766-889A-57
75	3	60.0	16	11	US-09-918-873-18
76	3	60.0	16	12	US-10-170-832-6
77	3	60.0	16	12	US-10-026-066-12
78	3	60.0	16	12	US-10-026-066-26
79	3	60.0	16	14	US-10-044-703-20
80	3	60.0	16	15	US-10-293-822-23
81	3	60.0	16	15	US-10-225-567A-2230
82	3	60.0	17	9	US-09-759-143-809
83	3	60.0	17	9	US-09-110-716-1
84	3	60.0	17	9	US-09-780-669-809
85	3	60.0	17	9	US-09-822-827-809
86	3	60.0	17	9	US-09-969-384-24
87	3	60.0	17	10	US-09-895-793-809
88	3	60.0	17	10	US-09-895-793-809
89	3	60.0	17	10	US-09-895-793-809
90	3	60.0	17	10	US-09-895-793-809
91	3	60.0	17	10	US-09-895-793-809
92	3	60.0	17	10	US-09-895-793-809
93	3	60.0	17	10	US-09-895-793-809
94	3	60.0	17	10	US-09-895-793-809
95	3	60.0	17	10	US-09-895-793-809
96	3	60.0	17	10	US-09-895-793-809
97	3	60.0	17	10	US-09-895-793-809
98	3	60.0	17	10	US-09-895-793-809
99	3	60.0	17	10	US-09-895-793-809
100	3	60.0	17	10	US-09-895-793-809

Sequence 294, Appl
Sequence 76, Appl
Sequence 24, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 26, Appl
Sequence 54, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 58, Appl
Sequence 59, Appl
Sequence 60, Appl
Sequence 13, Appl
Sequence 8, Appl
Sequence 269, Appl
Sequence 20, Appl
Sequence 59, Appl
Sequence 315, Appl
Sequence 607, Appl
Sequence 49, Appl
Sequence 42, Appl
Sequence 2, Appl
Sequence 295, Appl
Sequence 7, Appl
Sequence 14, Appl
Sequence 5, Appl
Sequence 83, Appl
Sequence 142, Appl
Sequence 269, Appl
Sequence 1, Appl
Sequence 35, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 300, Appl
Sequence 12, Appl
Sequence 808, Appl
Sequence 808, Appl
Sequence 84, Appl
Sequence 808, Appl
Sequence 20, Appl
Sequence 84, Appl
Sequence 808, Appl
Sequence 273, Appl
Sequence 808, Appl
Sequence 808, Appl
Sequence 2, Appl
Sequence 13, Appl
Sequence 181, Appl
Sequence 20, Appl
Sequence 57, Appl
Sequence 18, Appl
Sequence 6, Appl
Sequence 12, Appl
Sequence 26, Appl
Sequence 20, Appl
Sequence 23, Appl
Sequence 230, Appl
Sequence 809, Appl
Sequence 1, Appl
Sequence 809, Appl
Sequence 809, Appl
Sequence 24, Appl
Sequence 809, Appl

89 3 60.0 17 10 US-09-895-814-809 Sequence 809, App
90 3 60.0 17 12 US-10-158-825-139 Sequence 139, App
91 3 60.0 17 12 US-10-144-678A-809 Sequence 809, App
92 3 60.0 17 12 US-10-294-025-809 Sequence 809, App
93 3 60.0 17 12 US-10-239-956-16 Sequence 16, Appl
94 3 60.0 17 14 US-10-012-896-809 Sequence 809, App
95 3 60.0 17 15 US-10-158-847-139 Sequence 139, App
96 3 60.0 18 10 US-09-845-899A-8 Sequence 8, Appl
97 3 60.0 18 10 US-09-845-899A-11 Sequence 11, Appl
98 3 60.0 18 11 US-09-858-935B-117 Sequence 117, Appl
99 3 60.0 18 11 US-09-563-222-62 Sequence 62, Appl
100 3 60.0 18 12 US-10-194-801C-8 Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-9
; Sequence 9, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-9

Query Match 100.0%; Score 5; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VMEV 5
Db 1 VMEV 5
|||||

RESULT 2
US-09-994-595-121
; Sequence 121, Application US/09994595
; Publication No. US20030039981A1
; GENERAL INFORMATION:
; APPLICANT: Bhattacharjee, J.
; APPLICANT: Suvarna, Kalavati
; APPLICANT: Bhattacharjee, Vasker
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
; TITLE OF INVENTION: A BIOLOGICAL SAMPLE
; FILE REFERENCE: 96,247-A
; CURRENT APPLICATION NUMBER: US/09/994,595
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 08/650,809
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 121
; LENGTH: 12

; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide segment of GR5B_1BACB shown in Figure 4.
US-09-994-595-121
Query Match 100.0%; Score 5; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VMEV 5
Db 8 VMEV 12
|||||

RESULT 3
US-10-137-867-330
; Sequence 330, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 330
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-330

Query Match 80.0%; Score 4; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VMEV 5
Db 1 VMEV 4
|||||

RESULT 4
US-10-137-867-540
; Sequence 540, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 540
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-540

Query Match          60.0%; Score 3; DB 12; Length 3;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      1 MEV 3
|||||

RESULT 5
US-09-813-775C-6
; Sequence 6, Application US/09813775C
; Publication No. US20030054494A1
; GENERAL INFORMATION:
; APPLICANT: DeSavage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. US20030054494A1 chimpanzee erythropoietin
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT.057C52
; CURRENT APPLICATION NUMBER: US/09/813,775C
; CURRENT FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/552265
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-813-775C-6

Query Match          60.0%; Score 3; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      1 MEV 3
|||||

RESULT 6
US-09-731-092-4
; Sequence 4, Application US/09731092
; Publication No. US20030082621A1
; GENERAL INFORMATION:
; APPLICANT: MISEVIC, GRADIMIR
; TITLE OF INVENTION: FUCOSE CONTAINING PROTEOGLYCAN OR ACIDIC GLYCAN AND
; TITLE OF INVENTION: THEIR PHARMACEUTICAL USE
; FILE REFERENCE: MISE-001
; CURRENT APPLICATION NUMBER: US/09/731,092

```

```

; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 08/704,777
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: PCT/IB95/00208
; PRIOR FILING DATE: 1995-03-24
; PRIOR APPLICATION NUMBER: GB94-05 846.8
; PRIOR FILING DATE: 1994-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-731-092-4

Query Match          60.0%; Score 3; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
Db      2 VVM 4
|||||

RESULT 7
US-09-916-940-91
; Sequence 91, Application US/09916940
; Patent No. US20020127564A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020127564Alan, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A-64260-6/RMS/AMS
; CURRENT APPLICATION NUMBER: US/09/916,940
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/727,715
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/963,368
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 08/589,109
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/589,911
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/789,333
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 08/787,738
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-916-940-91

Query Match          60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      1 MEV 3
|||||

RESULT 8
US-10-096-550-91
; Sequence 91, Application US/10096550
; Publication No. US20030170641A1

```

```
; GENERAL INFORMATION:
; APPLICANT: No. US20030170641A1an, Garry P
; APPLICANT: Rothenburg, Michael S.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
; TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A-64259-1 correction
; CURRENT APPLICATION NUMBER: US/10/096,550
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 08/787,738
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-096-550-91

Query Match 60.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

RESULT 9
US-09-922-261-140
; Sequence 140, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Purnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-261-140

Query Match 60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

RESULT 10
US-09-884-767A-134
; Sequence 134, Application US/09884767A
```

```
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-134

Query Match 60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 1 VME 3

RESULT 11
US-09-110-716-4
; Sequence 4, Application US/09110716A
; Patent No. US20020034739A1
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Glasgow, Benjamin J.
; TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
; FILE REFERENCE: 22000-20596.00
; CURRENT APPLICATION NUMBER: US/09/110,716A
; CURRENT FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: unidentified
US-09-110-716-4

Query Match 60.0%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 2 MEV 4

RESULT 12
US-10-022-066-238
; Sequence 238, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
```

; CURRENT APPLICATION NUMBER: US/10/022,066
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/256,410
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 60/256,409
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 09/465,321
 ; PRIOR FILING DATE: 1999-12-17
 ; PRIOR APPLICATION NUMBER: 09/974,366
 ; PRIOR FILING DATE: 2001-10-10
 ; NUMBER OF SEQ ID NOS: 638
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 238
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-10-022-066-238

Query Match 60.0%; Score 3; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
 Db 1 VME 3

RESULT 13
 US-10-042-991-5
 ; Sequence 5, Application US/10042991
 ; Publication No. US20020142407A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ian M. Whitehead
 ; APPLICANT: Alan Slusarenko
 ; APPLICANT: Duncan Gaskin
 ; APPLICANT: Alan Brash
 ; APPLICANT: Nathalie Tijet
 ; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
 ; TITLE OF INVENTION: LYSASE AND USES THEREOF
 ; FILE REFERENCE: 06027.0001U3
 ; CURRENT APPLICATION NUMBER: US/10/042,991
 ; CURRENT FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Psidium Guajava (guava)
 US-10-042-991-5

Query Match 60.0%; Score 3; DB 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
 Db 4 VVM 6

RESULT 14
 US-10-046-801-18
 ; Sequence 18, Application US/10046801
 ; Publication No. US20030054027A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Unger, Evan C.
 ; TITLE OF INVENTION: Charged Lipids and Uses For The Same
 ; FILE REFERENCE: UNGR1592
 ; CURRENT APPLICATION NUMBER: US/10/046,801
 ; CURRENT FILING DATE: 2002-05-13
 ; PRIOR APPLICATION NUMBER: US/09/540,448

; PRIOR FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: 08/925,353
 ; PRIOR FILING DATE: 1997-09-08
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence
 US-10-046-801-18

Query Match 60.0%; Score 3; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
 Db 4 VVM 6

RESULT 15
 US-10-022-066-190
 ; Sequence 190, Application US/10022066
 ; Publication No. US2003016057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HILDEBRAND, WILLIAM H.
 ; APPLICANT: PRILLIMAN, KILEY RAE
 ; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: 6680.034
 ; CURRENT APPLICATION NUMBER: US/10/022,066
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/256,410
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 60/256,409
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 09/465,321
 ; PRIOR FILING DATE: 1999-12-17
 ; PRIOR APPLICATION NUMBER: 09/974,366
 ; PRIOR FILING DATE: 2001-10-10
 ; NUMBER OF SEQ ID NOS: 638
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 190
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 US-10-022-066-190

Query Match 60.0%; Score 3; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
 Db 2 VME 4

RESULT 16
 US-10-239-313A-294
 ; Sequence 294, Application US/10239313A
 ; Publication No. US20030175285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KLINGUER - HAMOUR, Christine
 ; APPLICANT: CORVAIA, Nathalie
 ; APPLICANT: BECK, Alain
 ; APPLICANT: GOETSCH, Liliane
 ; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
 ; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM

; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 294
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-294

Query Match 60.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
|||
Db 7 VME 9

RESULT 17

US-10-119-536A-76
; Sequence 76, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteria
; FILE REFERENCE: 4305/1J091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CPN0796 immunogenic peptide
US-10-119-536A-76

Query Match 60.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
|||
Db 2 VVM 4

RESULT 18

US-10-136-145-24
; Sequence 24, Application US/10136145
; Publication No. US20030216559A1
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.
; TITLE OF INVENTION: Melanoma associated antigenic polypeptide,
; epitopes thereof and vaccine against melanoma.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav
; STREET: Philips van Leydenlaan 25
; CITY: Nijmegen
; STATE: Brabant

; COUNTRY: the Netherlands
; ZIP: 6525 EX
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/136,145
; FILING DATE: 01-May-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,852B
; FILING DATE: February 15, 1995
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-136-145-24

Query Match 60.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
|||
Db 7 MEV 9

RESULT 19

US-10-026-001-5
; Sequence 5, Application US/10026001
; Publication No. US20020122791A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: ANTIGENIC CK-18 COMPOUNDS FOR THERAPY
; AND DIAGNOSIS AND METHODS FOR USING SAME
; FILE REFERENCE: GZ 210800
; CURRENT APPLICATION NUMBER: US/10/026,001
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,820
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-001-5

Query Match 60.0%; Score 3; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
|||
Db 7 MEV 9

RESULT 20

US-10-114-091-5
; Sequence 5, Application US/10114091
; Publication No. US20020197243A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: NOVEL p53BP2 COMPOUNDS FOR THERAPY AND DIAGNOSIS AND METHODS F
; TITLE OF INVENTION: SAME
; FILE REFERENCE: GZ 2106.00

; CURRENT APPLICATION NUMBER: US/10/114,091
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 60/280,794
 ; PRIOR FILING DATE: 2001-03-30
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: P53 BP2
 US-10-114-091-5

Query Match 60.0%; Score 3; DB 14; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
 ||||
 Db 5 MEV 7

RESULT 21
 US-10-195-117-26
 ; Sequence 26, Application US/10195117
 ; Publication No. US20030092083A1
 ; GENERAL INFORMATION:
 ; APPLICANT: In2Gen Co., Ltd.
 ; APPLICANT: Jeoung, Doo-il
 ; APPLICANT: Cho, Bomsou
 ; APPLICANT: Lim, Yoon
 ; APPLICANT: Park, Saeyoung
 ; APPLICANT: Lee, Daeyeon
 ; APPLICANT: Bang, Yung-Jue
 ; APPLICANT: Yang, Hankwang
 ; APPLICANT: Kim, Dae-Ke
 ; TITLE OF INVENTION: CAGE Antigen
 ; FILE REFERENCE: S9258-00002
 ; CURRENT APPLICATION NUMBER: US/10/195,117
 ; CURRENT FILING DATE: 2002-07-11
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 26
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(9)
 ; OTHER INFORMATION:
 US-10-195-117-26

Query Match 60.0%; Score 3; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
 ||||
 Db 1 VVM 3

RESULT 22
 US-08-344-824-54
 ; Sequence 54, Application US/08344824
 ; Publication No. US20030152580A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SETTE, Alessandro
 ; APPLICANT: SIDNEY, John
 ; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
 ; NUMBER OF SEQUENCES: 399
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: One Market Plaza, Steuart Street Tower, 20th
 ; STREET: Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/08/344,824
 ; APPLICATION NUMBER: US/08/344,824
 ; FILING DATE: 23-NOV-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/278,634
 ; FILING DATE: 21-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bastian, Kevin L.
 ; REGISTRATION NUMBER: 34,774
 ; REFERENCE/DOCKET NUMBER: 14137-80-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-3600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 US-08-344-824-54

Query Match 60.0%; Score 3; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
 ||||
 Db 4 VME 6

RESULT 23
 US-08-344-824-55
 ; Sequence 55, Application US/08344824
 ; Publication No. US20030152580A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SETTE, Alessandro
 ; APPLICANT: SIDNEY, John
 ; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
 ; NUMBER OF SEQUENCES: 399
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Steuart Street Tower, 20th
 ; STREET: Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/344,824
 ; FILING DATE: 23-NOV-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/278,634
 ; FILING DATE: 21-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-344-824-55

Query Match 60.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 VME 4
Db |||
4 VME 6

RESULT 24
US-08-344-824-56
Sequence 56, Application US/08344824
Publication No. US20030152580A1
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
FLOOR
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-344-824-56

Query Match 60.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 VME 4
Db |||
4 VME 6

RESULT 25
US-08-344-824-58
Sequence 58, Application US/08344824
Publication No. US20030152580A1
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
FLOOR
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-344-824-58

Query Match 60.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db |||
4 VME 6

RESULT 26
US-08-344-824-59
Sequence 59, Application US/08344824
Publication No. US20030152580A1
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
FLOOR
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-344-824-59

Query Match 60.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 2 VME 4
Db 4 VME 6

RESULT 27
US-08-344-824-60
Sequence 60, Application US/08344824
Publication No. US20030152580A1
GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-344-824-60

Query Match 60.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 2 VME 4
Db 4 VME 6

RESULT 28
US-09-012-135A-13
Sequence 13, Application US/09012135A
Patent No. US20020081578A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,135A
FILING DATE: January 22, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,268
FILING DATE: January 9, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. US20020081578A1ember 25, 1996
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide

US-09-012-135A-13

Query Match 60.0%; Score 3; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 1 VME 3

RESULT 29

US-09-923-831-8
; Sequence 8, Application US/09923831
; Patent No. US20020115142A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Val,rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/923.831
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-8

Query Match 60.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

RESULT 30

US-09-071-838-269
; Sequence 269, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yabegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071.838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:

; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 269:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-269

Query Match 60.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VME 3
Db 6 VME 8

RESULT 31

US-09-766-889A-20
; Sequence 20, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766.889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-20

Query Match 60.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

RESULT 32

US-09-766-889A-59
; Sequence 59, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766.889A

```

; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-59

Query Match      60.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      1 MEV 3

RESULT 33
US-09-983-802-315
; Sequence 315, Application US/09983802
; Publication No. US2003002185A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/983,802
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCY/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948

```

```

; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 315
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-315

Query Match      60.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      6 MEV 8

RESULT 34
US-10-022-066-607
; Sequence 607, Application US/10022066
; Publication No. US20030186057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE REFERENCE: 6680,034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 607
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

```

```

; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Unknown amino acid
US-10-022-066-607

Query Match      60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db 7 VME 9

RESULT 35
US-10-170-832-49
; Sequence 49, Application US/10170832
; Publication No. US20030170792A1
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgan
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-49

Query Match      60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 36
US-10-293-580-42
; Sequence 42, Application US/10293580
; Publication No. US20030170767A1
; GENERAL INFORMATION:
; APPLICANT: Aurora Biosciences Corporation
; APPLICANT: Cubitt, Andrew B.
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
; FILE REFERENCE: AURO1270 (08366/031001)
; CURRENT APPLICATION NUMBER: US/10/293,580
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/129,192
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: cytomegalovirus assemblin
US-10-293-580-42
```

```

Query Match      60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 2 VVM 4

RESULT 37
US-10-332-282-2
; Sequence 2, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Ethel D
; APPLICANT: Miller, Julie
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Titball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-332-282-2

Query Match      60.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 38
US-10-239-313A-295
; Sequence 295, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 295
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-295
```

Query Match 60.0%; Score 3; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
 |||
 Db 7 VME 9

RESULT 39

US-10-192-869-7
 ; Sequence 7, Application US/10192869
 ; Publication No. US20030022265A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Park, Woo-Jim
 ; APPLICANT: Kim, Sung-Yun
 ; TITLE OF INVENTION: Method for Determining Substrate Specificity of Protease
 ; FILE REFERENCE: HYLEE68.001AUS
 ; CURRENT APPLICATION NUMBER: US/10/192,869
 ; CURRENT FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: KR 10-2001-0041011
 ; PRIOR FILING DATE: 2001-07-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Fast-SEQ 4.0
 ; SEQ ID NO 7
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide substrate for kex2
 US-10-192-869-7

Query Match 60.0%; Score 3; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
 |||
 Db 1 VVM 3

RESULT 40

US-10-201-386-14
 ; Sequence 14, Application US/10201386
 ; Publication No. US20030091567A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alitalo, Kari
 ; APPLICANT: Joukov, Vladimir
 ; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR C (VEGF-C) PROTEIN
 ; FILE REFERENCE: 28967/34140A
 ; CURRENT APPLICATION NUMBER: US/10/201,386
 ; CURRENT FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: US/09/534,376
 ; PRIOR FILING DATE: 2000-03-24
 ; PRIOR APPLICATION NUMBER: 09/355,700
 ; PRIOR FILING DATE: 1999-11-05
 ; PRIOR APPLICATION NUMBER: PCT/US98/01973
 ; PRIOR FILING DATE: 1998-02-02
 ; PRIOR APPLICATION NUMBER: 08/795,430
 ; PRIOR FILING DATE: 1997-02-05
 ; PRIOR APPLICATION NUMBER: PCT/FR96/00427
 ; PRIOR FILING DATE: 1996-08-01
 ; PRIOR APPLICATION NUMBER: 08/671,573
 ; PRIOR FILING DATE: 1996-06-28
 ; PRIOR APPLICATION NUMBER: 08/601,132
 ; PRIOR FILING DATE: 1996-02-14
 ; PRIOR APPLICATION NUMBER: 08/585,895
 ; PRIOR FILING DATE: 1996-01-12
 ; PRIOR APPLICATION NUMBER: 08/510,133
 ; PRIOR FILING DATE: 1995-08-01
 ; PRIOR APPLICATION NUMBER: 08/340,011

; PRIOR FILING DATE: 1994-11-14
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: peptide
 ; OTHER INFORMATION: Igg-Kappa sequence
 US-10-201-386-14

Query Match 60.0%; Score 3; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
 |||
 Db 2 VVM 4

RESULT 41

US-10-161-097-5
 ; Sequence 5, Application US/10161097
 ; Publication No. US20030096404A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSENZWEIG, Michael
 ; APPLICANT: PYKEIT, Mark J.
 ; APPLICANT: SCADDEN, David T.
 ; APPLICANT: POZNANSKY, Mark C.
 ; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
 ; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
 ; TITLE OF INVENTION: DEVICES
 ; FILE REFERENCE: C1005/7012/KA/ERG
 ; CURRENT APPLICATION NUMBER: US/10/161,097
 ; CURRENT FILING DATE: 2002-05-31
 ; PRIOR APPLICATION NUMBER: US/09/574,749
 ; PRIOR FILING DATE: 2002-05-31
 ; PRIOR APPLICATION NUMBER: US 60/107,972
 ; PRIOR FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: PCT/US99/26795
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: US 09/524,749
 ; PRIOR FILING DATE: 2000-05-18
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Homo Sapiens source
 US-10-161-097-5

Query Match 60.0%; Score 3; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
 |||
 Db 1 MEV 3

RESULT 42

US-10-128-711-83
 ; Sequence 83, Application US/10128711
 ; Publication No. US20030099634A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VITTELLO, Maria A.
 ; APPLICANT: CHESTNUT, Robert W.
 ; APPLICANT: SETTE, Alessandro D.
 ; APPLICANT: CELIS, Esreban
 ; APPLICANT: GRAY, Howard

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
;
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
;
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 83:
US-10-128-711-83
;
;
; Query Match 60.0%; Score 3; DB 15; Length 10;
; Best Local Similarity 100.0%; Pred. No. 9.8e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 3 MEV 5
; Db |||
; 8 MEV 10
;
; RESULT 43
; US-10-128-711-142
; Sequence 142, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
;
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
;
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco

```

```

; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
;
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-128-711-142
;
;
; Query Match 60.0%; Score 3; DB 15; Length 10;
; Best Local Similarity 100.0%; Pred. No. 9.8e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 3 MEV 5
; Db |||
; 8 MEV 10
;
; RESULT 44
; US-10-213-512-269
; Sequence 269, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
;
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; FILE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0

```

```
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-269

Query Match      60.0%; Score 3; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 6 VVM 8

RESULT 45
US-10-060-019-1
; Sequence 1, Application US/10060019
; Publication No. US20030003564A1
; GENERAL INFORMATION:
; APPLICANT: Willems, Andrew
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; FILE REFERENCE: 11757.10USU1
; CURRENT APPLICATION NUMBER: US/10/060,019
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/177,165
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-060-019-1

Query Match      60.0%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 46
US-09-954-385-400
; Sequence 400, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gestel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 400
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-400

Query Match      60.0%; Score 3; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 6 MEV 8

RESULT 47
US-10-119-528-104
; Sequence 104, Application US/10119528
; Publication No. US20030175722A1
; GENERAL INFORMATION:
; APPLICANT: Mann, M.
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABASES
; FILE REFERENCE: MDSP-P01-004
; CURRENT APPLICATION NUMBER: US/10/119,528
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,551
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/285,362
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-119-528-104

Query Match      60.0%; Score 3; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 3 VVM 5

RESULT 48
US-09-012-135A-25
; Sequence 25, Application US/09012135A
; Patent No. US20020081578A1
; GENERAL INFORMATION:
; APPLICANT: Flowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,135A
; FILING DATE: January 22, 1998
; CLASSIFICATION: 435
```



```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/005,268
; FILING DATE: January 9, 1998
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. US20020081578A1ember 25, 1996
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 231/282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-9440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-012-135A-25

```

```

Query Match          60.0%; Score 3; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 VME 4
        |||
Db       5 VME 7

```

RESULT 49

```

US-09-813-333-30
; Sequence 30, Application US/0981333
; Patent No. US20020119160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-30

```

```

Query Match          60.0%; Score 3; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VVM 3
        |||
Db       5 VVM 7

```

RESULT 50

```

US-10-137-867-268
; Sequence 268, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc

```

```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-268

```

```

Query Match          60.0%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VVM 3
        |||
Db       1 VVM 3

```

RESULT 51

```

US-10-044-703-30
; Sequence 30, Application US/10044703
; Publication No. US20020192233A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/10/044,703
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-044-703-30

```

```

Query Match          60.0%; Score 3; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 VVM 3
        |||
Db       5 VVM 7

```

RESULT 52

```

US-09-229-173-35
; Sequence 35, Application US/09229173
; Publication No. US20030027296A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Deb K.
; TITLE OF INVENTION: Cloned DNA Polymerases from Thermotoga
; maritima and Mutants Thereof
; NUMBER OF SEQUENCES: 47

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/229,173
; FILING DATE: 13-JAN-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/706,702
; FILING DATE: 06-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/689,807
; FILING DATE: 14-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,400
; FILING DATE: 02-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/576,759
; FILING DATE: 21-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/537,397
; FILING DATE: 02-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/525,057
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Millonig, Robert C.
; REGISTRATION NUMBER: 34,395
; REFERENCE/DOCKET NUMBER: 0942.2800008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-09-229-173-35

Query Match 60.0%; Score 3; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 9 VVM 11

RESULT 53
US-10-176-416-19
; Sequence 19, Application US/10176416
; Publication No. US20030186864A1
; GENERAL INFORMATION:
; APPLICANT: Thorn, R.
; APPLICANT: Lanzer, M.
; APPLICANT: Moses, M.
; APPLICANT: Wiederschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING TROPONIN SUBUNITS,
; TITLE OF INVENTION: FRAGMENTS AND HOMOLOGS THEREOF AND METHODS OF THEIR USE TO
; TITLE OF INVENTION: INHIBIT ANGIOGENESIS
; FILE REFERENCE: 8657-043
; CURRENT APPLICATION NUMBER: US/10/176,416

; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 09/442,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tryptic peptide
US-10-176-416-19

Query Match 60.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 11 MEV 13

RESULT 54
US-10-192-806-19
; Sequence 19, Application US/10192806
; Publication No. US20030083255A1
; GENERAL INFORMATION:
; APPLICANT: Thorn, R.
; APPLICANT: Lanzer, M.
; APPLICANT: Moses, M.
; APPLICANT: Wiederschain, D.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: TROPONIN SUBUNITS, FRAGMENTS AND HOMOLOGS THEREOF AND
; TITLE OF INVENTION: METHODS OF THEIR USE TO INHIBIT ANGIOGENESIS
; FILE REFERENCE: 8657-042-999
; CURRENT APPLICATION NUMBER: US/10/192,806
; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: 09/612,421
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/268,274
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 08/961,264
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: 08/602,941
; PRIOR FILING DATE: 1996-02-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tryptic peptide
US-10-192-806-19

Query Match 60.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 11 MEV 13

RESULT 55
US-10-120-604-124
; Sequence 124, Application US/10120604

```
; Publication No. US20030096347A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: D0143NP
; CURRENT APPLICATION NUMBER: US/10/120,604
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/283,145
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/283,161
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/288,468
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/300,619
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-120-604-124

Query Match      60.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
Db      10 VVM 12

RESULT 56
US-10-207-655-300
; Sequence 300, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069,401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 300
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 14 amino acids deleted from IGAH-T4 (so that total
; OTHER INFORMATION: of 18 amino acids deleted from wild type IGA CH3
US-10-207-655-300

Query Match      60.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
Db      8 VVM 10

RESULT 57
US-10-286-134-12
; Sequence 12, Application US/10286134
; Publication No. US20030119747A1
; GENERAL INFORMATION:
; APPLICANT: THORN, RICHARD M.
; APPLICANT: LANSER, MARC E.
; APPLICANT: MOSES, MARSHA A.
; APPLICANT: WIEDERSCHAIN, DMITRI G.
```

```
; TITLE OF INVENTION: METHODS OF USING PHARMACEUTICAL COMPOSITIONS COMPRISING
; TITLE OF INVENTION: TROPONIN SUBUNITS AND HOMOLOGS THEREOF BEFORE, DURING, OR
; TITLE OF INVENTION: AFTER SURGICAL RESECTION OR RADIOLOGIC ABLATION OF A SOLID
; FILE REFERENCE: 057932-053421
; CURRENT APPLICATION NUMBER: US/10/286,134
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/335,133
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: tryptic peptide
US-10-286-134-12
```

```
Query Match      60.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 MEV 5
Db      11 MEV 13
```

```
RESULT 58
US-09-759-143-808
; Sequence 808, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121,427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-808
```

```
Query Match      60.0%; Score 3; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 VME 4
Db      3 VME 5
```

RESULT 59

US-09-780-669-808
; Sequence 808, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-669-808

Query Match 60.0%; Score 3; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 3 VME 5

RESULT 60

US-09-822-827-808
; Sequence 808, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-808

Query Match 60.0%; Score 3; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 3 VME 5

RESULT 61

US-09-791-171-84
; Sequence 84, Application US/09791171
; Patent No. US20020094336A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/791,171
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/050,739
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 0376/97
; PRIOR FILING DATE: 1997-04-02
; PRIOR APPLICATION NUMBER: 1277/97
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/044,624
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: 60/070,488
; PRIOR FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-84

Query Match 60.0%; Score 3; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 12 VVM 14

RESULT 62

US-09-945-249-88
; Sequence 88, Application US/09945249
; Patent No. US20020168748A1
; GENERAL INFORMATION:
; APPLICANT: BERLIN, VIVIAN
; APPLICANT: DAMAGNEZ, VERONIQUE
; APPLICANT: SMITH, SUSAN E.
; TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
; FILE REFERENCE: MIV-074.06
; CURRENT APPLICATION NUMBER: US/09/945,249
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/041,990
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: 08/771,212
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: 08/631,319
; PRIOR FILING DATE: 1996-04-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide that

; OTHER INFORMATION: corresponds to the C-termini of FTase or GGTase
; OTHER INFORMATION: substrates
US-09-945-249-88

Query Match 60.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
|||
Db 13 VWM 15

RESULT 63

US-09-895-793-808
; Sequence 808, Application US/09895793
; Publication No. US20020192763A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.534C2

; CURRENT APPLICATION NUMBER: US/09/895,793

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 982

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 808

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-895-793-808

Query Match 60.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
|||
Db 3 VME 5

RESULT 64

US-09-895-814-808

; Sequence 808, Application US/09895814

; Publication No. US20020193296A1

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.

; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C26

; CURRENT APPLICATION NUMBER: US/09/895,814

; CURRENT FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 990

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 808

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-895-814-808

Query Match 60.0%; Score 3; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
|||
Db 3 VME 5

RESULT 65

US-09-918-873-20

; Sequence 20, Application US/09918873

; Publication No. US20030032649A1

GENERAL INFORMATION:

; APPLICANT: Goldsmith, Elizabeth J.
; APPLICANT: Radha, Akella
; APPLICANT: Gaynor, Richard B.
; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
; TITLE OF INVENTION: DISCOVERY
; FILE REFERENCE: A33864 090495.0232
; CURRENT APPLICATION NUMBER: US/09/918,873
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; DATABASE ACCESSION NUMBER: P47197
; DATABASE ENTRY DATE: 1996-06-01
US-09-918-873-20

Query Match 60.0%; Score 3; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
|||
Db 3 VME 5

RESULT 66

US-09-804-980-84

; Sequence 84, Application US/09804980

```

; Publication No. US20030147897A1
; GENERAL INFORMATION:
; APPLICANT: Statens Serum Institut
; APPLICANT: Anderson, Peter
; TITLE OF INVENTION: M. Tuberculosis Antigens
; FILE REFERENCE: 67001-2002.4
; CURRENT APPLICATION NUMBER: US/09/804,980
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-804-980-84

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 12 VVM 14

RESULT 67
US-10-144-678A-808
; Sequence 808, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriack
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Hepler, William T.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals y de Bassols, Carlota
; APPLICANT: Foy, Teresa M.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-678A-808

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 12 VVM 14

RESULT 68
US-10-199-820-273
; Sequence 273, Application US/10199820
; Publication No. US20030180739A1
; GENERAL INFORMATION:
; APPLICANT: Board of Trustees of the University of Illinois
; APPLICANT: Primiano, Thomas
; APPLICANT: Chang, Bey-dih
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: Methods and Reagents for Identifying Gene Targets for Treating
; FILE REFERENCE: 99,216-U
; CURRENT APPLICATION NUMBER: US/10/199,820
; CURRENT FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-820-273

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 7 VME 9

RESULT 69
US-10-294-025-808
; Sequence 808, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-808

Query Match      60.0%; Score 3; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
Db 3 VME 5

RESULT 70
US-10-012-896-808
; Sequence 808, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu

```

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 808
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-896-808

Query Match      60.0%; Score 3; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VME 4
Db      3 VME 5

RESULT 71
US-10-060-019-2
; Sequence 2, Application US/10060019
; Publication No. US20030003564A1
; GENERAL INFORMATION:
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING UBIQUITIN
; FILE REFERENCE: 11757.10USU1
; CURRENT APPLICATION NUMBER: US/10/060,019
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/177,165
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/092,443
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/063,254
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-060-019-2

Query Match      60.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
      |||

```

```

Db      2 MEV 4

RESULT 72
US-10-293-822-13
; Sequence 13, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/10/293,822
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/418,780
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-822-13

Query Match      60.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
      |||
Db      5 VVM 7

RESULT 73
US-08-424-550B-181
; Sequence 181, Application US/08424550B
; Publication No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMESKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207

```

```
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 181:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-181

Query Match          60.0%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      10 MEV 12

RESULT 74
US-09-813-333-20
; Sequence 20, Application US/09813333
; Patent No. US2002019160A1
; GENERAL INFORMATION:
; APPLICANT: DeGroot, Anne S
; TITLE OF INVENTION: Human T Cell Response to MHC-Binding Motif Clusters
; FILE REFERENCE: 17999-004 US
; CURRENT APPLICATION NUMBER: US/09/813,333
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,834
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-813-333-20

Query Match          60.0%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
Db      2 VVM 4

RESULT 75
US-09-766-889A-57
; Sequence 57, Application US/09766889A
; Patent No. US2002016465A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 16

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-57

Query Match          60.0%; Score 3; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
Db      1 MEV 3

Search completed: November 25, 2003, 20:25:36
Job time : 11.9468 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 5.45213 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-9

Perfect score: 5
Sequence: 1 VMEV 5

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	5	4	US-09-641-803-9
2	5	100.0	12	4	US-09-106-568E-121
3	5	100.0	15	6	5252466-12
4	4	80.0	9	3	US-08-159-339A-603
5	4	80.0	10	3	US-08-159-339A-101
6	4	80.0	10	3	US-08-159-339A-596
7	3	60.0	4	1	US-08-062-287-7
8	3	60.0	4	2	US-08-464-203-7
9	3	60.0	4	2	US-08-429-964-18
10	3	60.0	4	3	US-09-195-578-3
11	3	60.0	4	3	US-09-140-951-3
12	3	60.0	4	3	US-09-170-951-3
13	3	60.0	4	3	US-09-164-482-3
14	3	60.0	4	3	US-09-167-180-3
15	3	60.0	4	4	US-09-552-265B-6
16	3	60.0	4	5	PCT-US93-08062-18
17	3	60.0	5	1	US-08-029-333-5
18	3	60.0	5	1	US-08-029-333-6
19	3	60.0	5	1	US-08-029-333-7
20	3	60.0	5	1	US-08-347-000-5
21	3	60.0	5	4	US-08-391-820-5
22	3	60.0	5	4	US-08-391-820-6
23	3	60.0	5	4	US-08-391-820-7
24	3	60.0	5	4	US-08-541-939-3
25	3	60.0	5	4	US-08-877-605-296
26	3	60.0	6	1	US-08-029-333-3
27	3	60.0	6	1	US-08-347-000-3
28	3	60.0	3	1	US-08-457-274A-14
29	3	60.0	3	3	US-08-981-256A-1
30	3	60.0	3	6	US-08-789-333F-91
31	3	60.0	3	6	US-08-787-738B-91
32	3	60.0	3	6	US-08-391-820-3
33	3	60.0	3	6	PCT-US95-05758-14
34	3	60.0	3	7	US-07-968-781A-67
35	3	60.0	3	7	US-08-266-570A-8
36	3	60.0	3	7	US-08-719-758-20
37	3	60.0	3	7	US-09-119-827-20
38	3	60.0	3	7	US-09-461-697-140
39	3	60.0	3	7	US-09-354-147C-38
40	3	60.0	3	8	US-08-029-333-2
41	3	60.0	3	8	US-08-347-000-2
42	3	60.0	3	8	US-08-993-165-18
43	3	60.0	3	8	US-09-078-173A-5
44	3	60.0	3	8	US-09-540-448-18
45	3	60.0	3	8	US-08-391-820-2
46	3	60.0	3	8	US-09-243-640-16
47	3	60.0	3	8	US-08-929-847-18
48	3	60.0	3	9	US-08-951-309-1
49	3	60.0	3	9	US-08-951-309-2
50	3	60.0	3	9	US-09-644-600-73
51	3	60.0	3	9	US-08-388-852B-24
52	3	60.0	3	10	US-08-331-398A-40
53	3	60.0	3	10	US-08-331-398A-41
54	3	60.0	3	10	US-08-331-398A-42
55	3	60.0	3	10	US-08-347-000-7
56	3	60.0	3	10	US-08-796-883-17
57	3	60.0	3	10	US-08-796-883-29
58	3	60.0	3	10	US-08-755-728-13
59	3	60.0	3	10	US-09-036-582-5
60	3	60.0	3	10	US-08-974-655-13
61	3	60.0	3	10	US-08-531-864-17
62	3	60.0	3	10	US-08-331-397B-40
63	3	60.0	3	10	US-08-331-397B-41
64	3	60.0	3	10	US-08-331-397B-42
65	3	60.0	3	10	US-08-759-804A-40
66	3	60.0	3	10	US-08-759-804A-41
67	3	60.0	3	10	US-08-759-804A-42
68	3	60.0	3	10	US-08-602-506A-17
69	3	60.0	3	10	US-08-602-506A-29
70	3	60.0	3	10	US-08-795-430-14
71	3	60.0	3	10	US-08-613-557-12
72	3	60.0	3	10	US-09-266-294-17
73	3	60.0	3	10	US-09-283-011-13
74	3	60.0	3	10	US-09-183-931-37
75	3	60.0	3	10	US-09-177-249-269
76	3	60.0	3	10	US-09-183-706-8
77	3	60.0	3	10	US-09-227-693-40
78	3	60.0	3	10	US-09-227-693-41
79	3	60.0	3	10	US-09-227-693-42
80	3	60.0	3	10	US-09-166-448-49
81	3	60.0	3	10	US-09-567-995-8
82	3	60.0	3	10	US-09-227-357-315
83	3	60.0	3	10	US-09-355-700-14
84	3	60.0	3	10	US-09-705-160-37
85	3	60.0	3	10	US-09-165-863-5
86	3	60.0	3	10	US-08-197-484-83
87	3	60.0	3	10	US-08-197-484-142
88	3	60.0	3	10	US-09-697-894-49
89	3	60.0	3	10	US-09-123-192C-42
90	3	60.0	3	10	US-09-289-350-5
91	3	60.0	3	10	US-09-574-749B-5
92	3	60.0	3	10	PCT-US95-02121-83
93	3	60.0	3	10	PCT-US95-02121-142
94	3	60.0	3	11	US-08-029-333-4
95	3	60.0	3	11	US-08-029-333-30
96	3	60.0	3	11	US-08-029-333-32
97	3	60.0	3	11	US-08-029-333-33
98	3	60.0	3	11	US-08-029-333-39
99	3	60.0	3	11	US-08-029-333-40
100	3	60.0	3	11	US-08-029-333-41

Sequence 14, Appl
Sequence 1, Appl
Sequence 91, Appl
Sequence 91, Appl
Sequence 3, Appl
Sequence 14, Appl
Sequence 67, Appl
Sequence 8, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 140, Appl
Sequence 38, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 18, Appl
Sequence 5, Appl
Sequence 18, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 73, Appl
Sequence 24, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 7, Appl
Sequence 17, Appl
Sequence 29, Appl
Sequence 13, Appl
Sequence 5, Appl
Sequence 13, Appl
Sequence 17, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 7, Appl
Sequence 17, Appl
Sequence 29, Appl
Sequence 14, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 13, Appl
Sequence 37, Appl
Sequence 269, Appl
Sequence 8, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 49, Appl
Sequence 8, Appl
Sequence 315, Appl
Sequence 14, Appl
Sequence 37, Appl
Sequence 5, Appl
Sequence 142, Appl
Sequence 83, Appl
Sequence 49, Appl
Sequence 42, Appl
Sequence 5, Appl
Sequence 83, Appl
Sequence 142, Appl
Sequence 4, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 33, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 41, Appl

ALIGNMENTS

```
RESULT 1
US-09-641-803-9
; Sequence 9, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
;
US-09-641-803-9

Query Match      100.0%; Score 5; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVMEV 5
      |||||
Db      1 VVMEV 5

RESULT 2
US-09-106-568E-121
; Sequence 121, Application US/09106568E
; Patent No. 6455248
; GENERAL INFORMATION:
; APPLICANT: Bhattacharjee, J..
; APPLICANT: Suvarna, Kalavati
; APPLICANT: Bhattacharjee, Vasker
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS IN
; FILE REFERENCE: 96,247-A
; CURRENT APPLICATION NUMBER: US/09/106,568E
; CURRENT FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: 08/650,809
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 121
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide segment of GRSB_1BACB shown in Figure 4.
;
US-09-106-568E-121

Query Match      100.0%; Score 5; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVMEV 5
      |||||
Db      8 VVMEV 12
```

```
RESULT 3
5252466-12
; Patent No. 5252466
; APPLICANT: CRONAN, JOHN E.
; TITLE OF INVENTION: FUSION PROTEINS HAVING A SITE FOR IN
; VIVO POST-TRANSLATION MODIFICATION AND METHODS OF MAKING AND
; PURIFYING THEM
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/525,568
; FILING DATE: 18-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 354,266
; FILING DATE: 19-MAY-1989
; SEQ ID NO:12;
; LENGTH: 15
5252466-12

Query Match      100.0%; Score 5; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVMEV 5
      |||||
Db      10 VVMEV 14

RESULT 4
US-08-159-339A-603
; Sequence 603, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 603:
; SEQUENCE CHARACTERISTICS:
```

; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-603

Query Match 80.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 VMEV 5
Db 2 VMEV 5

RESULT 5
US-08-159-339A-101
; Sequence 101, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-101

Query Match 80.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 VMEV 5

Db |||||
6 VMEV 9

RESULT 6
US-08-159-339A-596
; Sequence 596, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 596:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-596

Query Match 80.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 VMEV 5
Db |||||
3 VMEV 6

RESULT 7
US-08-062-287-7
; Sequence 7, Application US/08062287
; Patent No. 5602098
; GENERAL INFORMATION:
; APPLICANT: SEBTLI, SAID
; APPLICANT: HAMILTON, ANDREW
; APPLICANT: SEONG, CHURL M.

;
; TITLE OF INVENTION: INHIBITION OF FARNESYL TRANSFERASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/062,287
; FILING DATE: 18-MAY-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200385/6137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-062-287-7

Query Match 60.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 2 VVM 4
|||

RESULT 8
US-08-464-203-7
; Sequence 7, Application US/08464203
; Patent No. 5856310
; GENERAL INFORMATION:
; APPLICANT: SEBTI, SAID
; APPLICANT: HAMILTON, ANDREW
; APPLICANT: SEONG, CHURL M.
; TITLE OF INVENTION: INHIBITION OF FARNESYL TRANSFERASE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,203
; FILING DATE: 05-JUNE-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 200385/6137

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-203-7

Query Match 60.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 2 VVM 4
|||

RESULT 9
US-08-429-964-18
; Sequence 18, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; TRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,625
; FILING DATE: 16-FEB-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/615,715
; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990 (ABANDONED)
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924

```
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-429-964-18

Query Match      60.0%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VVM 3
      |||
Db      2 VVM 4

RESULT 10
US-09-195-578-3
; Sequence 3, Application US/09195578
; Patent No. 6054466
; GENERAL INFORMATION:
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: desolms, Jane S. J.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 20121Y
; CURRENT APPLICATION NUMBER: US/09/195,578
; CURRENT FILING DATE: 1998-11-18
; EARLIER APPLICATION NUMBER: 60/067,552
; EARLIER FILING DATE: 1997-12-04
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homosapien
US-09-195-578-3

Query Match      60.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VVM 3
      |||
Db      2 VVM 4

RESULT 11
US-09-140-557-3
; Sequence 3, Application US/09140557A
; Patent No. 6103487
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Barnett, Stanley F.
; APPLICANT: Heimbrock, David C.
; APPLICANT: Huber, Hans E.
; APPLICANT: Patrick, Denis R.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20034Y
; CURRENT APPLICATION NUMBER: US/09/140,557A
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/057,340
; EARLIER FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-terminus CAAX sequence of prenyl-protein
US-09-140-557-3

; OTHER INFORMATION: transferase substrate
US-09-140-557-3

Query Match      60.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VVM 3
      |||
Db      2 VVM 4

RESULT 12
US-09-170-951-3
; Sequence 3, Application US/09170951
; Patent No. 6103723
; GENERAL INFORMATION:
; APPLICANT: Bergman, Jeffrey M.
; APPLICANT: Dinsmore, Christopher J.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF FARNESYL-PROTEIN
; TITLE OF INVENTION: TRANSFERASE
; FILE REFERENCE: 19867Y
; CURRENT APPLICATION NUMBER: US/09/170,951
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 60/064,342
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homosapien
US-09-170-951-3

Query Match      60.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      1 VVM 3
      |||
Db      2 VVM 4

RESULT 13
US-09-164-482-3
; Sequence 3, Application US/09164482A
; Patent No. 6127390
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: desolms, S. Jane
; APPLICANT: Lumma, William C.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Sisko, John T.
; APPLICANT: Tucker, Thomas J.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20025Y
; CURRENT APPLICATION NUMBER: US/09/164,482A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/060,871
; EARLIER FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: C-terminus CAAX sequence of prenyl-protein
; OTHER INFORMATION: transferase substrate
US-09-164-482-3
```

Query Match 60.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
|||
Db 2 VVM 4

RESULT 14
US-09-167-180-3
; Sequence 3, Application US/09167180
; Patent No. 6297239
; GENERAL INFORMATION:
; APPLICANT: deSolms, S. Jane
; APPLICANT: Hutchinson, John H.
; APPLICANT: Shaw, Anthony W.
; APPLICANT: Graham, Samuel L.
; APPLICANT: Ciccarone, Terrence M.
; APPLICANT: Merck & Co., Inc.
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 19928Y
; CURRENT APPLICATION NUMBER: US/09/167,180
; CURRENT FILING DATE: 1998-10-06
; EARLIER APPLICATION NUMBER: 60/062,660
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homosapien
US-09-167-180-3

Query Match 60.0%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
|||
Db 2 VVM 4

RESULT 15
US-09-552-265B-6
; Sequence 6, Application US/09552265B
; Patent No. 6555343
; GENERAL INFORMATION:
; APPLICANT: DeSavage, Frederick
; APPLICANT: Henner, Dennis, J.
; TITLE OF INVENTION: No. 6555343el chimpanzee erythropoietin (chepo)
; TITLE OF INVENTION: polypeptides and nucleic acids encoding the same
; FILE REFERENCE: GENENT 057CP1
; CURRENT APPLICATION NUMBER: US/09/552,265B
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: US 09/307307
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-09-552-265B-6

Query Match 60.0%; Score 3; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
|||
Db 1 MEV 3

RESULT 16
PCT-US93-08062-18
; Sequence 18, Application PC/TUS9308062
; GENERAL INFORMATION:
; APPLICANT:
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
; SEQUENCE CHARACTERISTICS: REISS, YUVAL
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
; ADDRESSEE: METHODS AND COMPOSITIONS FOR
; ADDRESSEE: THE IDENTIFICATION,
; ADDRESSEE: CHARACTERIZATION AND
; ADDRESSEE: INHIBITION OF
; ADDRESSEE: FARNESYLTRANSFERASE
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK/ASKII
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08062
; FILING DATE: AUGUST 24, 1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/935,087
; FILING DATE: 24 AUGUST 1992 (24.08.92)
; NAME: UNKNOWN
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTFD377PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; TELEX: NOT APPLICABLE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US93-08062-18
Query Match 60.0%; Score 3; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
|||
Db 2 VVM 4

RESULT 17
US-08-029-333-5
; Sequence 5, Application US/08029333
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG

```
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-029-333-5

Query Match          60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
Db      3 VVM 5

RESULT 18
US-08-029-333-6
; Sequence 6, Application US/08029333
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-029-333-7

Query Match          60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
Db      3 VVM 5

RESULT 19
US-08-029-333-7
; Sequence 7, Application US/08029333
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-029-333-7

Query Match          60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
Db      3 VVM 5

RESULT 20
US-08-347-000-5
; Sequence 5, Application US/08347000
; Patent No. 5627265
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Gao, Ai-Guo
; TITLE OF INVENTION: Receptor for Cell-binding Domain of
; THROMBOSPONDIN
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,000
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US 08/029,333
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2848
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-347-000-5
;
; Query Match 60.0%; Score 3; DB 1; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 21
; US-08-391-820-5
; Sequence 5, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(1982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-820-6
;
; Query Match 60.0%; Score 3; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 21
; US-08-391-820-5
; Sequence 5, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
```

```
;
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(1982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-820-5
;
; Query Match 60.0%; Score 3; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 22
; US-08-391-820-6
; Sequence 6, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(1982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-820-6
;
; Query Match 60.0%; Score 3; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 22
; US-08-391-820-6
; Sequence 6, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(1982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-820-6
;
; Query Match 60.0%; Score 3; DB 4; Length 5;
; Best Local Similarity 100.0%; Pred. No. 2.5e+05;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 VWM 3
; Db 3 VWM 5
;
; RESULT 22
; US-08-391-820-6
; Sequence 6, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
```



```
Db          3 VVM 5

RESULT 23
US-08-391-820-7
; Sequence 7, Application US/08391820
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24 (982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-391-820-7

Query Match          60.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 VVM 3
           |||
Db          3 VVM 5

RESULT 24
US-08-541-939-3
; Sequence 3, Application US/08541939
; Patent No. 6541238
; GENERAL INFORMATION:
; APPLICANT: Saxena, Inder M.
; APPLICANT: Lin, Fong C.
; APPLICANT: Brown, R. M.
; TITLE OF INVENTION: Recombinant Cellulose Synthase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/541,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/222,322
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mayfield, Denise L.
; REGISTRATION NUMBER: 33,732
; REFERENCE/DOCKET NUMBER: UTSB:564/MAY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-541-939-3

Query Match          60.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 MEV 5
           |||
Db          1 MEV 3

RESULT 25
US-08-877-605-296
; Sequence 296, Application US/08877605
; Patent No. 6582965
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Z Library
US-08-877-605-296

Query Match          60.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 VVM 3
           |||
Db          3 VVM 5

RESULT 26
US-08-029-333-3
; Sequence 3, Application US/08029333
```

```
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24 (982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-029-333-3

Query Match 60.0%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 4 VVM 6

RESULT 27
US-08-347-000-3
; Sequence 3, Application US/08347000
; Patent No. 5627265
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Gao, Ai-Guo
; TITLE OF INVENTION: Receptor for Cell-binding Domain of
; Thrombospondins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,000
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US 08/029,333
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2848
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-347-000-3

Query Match 60.0%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 4 VVM 6

RESULT 28
US-08-457-274A-14
; Sequence 14, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Musca domestica
; STRAIN: Learn-Pyr
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 1
```

US-08-457-274A-14

Query Match 60.0%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db 2 VME 4

RESULT 29

US-08-981-256A-1
; Sequence 1, Application US/08981256A
; Patent No. 646042
; GENERAL INFORMATION:
; APPLICANT: Meinhard HASSLACHER et al.
; TITLE OF INVENTION: (S)-HYDROXY-NITRILE-LYASE FROM HEVEA BRASILIENSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/981,256A

FILING DATE: December 22, 1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Matthew Jacob

REGISTRATION NUMBER: 25,154

REFERENCE/DOCKET NUMBER: 1533-021112

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 721-8200

TELEFAX: (202) 721-8250

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acid residues

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-981-256A-1

Query Match 60.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 2 MEV 4

RESULT 30

US-08-789-333F-91
; Sequence 91, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A642601DJBRMSDSS

; CURRENT APPLICATION NUMBER: US/08/789,333F

; CURRENT FILING DATE: 1997-01-23

; PRIOR APPLICATION NUMBER: 08/589,108

; PRIOR FILING DATE: 1996-01-23

; PRIOR APPLICATION NUMBER: 08/589,911

; PRIOR FILING DATE: 1996-01-23

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 91

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-08-789-333F-91

Query Match 60.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 31

US-08-787-738B-91

; Sequence 91, Application US/08787738B

; Patent No. 6455247

; GENERAL INFORMATION:

; APPLICANT: No. 6455247an, Garry P

; APPLICANT: Rothenberg, Michael S.

; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR

; FILE REFERENCE: A-64259-1 correction

; CURRENT APPLICATION NUMBER: US/08/787,738B

; CURRENT FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 08/589,108

; PRIOR FILING DATE: 1996-01-23

; PRIOR APPLICATION NUMBER: 08/589,911

; PRIOR FILING DATE: 1996-01-23

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 91

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-08-787-738B-91

Query Match 60.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 32

US-08-391-820-3

; Sequence 3, Application US/08391820

; Patent No. 6469138

; GENERAL INFORMATION:

; APPLICANT: Frazier, William A.

; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG

; STREET: 800 N. Lindbergh Blvd.

; CITY: St. Louis

STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,820
FILING DATE: 21-Feb-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/029,333
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24(982)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-391-820-3

Query Match 60.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3
|||
Db 4 VWM 6

RESULT 33
PCT-US95-05758-14
Sequence 14, Application PC/TUS9505758
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Musca domestica
STRAIN: Learn-Pyr
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 1
PCT-US95-05758-14

Query Match 60.0%; Score 3; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
|||
Db 2 VME 4

RESULT 34
US-07-968-781A-67
Sequence 67, Application US/07968781A
Patent No. 5430137
GENERAL INFORMATION:
APPLICANT: Gaertner, Frank H.
APPLICANT: Sick, August J.
APPLICANT: Thompson, Mark
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Probes for the Identification of Bacillus
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/968,781A
FILING DATE: 19921030
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA44.FWCC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-968-781A-67

Query Match 60.0%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
|||
Db 2 VME 4

RESULT 35

US-08-266-570A-8
; Sequence 8, Application US/08266570A
; Patent No. 5484723
; GENERAL INFORMATION:
; APPLICANT: Zenno, Shuhei
; APPLICANT: Saigo, Kaoru
; TITLE OF INVENTION: FLAVIN REDUCTASE GENE FROM VIBRIO
; TITLE OF INVENTION: FISCHERI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: 700 Thirteenth Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,570A
; FILING DATE: 28-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 181850/1993
; FILING DATE: 28-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rose, Herbert C.
; REGISTRATION NUMBER: 29846
; REFERENCE/DOCKET NUMBER: 60257/No. 5484723aka
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 737-6770
; TELEFAX: (202) 737-6776
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-266-570A-8

Query Match 60.0%; Score 3; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
|||
Db 5 VVM 7

RESULT 36

US-08-719-758-20
; Sequence 20, Application US/08719758
; Patent No. 5837537
; GENERAL INFORMATION:
; APPLICANT: Campbell, Kevin P.
; APPLICANT: Jung, Daniel
; APPLICANT: Duclos, Franck
; APPLICANT: Straub, Volker
; TITLE OF INVENTION: k-SARCOGLYCAN NUCLEIC ACID SEQUENCES, AMINO
; TITLE OF INVENTION: ACID SEQUENCES AND APPLICATIONS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.

; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/719,758
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: UIRF-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-719-758-20

Query Match 60.0%; Score 3; DB 2; Length 7;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VME 4
|||
Db 3 VME 5

RESULT 37

US-09-119-827-20
; Sequence 20, Application US/09119827
; Patent No. 6211340
; GENERAL INFORMATION:
; APPLICANT: Campbell, Kevin P.
; APPLICANT: Jung, Daniel
; APPLICANT: Duclos, Franck
; APPLICANT: Straub, Volker
; TITLE OF INVENTION: k-SARCOGLYCAN NUCLEIC ACID SEQUENCES, AMINO
; TITLE OF INVENTION: ACID SEQUENCES AND APPLICATIONS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,827
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: UIRF-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558

```
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 7 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-119-827-20

Query Match          60.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 VME 4
      |||
Db      3 VME 5

RESULT 38
US-09-461-697-140
; Sequence 140, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-140

Query Match          60.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
      |||
Db      1 MEV 3

RESULT 39
US-09-354-147C-38
; Sequence 38, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 38
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: protein seq.
; OTHER INFORMATION: basis for rat Nan reverse primers
; NAME/KEY: VARIANT
; LOCATION: (3)
; OTHER INFORMATION: Xaa = Val or Asp
US-09-354-147C-38

Query Match          60.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MEV 5
      |||
Db      5 MEV 7

RESULT 40
US-08-029-333-2
; Sequence 2, Application US/08029333
; Patent No. 5399667
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24 (982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8 amino acids
;   TYPE: AMINO ACID
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-029-333-2

Query Match          60.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VVM 3
      |||
Db      4 VVM 6

RESULT 41
US-08-347-000-2
; Sequence 2, Application US/08347000
```

; Patent No. 5627265
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Gao, Ai-Guo
; TITLE OF INVENTION: Receptor for Cell-binding Domain of
; TITLE OF INVENTION: Thrombospondins
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,000
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,333
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2848
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-347-000-2

Query Match 60.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
|||
Db 4 VVM 6

RESULT 42
US-08-993-165-18
; Sequence 18, Application US/08993165A
; Patent No. 6123923
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Wu, Yungiu
; TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
; FILE REFERENCE: UNGR1224
; CURRENT APPLICATION NUMBER: US/08/993,165A
; CURRENT FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6123923el Sequence
US-08-993-165-18

Query Match 60.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVM 3
|||
Db 4 VVM 6
RESULT 43
US-09-078-173A-5
; Sequence 5, Application US/09078173A
; Patent No. 6200794
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskins
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Psidium Guajava (guava)
US-09-078-173A-5

Query Match 60.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
|||
Db 4 VVM 6

RESULT 44
US-09-540-448-18
; Sequence 18, Application US/09540448
; Patent No. 6403056
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Charged Lipids and Uses For The Same
; FILE REFERENCE: UNGR1592
; CURRENT APPLICATION NUMBER: US/09/540,448
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 08/925,353
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
US-09-540-448-18

Query Match 60.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
|||
Db 4 VVM 6

RESULT 45
US-08-391-820-2
; Sequence 2, Application US/08391820

```
; Patent No. 6469138
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
;           Kosfeld, Minh D.
; TITLE OF INVENTION: Thrombospondin Receptor Binding Peptides
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,820
; FILING DATE: 21-Feb-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(982)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; TELEFAX: (314)694-5435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-391-820-2

Query Match      60.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
      |||
Db      4 VVM 6

RESULT 46
US-09-243-640-16
; Sequence 16, Application US/09243640
; Patent No. 6521211
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C
; APPLICANT: Shen, Dekang
; APPLICANT: Wu, Guanli
; TITLE OF INVENTION: No. 6521211 Methods Of Imaging And Treatment With Targeted
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: DUP-0463
; CURRENT APPLICATION NUMBER: US/09/243,640
; CURRENT FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 08/660,032
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: 08/640,464
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/497,684
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 09/218,660
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 607,073,913
; PRIOR FILING DATE: 1998-02-06
```

```
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6521211el Sequence
US-09-243-640-16

Query Match      60.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
      |||
Db      4 VVM 6

RESULT 47
US-08-929-847-18
; Sequence 18, Application US/08929847
; Patent No. 6548047
; GENERAL INFORMATION:
; APPLICANT: Unger, Evan C.
; TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
; FILE REFERENCE: BMS0441
; CURRENT APPLICATION NUMBER: US/08/929,847
; CURRENT FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely synthetic sequence
US-08-929-847-18

Query Match      60.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VVM 3
      |||
Db      4 VVM 6

RESULT 48
US-08-951-309-1
; Sequence 1, Application US/08951309
; Patent No. 5952473
; GENERAL INFORMATION:
; APPLICANT: COHEN, Louis H.
; APPLICANT: NIEUWENHUIZEN, Willem
; TITLE OF INVENTION: REAGENT AND KIT FOR DETERMINING
; TITLE OF INVENTION: ISOPRENYLATING ACTIVITY AND INHIBITION THEREOF
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Young & Thompson
; STREET: Second Floor, 745 S. 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,309
; FILING DATE:
```



```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/230,522
; FILING DATE: 20-APR-1994
; APPLICATION NUMBER: EP 93201146.3
; FILING DATE: 20-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: BO 38354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703/521-2297
; TELEFAX: 703/585-0573
; TELEX: 248425
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-951-309-1

Query Match 60.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3
Db 7 VWM 9

RESULT 49
US-08-951-309-2
; Sequence 2, Application US/08951309
; Patent No. 5952473
; GENERAL INFORMATION:
; APPLICANT: COHEN, Louis H.
; APPLICANT: NIEUWENHUIZEN, Willem
; TITLE OF INVENTION: REAGENT AND KIT FOR DETERMINING
; TITLE OF INVENTION: ISOPRENYLATING ACTIVITY AND INHIBITION THEREOF
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Young & Thompson
; STREET: Second Floor, 745 S. 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/230,522
; FILING DATE: 20-APR-1994
; APPLICATION NUMBER: EP 93201146.3
; FILING DATE: 20-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; REFERENCE/DOCKET NUMBER: BO 38354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703/521-2297
; TELEFAX: 703/585-0573
; TELEX: 248425
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-951-309-2

Query Match 60.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3
Db 7 VWM 9

RESULT 50
US-09-644-600-73
; Sequence 73, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotsoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; FILE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 173-181 of the TADG-15 protein
; US-09-644-600-73

Query Match 60.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VWM 3
Db 6 VWM 8

RESULT 51
US-08-388-852B-24
; Sequence 24, Application US/08388852B
; Patent No. 6500919
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan; Figdor, Carl Gustav.
; TITLE OF INVENTION: Melanoma associated antigenic polypeptide.
; TITLE OF INVENTION: epitopes thereof and vaccine against melanoma.
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Adema, Gosse Jan; Figdor, Carl Gustav
; STREET: Philips van Leydenlaan 25
; CITY: Nijmegen
; STATE: Brabant
; COUNTRY: the Netherlands
; ZIP: 6525 EX
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,852B
; FILING DATE: February 15, 1995
; INFORMATION FOR SEQ ID NO: 24:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-388-852B-24

Query Match 60.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
|||
DB 7 MEV 9

RESULT 52

US-08-331-398A-40
; Sequence 40, Application US/08331398A
; Patent No. 5608039

GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994

PRIOR APPLICATION DATA:
CLASSIFICATION: 435
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-331-398A-40

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
|||
DB 1 MEV 3

RESULT 53

US-08-331-398A-41
; Sequence 41, Application US/08331398A
; Patent No. 5608039

GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-331-398A-41

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
|||
DB 1 MEV 3

RESULT 54

US-08-331-398A-42
; Sequence 42, Application US/08331398A
; Patent No. 5608039

GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-398A-42

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 6 VWM 8

RESULT 55
US-08-347-000-7
; Sequence 7, Application US/08347000
; Patent No. 5627265
; GENERAL INFORMATION:
; APPLICANT: Frazier, William A.
; APPLICANT: Gao, Ai-Guo
; TITLE OF INVENTION: Receptor for Cell-binding Domain of
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto/Searle, A3SG
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,000
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/029,333
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-2848
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 694-3117
; TELEFAX: (314) 694-5435
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-347-000-7

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3
Db 5 VWM 7

RESULT 56
US-08-796-883-17
; Sequence 17, Application US/08796883
; Patent No. 5744353
; GENERAL INFORMATION:
; APPLICANT: Herman, Jean; Coulie, Pierre;
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Luescher, Immanuel.
; TITLE OF INVENTION: Tumor Rejection Antigens Presented By
; TITLE OF INVENTION: HLA-B44 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,883
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,506
; FILING DATE: 20-FEBRUARY-1996
; APPLICATION NUMBER: 08/531,864
; FILING DATE: 21-SEPTEMBER-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,636
; FILING DATE: 17-JANUARY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,503
; FILING DATE: 3-JUNE-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5744353man D.
; REGISTRATION NUMBER: 30,946

```

REFERENCE/DOCKET NUMBER: LUD 5436
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Mage-3 peptide
US-08-796-883-17

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 57

US-08-796-883-29
Sequence 29, Application US/08796883
Patent No. 5744353
GENERAL INFORMATION:
APPLICANT: Herman, Jean; Coullie, Pierre;
APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
APPLICANT: Luescher, Immanuel.
TITLE OF INVENTION: Tumor Rejection Antigens Presented By
TITLE OF INVENTION: HLA-B44 Molecules, And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,883
FILING DATE: 06-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,506
FILING DATE: 20-FEBRUARY-1996
APPLICATION NUMBER: 08/531,864
FILING DATE: 21-SEPTEMBER-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,636
FILING DATE: 17-JANUARY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253,503
FILING DATE: 3-JUNE-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, NO. 5744353man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5436
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
NAME/KEY: Mage-6/HLA-B44
US-08-796-883-29

Query Match 60.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 58

US-08-755-728-13
Sequence 13, Application US/08755728
Patent No. 5962312
GENERAL INFORMATION:
APPLICANT: Florman, Gregory
APPLICANT: Mossie, Kevin
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,728
FILING DATE: No. 5962312ember 25, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-755-728-13

Query Match 60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4
Db 1 VME 3

RESULT 59

```
US-09-036-582-5
; Sequence 5, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy R.
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human MAGE-3 peptide
US-09-036-582-5

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      1 MEV 3

RESULT 60
US-08-974-655-13
; Sequence 13, Application US/08974655
; Patent No. 5972676
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mossie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,655
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/755,728
; FILING DATE: No. 5972676ember 25, 1996
; APPLICATION NUMBER: 60/008,809
; FILING DATE: December 18, 1995
; APPLICATION NUMBER: 60/023,943
; FILING DATE: August 14, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/113
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

US-09-036-582-5
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-974-655-13

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 MEV 4
Db      1 MEV 3

RESULT 61
US-08-531-864-17
; Sequence 17, Application US/08531864
; Patent No. 5977300
; GENERAL INFORMATION:
; APPLICANT: Coulie, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated No. 5977300a- and Decapeptides Which
; TITLE OF INVENTION: Bind to HLA-B44 Molecules And The Use Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,864
; FILING DATE: 21-September-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,636
; FILING DATE: 17-JANUARY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,503
; FILING DATE: 3-JUNE-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5977300man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5378.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-531-864-17

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 MEV 5
Db      1 MEV 3

RESULT 62
US-08-331-397B-40
; Sequence 40, Application US/08331397B
```



```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-331-397B-42

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
Db 6 VVM 8

RESULT 65
US-08-759-804A-40
; Sequence 40, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
```

```
;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-759-804A-40

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
Db 1 MEV 3

RESULT 66
US-08-759-804A-41
; Sequence 41, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-759-804A-41

Query Match          60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 3 MEV 5
|||
Db 1 MEV 3

RESULT 67

US-08-759-804A-42
; Sequence 42, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Fastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-759-804A-42

Query Match 60.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVM 3
|||
Db 6 VVM 8

RESULT 68

US-08-602-506A-17
; Sequence 17, Application US/08602506A
; Patent No. 6060257
; GENERAL INFORMATION:

; APPLICANT: Herman, Jean; Coulie, Pierre;
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Luescher, Immanuel.
; TITLE OF INVENTION: Tumor Rejection Antigens Presented By HLA-
; TITLE OF INVENTION: B44 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,506A
; FILING DATE: 20-FEBRUARY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/531,864
; FILING DATE: 21-SEPTEMBER-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,636
; FILING DATE: 17-JANUARY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,503
; FILING DATE: 3-JUNE-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6060257man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 938-3884
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Mage-3 peptide
US-08-602-506A-17

Query Match 60.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MEV 5
|||
Db 1 MEV 3

RESULT 69

US-08-602-506A-29
; Sequence 29, Application US/08602506A
; Patent No. 6060257
; GENERAL INFORMATION:
; APPLICANT: Herman, Jean; Coulie, Pierre;
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Luescher, Immanuel.
; TITLE OF INVENTION: Tumor Rejection Antigens Presented By HLA-
; TITLE OF INVENTION: B44 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,506A
FILING DATE: 20-FEBRUARY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/531,864
FILING DATE: 21-SEPTEMBER-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,636
FILING DATE: 17-JANUARY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/253,503
FILING DATE: 3-JUNE-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6060257man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5436
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Wage-6/HLA-B44
US-08-602-506A-29

Query Match 60.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5
Db 1 MEV 3

RESULT 70
US-08-795-430-14
Sequence 14, Application US/08795430
Patent No. 6130071
GENERAL INFORMATION:
APPLICANT: Alitalo, Kari
APPLICANT: Joukov, Vladimir
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI96/00427
FILING DATE: 01-AUG-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-795-430-14

Query Match 60.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVM 3
Db 2 VVM 4

RESULT 71
US-08-619-557-12
Sequence 12, Application US/08619557
Patent No. 6160087
GENERAL INFORMATION:
APPLICANT: Tomohiko OGAWA
TITLE OF INVENTION: PEPTIDES HAVING AN AMINO ACID SEQUENCE FROM
TITLE OF INVENTION: THE FIMBRIAL PROTEIN OF PORPHYROMONAS GINGIVALIS AND THEIR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,557
FILING DATE: March 27, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-619-557-12

Query Match

Best Local Similarity 60.0%; Score 3; DB 3; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3

Db 4 VWM 6

RESULT 72

US-09-266-294-17

Sequence 17, Application US/09266294

Patent No. 6171806

GENERAL INFORMATION:

APPLICANT: Coullie, Pierre; Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated No. 6171806a- and Decapeptides Which

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/266,294

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/531,864

FILING DATE: 21-September-1995

APPLICATION NUMBER: 08/373,636

FILING DATE: 17-JANUARY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/253,503

FILING DATE: 3-JUNE-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6171806man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5378.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-266-294-17

Query Match

Best Local Similarity 60.0%; Score 3; DB 3; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5

Db 1 MEV 3

RESULT 73

US-09-283-011-13

Sequence 13, Application US/09283011

Patent No. 6207401

GENERAL INFORMATION:

APPLICANT: Plowman, Gregory

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSRQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/283,011

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/012,135

FILING DATE: January 22, 1998

APPLICATION NUMBER: 08/755,728

FILING DATE: No. 6207401ember 25, 1996

APPLICATION NUMBER: 60/023,943

FILING DATE: August 14, 1996

APPLICATION NUMBER: 60/008,809

FILING DATE: December 18, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 231/282

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-283-011-13

Query Match

Best Local Similarity 60.0%; Score 3; DB 3; Length 10;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VME 4

Db 1 VME 3

RESULT 74

US-09-183-931-37

Sequence 37, Application US/09183931C

Patent No. 6210886

GENERAL INFORMATION:

; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: IJD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183.931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018.422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 37
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-183-931-37

Query Match 60.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 MEV 5

Db 1 MEV 3

RESULT 75

US-09-177-249-269
; Sequence 269, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177.249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071.838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 269
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-269

Query Match 60.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VWM 3

Db 6 VWM 8

Search completed: November 25, 2003, 20:16:05
Job time : 6.45213 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:04:14 ; Search time 3.68085 Seconds
(without alignments)
104.507 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3	75.0	9	2	S77984	cytochrome-c oxida
2	3	75.0	12	2	S58502	43.2K bile stone p
3	3	75.0	12	2	S47363	T-cell antigen rec
4	3	75.0	14	2	S29209	avenin alpha-2 - o
5	3	75.0	15	2	S29207	avenin gamma-4 - o
6	3	75.0	15	4	I52698	hypothetical THRAL
7	3	75.0	20	2	C54052	phosphoribosyl-AMP
8	3	75.0	20	2	B46174	RNA-binding protei
9	2	50.0	4	2	I57745	D-mannosate hydrol
10	2	50.0	5	2	B37325	pap fibrial regul
11	2	50.0	5	2	D60274	major protein anti
12	2	50.0	5	2	B44823	synaptosomal-assoc
13	2	50.0	5	2	PT0610	T-cell receptor be
14	2	50.0	5	2	PT0535	T-cell receptor be
15	2	50.0	5	2	PT0684	T-cell receptor be
16	2	50.0	6	2	A61419	sarcosine dehydrog
17	2	50.0	6	2	T11779	phosphoglycerate t
18	2	50.0	6	2	S29637	jacalin beta-II ch
19	2	50.0	6	2	PT0648	T-cell receptor be
20	2	50.0	7	2	B39127	phosphotransferase
21	2	50.0	7	2	A44428	platelet aggregati
22	2	50.0	7	2	S71299	ICL2 protein - Par
23	2	50.0	7	2	PCI316	large granule L3 c
24	2	50.0	7	2	PT0283	Ig heavy chain CRD
25	2	50.0	7	2	PT0529	T-cell receptor be
26	2	50.0	7	2	PT0667	T-cell receptor be
27	2	50.0	7	2	PT0702	T-cell receptor be
28	2	50.0	7	2	A39690	neural cell adhesi
29	2	50.0	7	2	A58718	carnocin U149 - Ca

30	2	50.0	8	2	A32523	peptidyl-dipeptida
31	2	50.0	8	2	B24749	neuropeptide B - b
32	2	50.0	8	2	S43971	tumor-associated a
33	2	50.0	8	2	S43972	tumor-associated a
34	2	50.0	8	2	PT0030	inulinase (EC 3.2.
35	2	50.0	8	2	B27867	homeotic protein U
36	2	50.0	8	2	A14683	aspartate transami
37	2	50.0	8	2	PT0043	phosphatidylethano
38	2	50.0	8	2	PT0595	T-cell receptor be
39	2	50.0	8	2	C39690	neural cell adhesi
40	2	50.0	8	2	A35180	neutral proteinase
41	2	50.0	8	2	A25836	L-serine ammonia-1
42	2	50.0	9	2	S30494	cat gene leader pe
43	2	50.0	9	2	B24362	chloramphenicol O-
44	2	50.0	9	2	S55696	phosphoenolpyruvat
45	2	50.0	9	2	A61820	macustamyotropin I
46	2	50.0	9	2	A37027	macrophage chemota
47	2	50.0	9	2	PH0942	T-cell receptor be
48	2	50.0	9	2	PH0935	T-cell receptor be
49	2	50.0	9	2	PH0917	T-cell receptor be
50	2	50.0	9	2	PH0921	T-cell receptor be
51	2	50.0	10	1	RHAQ1	gonadoliberin 1 -
52	2	50.0	10	2	S39392	calpain (EC 3.4.22
53	2	50.0	10	2	A24196	acetylcholinestera
54	2	50.0	10	2	S26506	collagen alpha 1(V
55	2	50.0	10	2	S10785	enamelin, 22K - bo
56	2	50.0	10	2	PT0215	T-cell receptor be
57	2	50.0	10	2	PH0900	T-cell receptor be
58	2	50.0	10	2	PH0927	T-cell receptor be
59	2	50.0	10	2	PH0925	T-cell receptor be
60	2	50.0	10	2	PH0926	T-cell receptor be
61	2	50.0	10	2	PH0895	T-cell receptor be
62	2	50.0	10	2	PH0948	T-cell receptor be
63	2	50.0	10	2	B61218	alpha-gliadin 6Ha
64	2	50.0	11	1	EOOCC	eledoisin - curled
65	2	50.0	11	1	EOOCC	eledoisin - curly
66	2	50.0	11	1	GMROL	leucosulfakinin -
67	2	50.0	11	2	B49164	chromogranin-B - r
68	2	50.0	11	2	D60409	kassinin-like pept
69	2	50.0	11	2	P60409	substance P-like p
70	2	50.0	11	2	P60409	substance P-like p
71	2	50.0	11	2	YHRT	morphogenetic neur
72	2	50.0	11	2	YHRT	morphogenetic neur
73	2	50.0	11	2	YHBO	morphogenetic neur
74	2	50.0	11	2	YHXAE	morphogenetic neur
75	2	50.0	11	2	YHJFY	morphogenetic neur
76	2	50.0	11	2	B60409	kassinin-like pept
77	2	50.0	11	2	C60409	kassinin-like pept
78	2	50.0	11	2	S07203	uperolein - frog (
79	2	50.0	11	2	S04875	nifs protein - Bra
80	2	50.0	11	2	S21127	prescorin methyltr
81	2	50.0	11	2	B43689	hypothetical prote
82	2	50.0	11	2	PC2372	58K heat shock pro
83	2	50.0	11	2	PU0029	33K protein 3218 -
84	2	50.0	11	2	P80259	39K protein 3225 -
85	2	50.0	11	2	A60656	perisulfakinin - A
86	2	50.0	11	2	D56979	collagen alpha 1(I)
87	2	50.0	11	2	S23926	major glycoprotein
88	2	50.0	11	2	PT0044	protein kinase C 1
89	2	50.0	11	2	PT0214	T-cell receptor be
90	2	50.0	11	2	PH0941	T-cell receptor be
91	2	50.0	11	2	PH0929	T-cell receptor be
92	2	50.0	11	2	PH0947	T-cell receptor be
93	2	50.0	11	2	PH0924	T-cell receptor be
94	2	50.0	11	2	PH0914	T-cell receptor be
95	2	50.0	12	2	PN0577	tyrosine 3-monooxy
96	2	50.0	12	2	PN0578	tyrosine 3-monooxy
97	2	50.0	12	2	PN0579	tyrosine 3-monooxy
98	2	50.0	12	2	PN0580	tyrosine 3-monooxy
99	2	50.0	12	2	PN0581	tyrosine 3-monooxy
100	2	50.0	12	2	PN0576	tyrosine 3-monooxy

ALIGNMENTS

```
RESULT 1
S77984
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa - bigeye tuna (fragment)
C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A:Reference number: S77980
A:Accession: S77984
A:Molecule type: protein
A:Residues: 1-9 <ARN>
A:Experimental source: heart
C:Genetics:
A:Genome: nuclear
C:Function:
A:Pathway: oxidative phosphorylation; respiratory chain
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 75.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 2 EQP 4

RESULT 2
E58502
43.2K bile stone protein - unidentified bacterium (fragment)
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: E58502
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: E58502
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <BIN>
A:Experimental source: human bile with stones
A>Note: a secondary sequence DVKIGVAGS was also found

Query Match 75.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 7 EQP 9

RESULT 3
S47363
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47363
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47363
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <LEH>
A:Cross-references: EMBL:Z35671; NID:G527467; PIDN:CAA84740.1; PID:G527468
C:Keywords: T-cell receptor

Query Match 75.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 8 SEQ 10

RESULT 4
S29209
avenin alpha-2 - oat (fragment)
N:Alternate names: Cip-3; coeliac immunoreactive protein 3
C:Species: Avena sativa (oat)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S29209
R:Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.
FEBS Lett. 310, 37-40, 1992
A:Title: Identification of the three major coeliac immunoreactive proteins and one a
A:Reference number: S29207; MUID:92405739; PMID:1526282
A:Accession: S29209
A:Molecule type: protein
A:Residues: 1-14 <ROC>
A:Experimental source: endosperm
C:Superfamily: gliadin
C:Keywords: prolamin; seed

Query Match 75.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 9 SEQ 11

RESULT 5
S29207
avenin gamma-4 - oat (fragment)
N:Alternate names: Cip-1; coeliac immunoreactive protein 1
C:Species: Avena sativa (oat)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S29207
R:Rocher, A.; Collilla, F.; Ortiz, M.L.; Mendez, E.
FEBS Lett. 310, 37-40, 1992
A:Title: Identification of the three major coeliac immunoreactive proteins and one a
A:Reference number: S29207; MUID:92405739; PMID:1526282
A:Accession: S29207
A:Molecule type: protein
A:Residues: 1-15 <ROC>
A:Experimental source: endosperm
C:Superfamily: gliadin
C:Keywords: prolamin; seed

Query Match 75.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 2 SEQ 4

RESULT 6
I52698
hypothetical THRAl/BTR mutant fusion protein, cell line BT474 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C:Accession: I52698
R:Futreal, P.A.; Cochran, C.; Marks, J.R.; Iglehart, J.D.; Zimmerman, W.; Barrett, J
Cancer Res. 54, 1791-1794, 1994
A:Title: Mutation analysis of the THRAl gene in breast cancer: deletion/fusion of th
```

A;Reference number: I52698; MUID:94185019; PMID:7511052

A;Accession: I52698

A;Status: translated from GB/EMBL/DBSJ

A;Molecule type: mRNA

A;Residues: 1-15 <FUT>

A;Cross-references: GB:S71020; NID:G546112; PIDN:AAB30341.1; PID:G546112

C;Comment: This sequence is the chimeric product of a deletion or translocation mutation

C;Genetics:

A;Gene: THRAl/BTR

A;Map position: 17q11.2

C;Keywords: fusion protein

Query Match 75.0%; Score 3; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.7e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3

|||

Db 4 SEQ 6

RESULT 7

C54052 phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3.6.1.15)

C;Species: Klebsiella pneumoniae

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2002

C;Accession: C54052

R;Rieder, G.; Merrick, M.J.; Castorff, H.; Kleiner, D.

J. Biol. Chem. 269, 14386-14390, 1994

A;Title: Function of hisF and hisH gene products in histidine biosynthesis.

A;Reference number: A54052; MUID:94237842; PMID:8182043

A;Accession: C54052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-20 <RIE>

A;Experimental source: M5a1

A;Note: sequence extracted from NCBI backbone (NCBIN:148607, NCBIPI:148610)

C;Genetics:

A;Gene: hisE

C;Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein

C;Keywords: histidine biosynthesis; hydrolase; multifunctional enzyme

Query Match 75.0%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3

|||

Db 3 SEQ 5

RESULT 8

B46174

RNA-binding protein TIAR - human (fragment)

N;Alternate names: cytotoxic granule-associated RNA-binding protein; TIA-1 related protein

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jul-1998

C;Accession: B46174

R;Kawakami, A.; Tian, Q.; Duan, X.; Streuli, M.; Schlossman, S.F.; Anderson, P.

Proc. Natl. Acad. Sci. U.S.A. 89, 8681-8685, 1992

A;Title: Identification and functional characterization of a TIA-1-related nucleolysin.

A;Reference number: A46174; MUID:92409580; PMID:1326761

A;Accession: B46174

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-20 <KAW>

A;Note: sequence extracted from NCBI backbone (NCBIN:114067, NCBIPI:114068)

C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein

Query Match 75.0%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 7.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4

|||

Db 2 EQP 4

RESULT 9

I57745

D-mannonate hydrolase (uxuA) - Escherichia coli

C;Species: Escherichia coli

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999

C;Accession: I57745

R;Blanco, C.; Ritzenthaler, P.; Kolb, A.

Mol. Gen. Genet. 202, 112-119, 1986

A;Title: The regulatory region of the uxuA operon in Escherichia coli K12.

A;Reference number: I57745; MUID:86174344; PMID:3083215

A;Accession: I57745

A;Status: preliminary; translated from GB/EMBL/DBSJ

A;Molecule type: DNA

A;Residues: 1-4 <RES>

A;Cross-references: EMBL:X03411; NID:G43300; PIDN:CAA27147.1; PID:G581254

Query Match 50.0%; Score 2; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3

|||

Db 2 EQ 3

RESULT 10

B37325

pap fibrial regulatory protein papI - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 11-Sep-1992 #sequence_revision 11-Sep-1992 #text_change 23-Mar-1993

C;Accession: B37325

R;Bratzen, B.A.; Blyn, L.B.; Skinner, B.S.; Low, D.A.

J. Bacteriol. 173, 1789-1800, 1991

A;Title: Evidence for a methylation-blocking factor (mbf) locus involved in pap pilus

A;Reference number: A37325; MUID:91154136; PMID:1671857

A;Accession: B37325

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-5 <BRA>

A;Cross-references: GB:M63747

Query Match 50.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

|||

Db 2 SE 3

RESULT 11

D60274

major protein antigen MPT46 - Mycobacterium tuberculosis (fragment)

C;Species: Mycobacterium tuberculosis

C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993

C;Accession: D60274

R;Nagai, S.; Wiker, H.O.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the cult

A;Reference number: A60274; MUID:91099989; PMID:1898899

A;Accession: D60274

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <NAG>

Query Match 50.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
||
Db 3 SE 4

RESULT 12

B44823
synaptosomal-associated protein SNAP-25 peptide 10A - rabbit (fragment)
N;Alternate names: superprotein peptide 10A
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C;Accession: B44823
R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A;Reference number: A44823; MUID:92044785; PMID:1941090
A;Accession: B44823
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <LOE>
A;Experimental source: visual tissue
A;Note: sequence extracted from NCBI backbone (NCBIP:64255)
C;Keywords: membrane trafficking

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
||
Db 1 EQ 2

RESULT 13

PT0610
T-cell receptor beta chain V-D-J region (100-2E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0610
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0610
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <PEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
||
Db 3 SE 4

RESULT 14

PT0535
T-cell receptor beta chain V-D-J region (126-1AE) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0535
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0535
A;Status: translation not shown
A;Molecule type: mRNA

A;Residues: 1-5 <PEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
||
Db 3 SE 4

RESULT 15

PT0684
T-cell receptor beta chain V-D-J region (140-1BK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0684
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N region:
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0684
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <PEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
||
Db 3 SE 4

RESULT 16

A61419
sarcosine dehydrogenase (EC 1.5.99.1) - Pseudomonas sp. (strain WRF) (fragment)
C;Species: Pseudomonas sp.
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: A61419
R;Pinto, J.T.; Frisell, W.R.
Arch. Biochem. Biophys. 169, 483-491, 1975
A;Title: Characterization of the peptide-bound flavin of a bacterial sarcosine dehy:
A;Reference number: A61419; MUID:76038634; PMID:241294
A;Accession: A61419
A;Molecule type: protein
A;Residues: 1-6 <FIN>
C;Keywords: FAD; flavoprotein; oxidoreductase; phosphoprotein
F;6/Modified site: 3'-FAD-histidine (His) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 6;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
||
Db 3 SE 4

RESULT 17

T11779
phosphoglycerate transport regulatory protein pgTA - Salmonella typhimurium (fragmen:
C;Species: Salmonella typhimurium
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: T11779
R;Yang, Y.L.; Goldrick, D.; Hong, J.S.
J. Bacteriol. 170, 4299-4303, 1988
A;Title: Identification of the products and nucleotide sequences of two regulatory g:

A:Reference number: Z17339; MUID:88314933; PMID:2842311
 A:Accession: T11779
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <YAN>
 A:Cross-references: EMBL:M21279; NID:g858752; PID:g154260
 A:Experimental source: strain LT2

Query Match 50.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
 ||
 Db 3 EQ 4

RESULT 18
 S29637
 jacalin beta-II chain - Artocarpus champedon (fragment)
 C:Species: Artocarpus champedon
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
 C:Accession: S29637
 R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.
 Biochim. Biophys. Acta 1156, 219-222, 1993
 A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
 A:Reference number: S29635; MUID:93152601; PMID:8427879
 A:Accession: S29637
 A:Molecule type: protein
 A:Residues: 1-6 <NGO>
 A:Experimental source: seed
 A:Complex: heterotetramer; two alpha and two beta chains
 C:Function:

A:Description: seed storage protein
 A:Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine
 C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 50.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
 ||
 Db 2 EQ 3

RESULT 19
 PT0648
 T-cell receptor beta chain V-D-J region (121-3BK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0648
 R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0648
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-6 <FEE>
 A:Experimental source: day 4 postnatal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
 ||
 Db 3 SE 4

RESULT 20

B39127
 phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
 C:Species: Escherichia coli
 C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
 C:Accession: B39127
 R:Hardesty, C.; Ferran, C.; DiRienzo, J.M.
 J. Bacteriol. 173, 449-456, 1991
 A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of
 rin.
 A:Reference number: A39127; MUID:91100329; PMID:1846143
 A:Accession: B39127
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-7 <HAR>
 A:Cross-references: GB:M38416; NID:g155142; PIDN:AAA98418.1; PID:g155144
 C:Keywords: phosphotransferase

Query Match 50.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
 ||
 Db 4 EQ 5

RESULT 21
 A44428
 platelet aggregation-associated protein - Streptococcus sanguis (fragment)
 C:Species: Streptococcus sanguis
 C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 11-Nov-1994
 C:Accession: A44428
 R:Rickson, P.R.; Herzberg, M.C.
 J. Biol. Chem. 268, 1646-1649, 1993
 A:Title: The Streptococcus sanguis platelet aggregation-associated protein. Identific.
 A:Reference number: A44428; MUID:93131902; PMID:8420939
 A:Accession: A44428
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <ERI>
 C:Keywords: cell wall

Query Match 50.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
 ||
 Db 3 EQ 4

RESULT 22
 S71299
 ICL2 protein - Paramecium tetraurelia (fragment)
 C:Species: Paramecium tetraurelia
 C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C:Accession: S71299
 R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A:Title: Characterization of centrin genes in Paramecium.
 A:Reference number: S71299; MUID:96248429; PMID:8665928
 A:Accession: S71299
 A:Molecule type: protein
 A:Residues: 1-7 <MAD>
 A:Experimental source: strain d4-2
 C:Genetics:
 A:Genetic code: SGC5

Query Match 50.0%; Score 2; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

Db 2 QP 3
||

RESULT 23

PC1316
large granule L3 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
C;Species: Tachyplesus tridentatus
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: PC1316
R;Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
J. Biochem. 114, 307-316, 1993
A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)
A;Reference number: PC1309; MUID:94110249; PMID:8282718
A;Accession: PC1316
A;Molecule type: protein
A;Residues: 1-7 <SH1>
C;Comment: This protein participates in immobilization of invading microbes.

Query Match 50.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
Db 3 QP 4

RESULT 24

PT0283
Ig heavy chain CRD3 region (clone 4-94B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0283
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0283
A;Molecule type: DNA
A;Residues: 1-7 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 50.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
||
Db 3 EQ 4

RESULT 25

PT0529
T-cell receptor beta chain V-D-J region (100-4K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0529
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0529
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
Db 3 SE 4

RESULT 26

PT0667
T-cell receptor beta chain V-D-J region (121-2I) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0667
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0667
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
Db 3 SE 4

RESULT 27

PT0702
T-cell receptor beta chain V-D-J region (161-2AA) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0702
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0702
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-7 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
Db 3 SE 4

RESULT 28

A39690
neural cell adhesion molecule, cardiac splice form -, -, -, - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1993
C;Accession: A39690
R;Reyes, A.A.; Small, S.J.; Akesson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule
A;Reference number: A39690; MUID:91141516; PMID:1996115
A;Accession: A39690
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-7 <REY>
A;Cross-references: GB:M63970

C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
1 QP 2

RESULT 29
A58718
carnocin U149 - Carnobacterium sp. (fragment)
C;Species: Carnobacterium sp.
C;Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C;Accession: A58718
R;Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 1417-1422, 1992
A;Title: Purification and characterization of a new bacteriocin isolated from a Carnobac-
A;Reference number: A58718; MUID:92321768; PMID:1622206
A;Accession: A58718
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <STO>
C;Keywords: antibiotic; lanthionine

Query Match 50.0%; Score 2; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
2 SE 3

RESULT 30
A32523
peptidyl-dipeptidase A (EC 3.4.15.1) - bovine (fragment)
N;Alternate names: angiotensin I-converting enzyme; peptidyl-dipeptidase I
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 11-May-2000
C;Accession: A32523
R;Harris, R.B.
Adv. Exp. Med. Biol. 198, 513-521, 1986
A;Title: Isolation and sequencing of an active-site peptide from angiotensin I-converting
A;Reference number: A32523; MUID:87123961; PMID:3028071
A;Accession: A32523
A;Molecule type: protein
A;Residues: 1-8 <HAR>
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; blood pressure control; peptidyl-dipeptide hydrolase; z

Query Match 50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
7 SE 8

RESULT 31
B24749
neuropeptide B - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000
C;Accession: B24749
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b
A;Reference number: A94074; MUID:86067985; PMID:3865193
A;Accession: B24749

A;Molecule type: protein
A;Residues: 1-8 <YAN>
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide

Query Match 50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
4 QP 5

RESULT 32
S43971
tumor-associated antigen MUT1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C;Accession: S43971
R;Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murin
A;Reference number: S43971; MUID:94217811; PMID:8164742
A;Accession: S43971
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAN>
C;Superfamily: unassigned animal peptides

Query Match 50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
||
2 EQ 3

RESULT 33
S43972
tumor-associated antigen MUT2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 18-Aug-2000
C;Accession: S43972
R;Mandelblom, O.; Berke, G.; Fridkin, M.; Feldman, M.; Eisenstein, M.; Eisenbach, L.
Nature 369, 67-71, 1994
A;Title: CTL induction by a tumour-associated antigen octapeptide derived from a murin
A;Reference number: S43971; MUID:94217811; PMID:8164742
A;Accession: S43972
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAN>
C;Superfamily: unassigned animal peptides

Query Match 50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
||
2 EQ 3

RESULT 34
PT0030
inulinase (EC 3.2.1.7) - Aspergillus ficuum (fragment)
N;Alternate names: inulase
C;Species: Aspergillus ficuum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 07-May-1999
C;Accession: PT0030
R;Etalibi, M.; Barattii, J.C.
Agric. Biol. Chem. 54, 61-68, 1990

A;Title: Molecular and kinetic properties of Aspergillus ficum inulinases.
 A;Reference number: PT0030; MUID:90344234; PMID:1368526
 A;Accession: PT0030
 A;Molecule type: protein
 A;Residues: 1-8 <ETT>
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 50.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
 ||
 Db 5 QP 6

RESULT 35

B27867 homeotic protein Ultrabithorax - fruit fly (Drosophila melanogaster) (fragment)
 C;Species: Drosophila melanogaster
 C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 23-Feb-1997
 A;Accession: B27867

R;Saari, G.; Bienz, M.
 EMBO J. 6, 1775-1779, 1987
 A;Title: The structure of the ultrabithorax promoter of Drosophila melanogaster.
 A;Reference number: A91072
 A;Accession: B27867

A;Molecule type: mRNA
 A;Residues: 1-8 <SAA>
 C;Genetics:
 A;Gene: FlyBase:Ubx
 A;Cross-references: FlyBase:FBgn0003944
 C;Keywords: DNA binding; nucleus; transcription regulation

Query Match 50.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
 ||
 Db 6 EQ 7

RESULT 36

Al4683 aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragment)
 N;Alternate names: aspartate aminotransferase, mitochondrial
 C;Species: Gallus gallus (chicken)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000
 A;Accession: Al4683

R;Wilson, K.J.; Hunziker, P.; Hughes, G.J.
 FEBS Lett. 108, 98-102, 1979
 A;Title: Microsequence analysis. IV. Automatic liquid-phase sequencing using DABITC.
 A;Reference number: Al4683; MUID:80092116; PMID:520566
 A;Accession: Al4683

A;Molecule type: protein
 A;Residues: 1-8 <ML>
 C;Keywords: aminotransferase; mitochondrion

Query Match 50.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
 ||
 Db 1 SE 2

RESULT 37

PN0043 phosphatidylethanol amine-binding protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998

C;Accession: PN0043

R;Kato, H.
 Kawasaki Igakkaishi 22, 245-259, 1996
 A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse ne
 A;Reference number: PN0041
 A;Accession: PN0043

A;Molecule type: protein
 A;Residues: 1-8 <KAR>
 A;Experimental source: neuroblastoma cell
 C;Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is bloc
 C;Keywords: brain

Query Match 50.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
 ||
 Db 3 EQ 4

RESULT 38

PT0595 T-cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)

C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 A;Accession: PT0595
 R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0595

A;Status: translation not shown
 A;Molecule type: mRNA

A;Residues: 1-8 <FEE>
 A;Experimental source: newborn thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
 ||
 Db 3 SE 4

RESULT 39

C39690 neural cell adhesion molecule, cardiac splice form -, -, -, + - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
 C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
 A;Accession: C39690

R;Reyes, A.A.; Small, S.J.; Akeson, R.
 Mol. Cell. Biol. 11, 1654-1661, 1991
 A;Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule

A;Reference number: A39690; MUID:91141516; PMID:1996115
 A;Accession: C39690
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A;Molecule type: mRNA
 A;Residues: 1-8 <KEY>
 A;Cross-references: GB:M63970
 C;Keywords: cardiac muscle; cell adhesion; heart

Query Match 50.0%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
 ||
 Db 1 QP 2

```

RESULT 40
A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C:Accession: A35180
R:Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Sato, M.
J. Biol. Chem. 265, 5809-5815, 1990
A:Title: Purification of a novel type of calcium-activated neutral protease from rat brain
A:Reference number: A35180; MUID:90202830; PMID:2318836
C:Accession: A35180
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <YOS>
C:Keywords: hydrolase

Query Match          50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
    ||
Db 4 SE 5

RESULT 41
A25836
L-serine ammonia-lyase (EC 4.3.1.17) - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 24-Jan-1988 #sequence_revision 24-Jan-1988 #text_change 21-Jun-2002
C:Accession: A25836
R:Heinacz, M.C.; McFall, E.
J. Bacteriol. 123, 1163-1169, 1975
A:Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operator
A:Reference number: A25836; MUID:76005414; PMID:1099073
A:Contents: K12
A:Accession: A25836
A:Molecule type: protein
A:Residues: 1-8 <HEI>
C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; seri

Query Match          50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
    ||
Db 2 SE 3

RESULT 42
S30494
cat gene leader peptide - Streptococcus agalactiae plasmid pIP501
C:Species: Streptococcus agalactiae
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 24-Sep-1999
C:Accession: S30494
R:Trieu-Cuot, P.; de Cespedes, G.; Haraud, T.
Plasmid 28, 272-276, 1992
A:Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Strept
A:Reference number: JQ1950; MUID:93096867; PMID:1461942
A:Accession: S30494
A:Molecule type: DNA
A:Residues: 1-9 <TRI>
A:Cross-references: EMBL:X65462; NID:g49071; PIDN:CAA46454.1; PID:g581554
C:Genetics:
A:Genome: plasmid pIP501
C:Superfamily: unassigned leader peptides

Query Match          50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

```

```

Db 4 SE 5
    ||

RESULT 43
B24362
chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid pU1
C:Species: Staphylococcus aureus
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 11-May-2000
C:Accession: B24362
R:Bruckner, R.; Matzura, H.
EMBO J. 4, 2295-2300, 1985
A:Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the St.
A:Reference number: A24362; MUID:86081739; PMID:3865770
A:Accession: B24362
A:Molecule type: DNA
A:Residues: 1-9 <BRU>
A:Cross-references: GB:X02872; NID:g46536; PIDN:CAA26630.1; PID:g581555
C:Comment: Ribosome stalling in the translation of this leader peptide, caused by the
relation of the chloramphenicol O-acetyltransferase from a ribosome binding site loca
C:Genetics:
A:Genome: plasmid
C:Superfamily: unassigned leader peptides

Query Match          50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
    ||
Db 4 SE 5

RESULT 44
S55696
phosphoenolpyruvate carboxykinase - Trypanosoma brucei
C:Species: Trypanosoma brucei
C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S55696
R:Hunt, M.; Koehler, P.
Biochim. Biophys. Acta 1249, 15-22, 1995
A:Title: Purification and characterization of phosphoenolpyruvate carboxykinase from
A:Reference number: S55696; MUID:95284106; PMID:7766679
A:Accession: S55696
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <HUN>

Query Match          50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
    ||
Db 1 QP 2

RESULT 45
A61620
locustamyotropin III - migratory locust
C:Species: Locusta migratoria (migratory locust)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C:Accession: A61620
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
Insect Biochem. Mol. Biol. 22, 447-452, 1992
A:Title: Isolation, identification and synthesis of locustamyotropin III and IV, two
A:Reference number: A61620
A:Accession: A61620
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <SCH>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Leu) #status experimental

```

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
3 QP 4

Db

RESULT 46
A37027
macrophage chemotactic factor - human (fragment)
N;Alternate names: T-cell hybridoma D6-18 protein
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 23-Feb-1997
C;Accession: A37027
R;Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.
Cell. Immunol. 123, 212-225, 1989
A;Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clone.
A;Reference number: A37027; MUID:89376581; PMID:2505934
A;Accession: A37027
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <YOS>

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
8 SE 9

Db

RESULT 47
PH0942
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0942
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0942
A;Molecule type: mRNA
A;Residues: 1-9 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon TGC for residue 2 as Ala
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
||
8 EQ 9

Db

RESULT 48
PH0935
T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0935
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0935
A;Molecule type: mRNA

A;Residues: 1-9 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
4 SE 5

Db

RESULT 49
PH0917
T-cell receptor beta chain V-D-J region (isolate 3) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0917
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0917
A;Molecule type: mRNA
A;Residues: 1-9 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
4 SE 5

Db

RESULT 50
PH0921
T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0921
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0921
A;Molecule type: mRNA
A;Residues: 1-9 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
4 SE 5

Db

RESULT 51
RHAQ1
gonadoliberin I - American alligator
N;Alternate names: gonadotropin-releasing hormone I
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C;Accession: A60066
R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swar
Regul. Pept. 33, 105-116, 1991
A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains

A;Reference number: A60066; MUID:91352338; PMID:1882082

A;Accession: A60066

A;Molecule type: protein

A;Residues: 1-10 <LOV>

C;Superfamily: gonadoliberin

C;Keywords: amidated carboxylic acid (Gln) #status experimental

F;1/Modified site: pyrrolidone carboxylic acid (Gly) #status experimental

F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 50.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

DB 8 QP 9

RESULT 52

S39392

calpain (EC 3.4.22.17) II light chain - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 18-Feb-1994 #sequence_revision 24-Jul-1998 #text_change 29-Sep-1999

C;Accession: S39392

R;Crawford, C.; Brown, N.R.; Willis, A.C.

Biochem. J. 296, 135-142, 1993

A;Title: Studies of the active site of m-calpain and the interaction with calpastatin.

A;Reference number: S39391; MUID:94071815; PMID:8250833

A;Accession: S39392

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <CRA>

C;Superfamily: calpain small chain; calmodulin repeat homology

C;Keywords: cysteine proteinase; EF hand; hydrolase

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 4 SE 5

RESULT 53

A24196

acetylcholinesterase (EC 3.1.1.7) - electric eel (fragment)

C;Species: Electrophorus electricus (electric eel)

C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 28-Apr-1993

C;Accession: A24196

R;Kieffer, B.; Goeldner, M.; Hirth, C.; Abersold, R.; Chang, J.Y.

FEBS Lett. 202, 91-96, 1986

A;Title: Sequence determination of a peptide fragment from electric eel acetylcholinesterase

A;Reference number: A24196

A;Accession: A24196

A;Molecule type: protein

A;Residues: 1-10 <MIE>

C;Keywords: carboxylic ester hydrolase

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

DB 5 SE 6

RESULT 54

S26506

collagen alpha 1(VI) chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Dec-1998

C;Accession: S26506

R;Jander, R.; Rautenberg, J.; Giarville, R.W.

Eur. J. Biochem. 133, 39-46, 1983

A;Title: Further characterization of the three polypeptide chains of bovine and human

A;Reference number: S26506; MUID:83209648; PMID:6852033

A;Accession: S26506

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <JAN>

C;Keywords: hydroxyproline

F;9/Modified site: hydroxyproline (Pro) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

DB 3 QP 4

RESULT 55

S10785

enamelin, 22K - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998

C;Accession: S10785

R;Strawich, E.; Gilmcher, M.J.

Eur. J. Biochem. 191, 47-56, 1990

A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is a

A;Reference number: S10780; MUID:90336641; PMID:2379503

A;Accession: S10785

A;Molecule type: protein

A;Residues: 1-10 <STR>

C;Keywords: enamel; phosphoprotein

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

DB 3 QP 4

RESULT 56

PT0215

T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0215

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not rest

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0215

A;Molecule type: mRNA

A;Residues: 1-10 <NAK>

C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3

DB 7 EQ 8

RESULT 57

PH0900

T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

```

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0900
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0900
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQ 3
      ||
Db      9 EQ 10

RESULT 58
PH0927
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0927
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0927
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQ 3
      ||
Db      9 EQ 10

RESULT 59
PH0925
T-cell receptor beta chain V-D-J region (isolate 11) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0925
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0925
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQ 3
      ||
Db      9 EQ 10

RESULT 60
PH0926
T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0926
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0926
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
A;Note: the authors translated the codon AGA for residue 4 as Thr
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQ 3
      ||
Db      9 EQ 10

RESULT 61
PH0895
T-cell receptor beta chain V-D-J region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0895; PH0896
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0895
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: myelin basic protein-immunized T-cell; clones 15 and 16
C;Keywords: T-cell receptor

Query Match      50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SE 2
      ||
Db      7 SE 8

RESULT 62
PH0948
T-cell receptor beta chain V-D-J region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 19-Oct-1995 #text_change 30-May-1997
C;Accession: PH0948; PH0897; PH0909; PH0899
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0948
A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered from
A;Accession: PH0897
A;Molecule type: mRNA
A;Residues: 1-10 <GO2>
A;Experimental source: myelin basic protein-immunized T-cell, clones 3, 6-2, 14, hyb;
A;Accession: PH0909
A;Molecule type: mRNA
A;Residues: 1-10 <GO3>
A;Accession: PH0899
A;Status: preliminary
A;Molecule type: mRNA

```

A;Residues: 1-10 <G04>
A;Experimental source: clone 14
C;Keywords: T-cell receptor

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
||
Db 9 EQ 10

RESULT 63

B61218
alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)
C;Species: Haynaldia villosa, Dasypyrum villosum
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 17-Mar-1999
C;Accession: B61218
R;Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.
Biochem. Genet. 29, 207-211, 1991
A;Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa
A;Reference number: A61218; MUID:91315394; PMID:1859356
A;Accession: B61218
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SHE>
C;Keywords: seed; storage protein

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
Db 9 QP 10

RESULT 64

EOOCC
eledoisin - curled octopus
C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
C;Accession: B01561; A01561
R;Anastasi, A.; Erspaner, V.
Arch. Biochem. Biophys. 101, 56-65, 1963
A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of eledoisin
A;Reference number: A01561
A;Accession: B01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagog
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
Db 1 QP 2

RESULT 65

EOOCC
eledoisin - musky octopus
C;Species: Eledone moschata, Ozaena moschata (musky octopus)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998
C;Accession: A01561
R;Anastasi, A.; Erspaner, V.
Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide
A;Reference number: A01561
A;Accession: A01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagog
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
Db 1 QP 2

RESULT 66

GNROL
leucosulfakinin - Madeira cockroach
N;Alternate names: LSK
C;Species: Leucophaea madeirae (Madeira cockroach)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 13-Sep-1996
C;Accession: A01622
R;Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
Science 234, 71-73, 1986
A;Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and leucosulfakinin
A;Reference number: A01622; MUID:86315858; PMID:3749893
A;Accession: A01622
A;Molecule type: protein
A;Residues: 1-11 <NAC>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; sulfoprotein
F;6/Binding site: sulfate (Tyr) (covalent) #status experimental
F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
||
Db 1 EQ 2

RESULT 67

B49164
chromogranin-B - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: B49164
R;Nielsen, E.; Welinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991
A;Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides
A;Reference number: A49164; MUID:92063871; PMID:1954895
A;Accession: B49164
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <NIE>
A;Note: sequence extracted from NCBI backbone (NCBIP:66370)
C;Superfamily: chromogranin B precursor

Query Match 50.0%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
Db 3 SE 4


```

RESULT 68
D60409
C:Species: Pseudophryne guentheri
C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: D60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: D60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 69
F60409
substance P-like peptide II - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: F60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: F60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 70
E60409
substance P-like peptide I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: E60409
R:Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austr
A:Reference number: A60409; MUID:90287814; PMID:2356157
A:Accession: E60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

```

```

Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 71
YHRT
morphogenetic neuropeptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from co
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: A01427
A:Molecule type: protein
A:Residues: 1-11 <BOB>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical stru
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h
een found in mammalian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutam
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 72
YHHT
morphogenetic neuropeptide - human
C:Species: Homo sapiens (man)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: B01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from co
A:Reference number: A93266; MUID:82035850; PMID:7290191
A:Accession: B01427
A:Molecule type: protein
A:Residues: 1-11 <BOB>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803; PMID:7297679
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical stru
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h
malian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuro
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #st

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

```

Db 1 QP 2

RESULT 73

YHBO

morphogenetic neuropeptide - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C:Accession: Col427; A01427
 R:Bodenmuller, H.; Schaller, H.C.
 Nature 293, 579-580, 1981
 A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coelestis
 A:Reference number: A93266; MUID:82035850; PMID:7290191
 A:Accession: Col427

A:Molecule type: protein
 A:Residues: 1-11 <SCH>
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679
 A:Contents: annotation; synthesis
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
 C:Superfamily: unassigned animal peptides
 C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropeptide
 F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4

| |

Db 1 QP 2

RESULT 74

YHXA

morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)
 N:Alternate names: head activator
 C:Species: Anthopleura elegantissima
 C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C:Accession: A93900; A01427
 R:Schaller, H.C.; Bodenmuller, H.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
 A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
 A:Reference number: A93900

A:Accession: A93900
 A:Molecule type: protein
 A:Residues: 1-11 <SCH>
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
 C:Superfamily: unassigned animal peptides
 C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4

| |

Db 1 QP 2

RESULT 75

YHBY

morphogenetic neuropeptide - Hydra attenuata
 N:Alternate names: head activator
 C:Species: Hydra attenuata
 C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
 C:Accession: B93900; A01427
 R:Schaller, H.C.; Bodenmuller, H.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
 A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
 A:Reference number: A93900

A:Accession: B93900
 A:Molecule type: protein
 A:Residues: 1-11 <SCH>
 R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
 FEBS Lett. 131, 317-321, 1981
 A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
 A:Reference number: A91296; MUID:82050803; PMID:7297679

A:Contents: annotation; synthesis
 A:Note: the synthetic peptide was identical with the natural peptide in chemical structure
 C:Comment: This peptide was first isolated from nerve cells of hydra and was called head activator
 C:Superfamily: unassigned animal peptides
 C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 50.0%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
 | |
 Db 1 QP 2

Search completed: November 25, 2003, 18:28:20
 Job time : 3.68085 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:02:54 ; Search time 1.93617 Seconds
(without alignments)
97.154 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	100.0	9	1	RT33_BOVIN
2	3	75.0	9	1	COXE_THUOB
3	2	50.0	4	1	BOSI_HUMAN
4	2	50.0	7	1	LANC_CARUI
5	2	50.0	7	1	UHL1_RAT
6	2	50.0	8	1	NPB_BOVIN
7	2	50.0	8	1	UF06_MOUSE
8	2	50.0	9	1	AL10_CARMA
9	2	50.0	9	1	D1_NEPNO
10	2	50.0	9	1	FAR3_PENNO
11	2	50.0	9	1	FAR4_PENNO
12	2	50.0	9	1	FRF1_SARBU
13	2	50.0	9	1	LMT3_LOCOMI
14	2	50.0	9	1	LPCA_STAAU
15	2	50.0	10	1	CATB_SHEEP
16	2	50.0	10	1	FAR6_PANRE
17	2	50.0	10	1	GONI_ALLMI
18	2	50.0	10	1	PORB_METTM
19	2	50.0	10	1	SVK_CAMUP
20	2	50.0	10	1	UPA4_HUMAN
21	2	50.0	10	1	UPA5_HUMAN
22	2	50.0	10	1	URA6_HUMAN
23	2	50.0	11	1	LSK1_LEUNA
24	2	50.0	11	1	LSKP_PERAM
25	2	50.0	11	1	MORN_HUMAN
26	2	50.0	11	1	TKN1_PSEGU
27	2	50.0	11	1	TKN1_UPERU
28	2	50.0	11	1	TKN2_PSEGU
29	2	50.0	11	1	TKN3_PSEGU
30	2	50.0	11	1	TKN4_PSEGU
31	2	50.0	11	1	TKN5_PSEGU
32	2	50.0	11	1	TKN5_ELEMO
33	2	50.0	12	1	CALM_TETTH

Q05055 tetrahymena

34	2	50.0	12	1	FARI_CALVO
35	2	50.0	12	1	FIFI_SARBU
36	2	50.0	12	1	H59A_RAT
37	2	50.0	12	1	UR2_POLSP
38	2	50.0	13	1	ACT7_SOYBN
39	2	50.0	13	1	CPI_APLCA
40	2	50.0	13	1	CRTC_BOVIN
41	2	50.0	13	1	ECDE_LYMDI
42	2	50.0	13	1	ET22_LITRU
43	2	50.0	13	1	EP65_HUMAN
44	2	50.0	13	1	FARB_ASCSU
45	2	50.0	13	1	PEDI_HYDAT
46	2	50.0	13	1	PSAE_PEA
47	2	50.0	13	1	UHA3_CANPA
48	2	50.0	14	1	ATP6_SPIOL
49	2	50.0	14	1	MARI_ALTSP
50	2	50.0	14	1	NSK2_SARBU
51	2	50.0	14	1	PKK6_PERAM
52	2	50.0	14	1	TAT_HV128
53	2	50.0	14	1	TAT_HV128
54	2	50.0	15	1	APF3_MALPA
55	2	50.0	15	1	ARCA_STRPS
56	2	50.0	15	1	CHI1_PEA
57	2	50.0	15	1	IRBP_CRISP
58	2	50.0	15	1	LEC2_PSOSC
59	2	50.0	15	1	MM01_RAT
60	2	50.0	15	1	PGKH_PHYPA
61	2	50.0	15	1	PGTS_PELAC
62	2	50.0	15	1	RBS_PHYPA
63	2	50.0	15	1	RS20_BACST
64	2	50.0	15	1	RT32_BOVIN
65	2	50.0	15	1	UC13_WAIZE
66	2	50.0	15	1	UC27_WAIZE
67	2	50.0	15	1	UN01_PINPS
68	2	50.0	15	1	URE2_MORMO
69	2	50.0	16	1	BRB_BASAL
70	2	50.0	16	1	FIBA_EQUAS
71	2	50.0	16	1	FIBA_MEIME
72	2	50.0	16	1	FIBA_MUSVI
73	2	50.0	16	1	HTPG_ACICA
74	2	50.0	16	1	IBP4_PIG
75	2	50.0	16	1	LPK1_LOCOMI
76	2	50.0	17	1	ACT6_SOYBN
77	2	50.0	17	1	PH4_PERAM
78	2	50.0	17	1	PSBL_SXNVU
79	2	50.0	17	1	RM35_YEAST
80	2	50.0	17	1	TPIS_PINPS
81	2	50.0	17	1	UN15_CLOPA
82	2	50.0	18	1	A2M_OCTVU
83	2	50.0	18	1	AGI_EUPCH
84	2	50.0	18	1	ALL2_CVDPO
85	2	50.0	18	1	D7AL_ACASC
86	2	50.0	18	1	DRPH_UCAPU
87	2	50.0	18	1	LCTN_LAMGL
88	2	50.0	18	1	LUXB_KRYAS
89	2	50.0	18	1	RL24_SERMA
90	2	50.0	19	1	ADC_CLOPA
91	2	50.0	19	1	AL22_HORSE
92	2	50.0	19	1	ETFA_CLOPA
93	2	50.0	19	1	FIBA_CERNI
94	2	50.0	19	1	IRBP_CAVPO
95	2	50.0	19	1	LPRM_STAAU
96	2	50.0	19	1	RL10_CITFR
97	2	50.0	20	1	TPIS_CLOPA
98	2	50.0	20	1	ALBG_EQUAS
99	2	50.0	20	1	COGC_PARCM
100	2	50.0	20	1	COXE_THUOB

ALIGNMENTS

RESULT 1

```

RT33_BOVIN
ID RT33_BOVIN STANDARD; PRT; 9 AA.
AC P82926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Fragment).
GN MRPS33.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C. Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1032 MW; D341D73776DB05B9 CRC64;

Query Match 100.0%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 4
Db 3 SEQ 6

RESULT 2
COXE_THUOB
ID COXE_THUOB STANDARD; PRT; 9 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide Via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8241;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310366;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver";
RL Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) = 4 ferriocytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR; S77984; S77984.
DR InterPro; IPR001349; COX6A.
DR PROSITE; PS01329; COX6A; PARTIAL.
KW Cytochrome oxidase; Inner membrane; Mitochondrion.
FT NON_TER 1 1

```

```

FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

Query Match 75.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 2 EQP 4

RESULT 3
EOSI_HUMAN
ID EOSI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Eosinophilic peptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -!- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR GO; GO:0030105; P:anaphylaxis; IDA.
DR GO; GO:0006935; P:chemotaxis; IDA.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 3 SE 4

RESULT 4
LANC_CARUI
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin U149 (Fragment).
OS Carnobacterium sp. (strain U149).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).

```

CC ACTIVE ON GRAM-POSITIVE BACTERIA.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON TER 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
2 SE 3

Db

RESULT 5
UH11_RAT
ID UH11_RAT STANDARD; PRT; 7 AA.
AC P65576;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Histar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RL Jungblut P.R.;
RA Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5, ITS MW IS: 42 kDa.
FT UNSURE 2 2 OR A.
FT NON_TER 7
SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5ACB0 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
||
5 EQ 6

Db

RESULT 6
NPB_BOVIN
ID NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067995; PubMed=3865193;
RY Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
||
4 QP 5

Db

RESULT 7
UF06_MOUSE
ID UF06_MOUSE STANDARD; PRT; 8 AA.
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
FT NON_TER 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
||
2 SE 3

Db

RESULT 8
AL10_CARMA
ID AL10_CARMA STANDARD; PRT; 9 AA.
AC P81813;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
 ||
 Db 3 QP 4

RESULT 9
 DI_NEPNO
 ID DI_NEPNO STANDARD; PRT; 9 AA.
 AC P24816;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE Gastrin/cholecystokinin-like peptide DI.
 OS Nephrops norvegicus (Norway lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Nephrops.
 OC NCBI_TaxID=6929;
 RN [1]
 RN SEQUENCE.
 RP TISSUE=Stomach;
 RC MEDLINE=92082847; PubMed=1747388;
 RA Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;
 RT "Structure and biological activity of crustacean gastrointestinal
 peptides identified with antibodies to gastrin/cholecystokinin";
 RL Biochimie 73:1233-1239(1991).
 CC -!- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PIR; S47432; S47432.
 KW Hormone.
 SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
 ||
 Db 1 SE 2

RESULT 10
 FAR3_PENMO
 ID FAR3_PENMO STANDARD; PRT; 9 AA.
 AC P83318;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP3 (AQPSMRLRF-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OC NCBI_TaxID=6687;
 RN [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RP TISSUE=Eyestalk;
 RC MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn Penaeus monodon.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
 ||
 Db 2 QP 3

RESULT 11
 FAR4_PENMO
 ID FAR4_PENMO STANDARD; PRT; 9 AA.
 AC P83319;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP4 (SQPSMRLRF-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OC NCBI_TaxID=6687;
 RN [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RP TISSUE=Eyestalk;
 RC MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn Penaeus monodon.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
 ||
 Db 2 QP 3

RESULT 12
 FRF1_SARBU
 ID FRF1_SARBU STANDARD; PRT; 9 AA.
 AC P83350;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FMRFamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OC NCBI_TaxID=7385;
 RN [1]
 RN SEQUENCE, AMIDATION, AND FUNCTION.
 RP TISSUE=CNS;
 RC MEDLINE=23342733; PubMed=12438685;
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
 RT "Identification in Drosophila melanogaster of the invertebrate G
 protein-coupled FMRFamide receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular

```

CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRP/AMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
KW MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1155 MW; 2DB10699CAB6C5A7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 13
LMT3_LOGMI
ID LMT3 LOGMI STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytotropin 3 (LOM-WT-3).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytotropin III and
RT IV, two additional neuropeptides of Locusta migratoria: members of the
RT locustamytotropin peptide family.";
RT Locustamytotropin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A61620; A61620.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 3 QP 4

RESULT 14
LPCA-STAAU
ID LPCA STAAU STANDARD; PRT; 9 AA.
AC P36884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OS Streptococcus agalactiae.
OG Plasmid pSCS6, Plasmid pSCS7, Plasmid PUB112, and Plasmid pIP501.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=436; PLASMID=pSCS7;
RX MEDLINE=92021652; PubMed=1929326;
RA Schwarz S., Cardoso M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
RT aureus.";
RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; PLASMID=pSCS6;
RX MEDLINE=92388047; PubMed=1517170;
RA Cardoso M., Schwarz S.;
RT "Nucleotide sequence and structural relationships of a
RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
RT Staphylococcus aureus.";
RL J. Appl. Bacteriol. 72:289-293(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; PLASMID=pUB112;
RX MEDLINE=86081739; PubMed=3865770;
RA Brueckner R., Matzura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
RT of the Staphylococcus aureus plasmid PUB112.";
RL EMBO J. 4:2295-2300(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.agalactiae; PLASMID=pIP501;
RX MEDLINE=93096867; PubMed=1461942;
RA Trieu-Cuot P., de Cespedes G., Haraud T.;
RT "Nucleotide sequence of the chloramphenicol resistance determinant of
RT the streptococcal plasmid pIP501.";
RL Plasmid 28:272-276(1992).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M58515; AAA26612.1; -
CC EMBL; M58516; AAA16528.1; -
CC EMBL; X02872; CAA26630.1; -
CC EMBL; X60827; CAA43217.1; -
CC EMBL; X65462; CAA46454.1; -
CC PIR; B24362; B24362.
CC PIR; S30494; S30494.
KW Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 9 AA; 1074 MW; 5D9CAB5AAB05B333 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 4 SE 5

RESULT 15
CATB-SHEEP
ID CATB SHEEP STANDARD; PRT; 10 AA.
AC P83205;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
GN CTSB.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

```

Wed Nov 26 09:06:32 2003

```
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN SEQUENCE.
RP
RC TISSUE=Placenta;
RX MEDLINE=22394055; PubMed=12506352;
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
RA Mboko H.B., Beckers J.-F.M.P.;
RT "Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.";
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides.
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro; IPR000169; Shprot_acsite.
DR PROSITE; PS00640; THIOL PROTEASE ASN; PARTIAL.
DR PROSITE; PS00139; THIOL PROTEASE CYS; PARTIAL.
DR PROSITE; PS00639; THIOL PROTEASE HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 50.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 9 EQ 10

RESULT 16
FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRamide-like neuropptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRamide-related
RT peptides (FaRs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: MYOACTIVE.
CC -!- SIMILARITY: BELONGS TO THE FAP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 50.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 5 QP 6

RESULT 17
GONI_ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)
DE (Luliberin I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1882082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR InterPro; IPR002012; GnRH.
DR PIR; A60066; RHAQ1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 8 QP 9

RESULT 18
PORB_METTM STANDARD; PRT; 10 AA.
AC P80901;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase
DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)
DE (Fragment).
GN PORB
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE
RX MEDLINE=97261844; PubMed=9108258;
RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases
RT in Methanobacterium thermoautotrophicum.";
RL Eur. J. Biochem. 244:862-868(1997).
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC GAMMA CHAIN.
CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature
CC of 80 degrees Celsius.
```


KW Oxidoreductase.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EQ 3
 Db ||
 5 EQ 6

RESULT 19
 SYK CAMUP STANDARD; PRT; 10 AA.
 AC Q46464;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS) (Fragment)
 GN LYSS.
 OS Campylobacter upsaliensis.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=28080;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 43954;
 RX MEDLINE=97149302; PubMed=8996110;
 RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
 RT "Characterization of Campylobacter upsaliensis fur and its
 RT localization in a highly conserved region of the Campylobacter
 RT genome";
 RL Gene 183:219-224(1996).
 CC -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
 CC + L-lysyl-tRNA(Lys).
 CC -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to Class-II aminoacyl-tRNA synthetase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L77076; AAB41342.1; -.
 DR HAMAP; MF_00252; -; 1.
 DR InterPro; IPR006195; tRNA ligase II.
 DR PROSITE; PS50862; AA_TRNA_LIGASE-II; PARTIAL.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; Magnesium.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SE 2
 Db ||
 3 SE 4

RESULT 20
 UP44 HUMAN STANDARD; PRT; 10 AA.
 ID UP44 HUMAN
 AC P30090;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30091; HUMAN.
 FT NON_TER 1
 FT VARIANT 9 9 G -> Y.
 FT /FTId=VAR_000002.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.8, ITS MW IS: 40.5 kDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30090; HUMAN.
 FT NON_TER 1
 FT UNSURE 4 4
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SE 2
 Db ||
 6 SE 7

RESULT 21
 UP45 HUMAN STANDARD; PRT; 10 AA.
 ID UP45 HUMAN
 AC P30091;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.;
 RT "Plasma protein map: an update by microsequencing";
 RL Electrophoresis 13:707-714(1992).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
 CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
 CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
 CC PROTEIN.
 DR SWISS-2DPAGE; P30091; HUMAN.
 FT NON_TER 1
 FT VARIANT 9 9 G -> Y.
 FT /FTId=VAR_000002.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 3 QP 4

RESULT 22
URAG HUMAN STANDARD; PRT; 10 AA.
AC P32080;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of red blood cells (Spot 17) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Erythrocyte; PubMed=8313871;
RX MEDLINE=94147970; Fruiger S., Paquet M., Bairoch A.,
RA Golaz O., Hughes G.J., Tassot J.-D., Appel R.D., Walzer C.,
RA Pasquali C., Sanchez J.-C., Tassot J.-D., Appel R.D., Walzer C.,
RA Baalant L., Hochstrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
RL Electrophoresis 14:1223-1231(1993).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P32080; HUMAN.
FT NON TER 10
SQ SEQUENCE 10 AA; 965 MW; 63DDC8D9GAE1EDDB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 23
LSK1 LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Leucosulfakinin-I (LSK-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -!- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF
CC THE COCKROACH HINGUT. INHIBITS MUSCLE CONTRACTION OF HINDGUT.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
CC PIR; A01622; GNROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 1 EQ 2

RESULT 24
LSKP PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CKK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -!- FUNCTION: STIMULATES HINDGUT CONTRACTIONS.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 1 EQ 2

RESULT 25
MORN HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human).
OS Rattus norvegicus (Rat).
OS Bos taurus (Bovine).
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).

RN [2]
 RP SEQUENCE.
 RC SPECIES=A.elegantissima, and H.attenuata;
 RA Schaller H.C., Bodenmuller H.;
 RT "Isolation and amino acid sequence of a morphogenetic peptide from hydra.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
 RN [3]
 RP SYNTHESIS.
 RX MEDLINE=82050803; PubMed=7297679;
 RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
 RT "Synthesis of a new neuropeptide, the head activator from hydra.";
 RL FEBS Lett. 131:317-321(1981).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=90059923; PubMed=2583101;
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells in the G2/mitosis transition.";
 RL EMBO J. 8:3311-3318(1989).
 CC -!- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS IN THE G2/MITOSIS TRANSITION.
 CC -!- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
 DR PIR; A01427; YHRT.
 DR PIR; A33900; YHXA.
 DR PIR; B01427; YHHU.
 DR PIR; B93900; YHJPHY.
 DR PIR; C01427; YHBO.
 DR GK; P01163; --
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

 Query Match 50.0%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;
 QY 3 QP 4
 Db 1 QP 2

 RESULT 26
 TKN1_PSEGU STANDARD; PRT; 11 AA.
 AC P42986;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DE Kassinin-like peptide K-I (PG-KI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae; Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F., Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; B60409; B60409.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1269 MW; 3DEA7C37C9CB1AB7 CRC64;

 Query Match 50.0%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;
 QY 3 QP 4
 Db 1 QP 2

 RESULT 27
 TKN1_UPERU STANDARD; PRT; 11 AA.
 AC P08612;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperolein.
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae; Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Eudean R.;
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR InterPro; IPR003580; Protachykinin.
 DR InterPro; IPR002040; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

 Query Match 50.0%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;
 QY 3 QP 4
 Db 1 QP 2

 RESULT 28
 TKN2_PSEGU STANDARD; PRT; 11 AA.
 ID TKN2_PSEGU

P42987;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 CC Myobatrachinae; Pseudophryne.
 CC NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.,
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; C60409; C60409.
 DR InterPro; IPR003580; Protachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 CC Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 1 1
 FT MOD_RES 11 11
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QP 4
 Db 1 QP 2

RESULT 29
 TKN3_PSEGU
 ID TKN3_PSEGU STANDARD; PRT; 11 AA.
 AC P42988;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-III (PG-KIII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 CC Myobatrachinae; Pseudophryne.
 CC NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.,
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; D60409; D60409.
 DR InterPro; IPR003580; Protachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 CC Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 1 1
 FT MOD_RES 11 11
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1268 MW; 3DEA7C37C9CB1457 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QP 4
 Db 1 QP 2

RESULT 30
 TKN4_PSEGU
 ID TKN4_PSEGU STANDARD; PRT; 11 AA.
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide I (PG-SP1).
 OS Pseudophryne guentheri (Guenther's toadlet).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 CC Myobatrachinae; Pseudophryne.
 CC NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.,
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR; E60409; E60409.
 DR InterPro; IPR003580; Protachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 CC Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 1 1
 FT MOD_RES 11 11
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;
 Query Match 50.0%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 QP 4
 Db 1 QP 2

```
RESULT 31
TKN5_PSEGU          STANDARD;          PRT;          11 AA.
ID  TKN5_PSEGU          STANDARD;          PRT;          11 AA.
AC  P42990;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Substance P-like peptide II (PG-SPII).
OS  Pseudophryne guentheri (Guenther's toadlet).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC  Myobatrachinae; Pseudophryne.
OX  NCBI_TaxID=30349;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Skin secretion;
RX  MEDLINE=90287814; PubMed=2356157;
RA  Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA  Roberts J.D., Melchiorri P., Erspamer V.;
RT  "Six novel tachykinin- and bombesin-related peptides from the skin of
RT  the Australian frog Pseudophryne guntheri.",
RL  Peptides 11:299-304 (1990).
CC  -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC  EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC  SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC  MUSCLES.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
CC  -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR  PIR; F60409; F60409.
DR  InterPro; IPR003580; Protachykinin.
DR  InterPro; IPR002040; Tachykinin.
DR  Pfam; PF02202; Tachykinin; 1.
DR  SMART; SM00203; TK; 1.
DR  PROSITE; PS00267; TACHYKININ; 1.
KW  Amphibian defense peptide; tachykinin; Neuropeptide; Amidation;
KW  Pyrrolidone carboxylic acid.
FT  MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT  MOD_RES 11 11 AMIDATION.
SQ  SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 32
TKN_ELEMO          STANDARD;          PRT;          11 AA.
ID  TKN_ELEMO          STANDARD;          PRT;          11 AA.
AC  F01293;
DT  21-JUL-1986 (Rel. 01, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Eledoisin.
OS  Eledone moschata (Musk octopus) (Ozaena moschata), and
OS  Eledone cirrhosa (Curled octopus) (Ozaena cirrhosa).
OC  Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC  Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
OX  NCBI_TaxID=6641, 102876;
RN  [1]
RP  SEQUENCE.
RA  Anastasi A., Erspamer V.;
RT  "The isolation and amino acid sequence of eledoisin, the active
RT  endecapeptide of the posterior salivary glands of Eledone.",
RL  Arch. Biochem. Biophys. 101:56-65 (1963).
CC  -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC  EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC  SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
```

```
CC  MUSCLES.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- TISSUE SPECIFICITY: Skin.
CC  -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR  PIR; B01561; E00CC.
DR  PDB; 1MXQ; 18-FEB-03.
DR  InterPro; IPR002040; Tachykinin.
DR  PROSITE; PS00267; TACHYKININ; 1.
KW  Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
KW  3D-structure.
FT  MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT  MOD_RES 11 11 AMIDATION.
SQ  SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 33
CALM_TETTH          STANDARD;          PRT;          12 AA.
ID  CALM_TETTH          STANDARD;          PRT;          12 AA.
AC  Q05055;
DT  01-FEB-1994 (Rel. 28, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Calmodulin (Fragment).
OS  Tetrahymena thermophila.
OC  Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC  Tetrahymenina; Tetrahymena.
OX  NCBI_TaxID=5911;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=93281388; PubMed=8506136;
RA  Katoh M., Hirono M., Takemasa T., Kimura M., Watanabe Y.;
RT  "A microtubule-specific sequence exists in the 5'-upstream region of
RT  calmodulin gene in Tetrahymena thermophila.",
RL  Nucleic Acids Res. 21:2409-2414 (1993).
CC  -!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
CC  ENZYMES BY CA(++) . AMONG THE ENZYMES TO BE STIMULATED BY THE
CC  CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
CC  PHOSPHATASES.
CC  -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
CC  SITES.
CC  -!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  EMBL; D12774; BAA02239.1; -.
DR  InterPro; IPR002048; EF-hand.
DR  PROSITE; PS00018; EF_HAND; PARTIAL.
KW  Calcium-binding; Repeat; Acetylation.
FT  INIT_MET 0 0 BY SIMILARITY.
FT  MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT  NON_TER 12 12
SQ  SEQUENCE 12 AA; 1393 MW; 83F31CD443DB1B01 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
```

7 EQ 8

Query Match 50.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 4 QP 5

RESULT 34

FARI-CALVO STANDARD; PRT; 12 AA.
AC P41869;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Calliphora vomitoria (Blue blowfly).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Jonsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; E44787; E44787.
KW Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1390 MW; 2DDDB316914AB5A7 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 4 QP 5

RESULT 35

FIF1-SARBU STANDARD; PRT; 12 AA.
AC P83349;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neb-FIRFamide 1.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AMIDATION, AND FUNCTION.
RC TISSUE-CNS;
RX MEDLINE=22342733; PubMed=12438685;
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 12 12
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;

RESULT 36

HS9A-RAT STANDARD; PRT; 12 AA.
ID HS9A-RAT
AC P82995;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heat shock protein HSP 90-alpha (Fragment).
GN HSPCA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=21589773; PubMed=11732320;
RA Langer T., Fasold H.;
RT "Isolation and quantification of the heat shock protein 90 alpha and
RT beta isoforms from rat liver.";
RL Proteoloma 218:54-56(2001).
CC -!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.

DR InterPro; IPR001404; Hsp90.
DR PROSITE; PS00298; HSP90; PARTIAL.
KW Chaperone; ATP-binding; Heat shock; Phosphorylation.
FT MOD_RES 4 4
FT MOD_RES 6 6
FT MOD_RES 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; DE47C322CAB6C1B6 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 9 QP 10

RESULT 37

UR2-POLSP STANDARD; PRT; 12 AA.
ID UR2-POLSP
AC P81022;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II (U-II) (UII).
OS Polyodon spathula (North American paddlefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;
OC Polyodon.
OX NCBI_TaxID=7913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=96051494; PubMed=8536944;
RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;

```

RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon
RT spathula).";
RL Gen. Comp. Endocrinol. 99:323-332(1995).
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
CC -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW HORMONE.
FT DISULFID 6 11 BY SIMILARITY.
SQ SEQUENCE 12 AA; 1410 MW; 7551E9DBB879CEBB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 4 SE 5

RESULT 38
ACT7_SOYBN ID ACT7_SOYBN STANDARD; PRT; 13 AA.
AC P15987;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin 7 (Fragment).
GN SACT7.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wayne;
RX MEDLINE=91346640; PubMed=2102831;
RA Pearson L., Meagher R.B.;
RT "Diverse soybean actin transcripts contain a large intron in the 5'
RT untranslated leader: structural similarity to vertebrate muscle actin
RT genes.";
RL Plant Mol. Biol. 14:513-526(1990).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS.
CC -!- FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN
CC IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION,
CC CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.
CC -!- SIMILARITY: Belongs to the actin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X17120; CAA34980.1; --
CC FIR; S15755; S15755.
CC InterPro; IPR004001; Actin.
CC InterPro; IPR004000; Actin like.
CC PROSITE; PS00406; ACTINS 1; PARTIAL.
CC PROSITE; PS00432; ACTINS 2; PARTIAL.
CC PROSITE; PS01132; ACTINS_ACT-LIKE; PARTIAL.
KW Structural protein; Multigene family.

```

```

FT NON TER 13 13
SQ SEQUENCE 13 AA; 1420 MW; 8BEFF3C36D4FD05A CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 8 QP 9

RESULT 39
CPI_APLCA ID CPI_APLCA STANDARD; PRT; 13 AA.
AC Q10598;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Cerebral peptide 1 (CPI)
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=97001771; PubMed=8844763;
RA Phares G.A., Lloyd P.E.;
RT "Purification, primary structure, and neuronal localization of
RT cerebral peptide 1 from Aplysia.";
RL Peptides 17:753-761(1996).
CC -!- FUNCTION: MAY FUNCTION AS A PEPTIDE TRANSMITTER.
CC -!- TISSUE SPECIFICITY: FOUND PREDOMINANTLY IN THE CEREBRAL AND PEDAL
CC GANGLIA.
SQ SEQUENCE 13 AA; 1314 MW; 9DBC3CE82C667B05 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 6 SE 7

RESULT 40
CRTC_BOVIN ID CRTC_BOVIN STANDARD; PRT; 13 AA.
AC P28489;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin (CRP55) (Calregulin) (HACBP) (ERP60) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RT reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).
CC -!- FUNCTION: THIS PROTEIN BINDS CALCIUM. THERE ARE BOTH HIGH AND
CC LOW AFFINITY CALCIUM-BINDING SITES.
CC -!- SUBUNIT: Monomer (By similarity).

```

```

CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CALRETICULIN FAMILY.
DR PIR; A33208; A33208.
DR InterPro; IPR001580; Calreticulin.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
KW Endoplasmic reticulum; Calcium-binding.
FT NON TER 13
SQ SEQUENCE 13 AA; 1557 MW; C85DDA6993CA1339 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 8 EQ 9

RESULT 41
ECDE LYMDI STANDARD; PRT; 13 AA.
AC P80941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Testis ecdysiotropin peptide E (TE).
OS Lymantria dispar (Gypsy moth).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;
OC Lymantriidae; Lymantria.
OX NCBI_TaxID=13123;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=97387807; PubMed=9243792;
RA Loeb M.J., Wagner R.M., Woods C.W., Gelman D.G., Harrison D.,
RA Bell R.A.;
RT "Naturally occurring analogs of Lymantria testis ecdysiotropin, a
RT gonadotropin isolated from brains of Lymantria dispar pupae.";
RL Arch. Insect Biochem. Physiol. 36:37-50(1997).
CC -1- FUNCTION: STIMULATES SYNTHESIS OF ECDYSTEROID IN THE TESTES
CC OF LARVAE AND PUPAE.
SQ SEQUENCE 13 AA; 1357 MW; 1841B4CA3275B764 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 12 SE 13

RESULT 42
EI22 LITRU STANDARD; PRT; 13 AA.
ID EI22 LITRU
AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog

```

```

RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1598 MW; C1808EF3B357322 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 9 QP 10

RESULT 43
EP65 HUMAN STANDARD; PRT; 13 AA.
ID EP65 HUMAN
AC P54963;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Erythrocyte 65 kDa protein (P65) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE. AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=9004678; PubMed=2507249;
RA Hart G.W., Hailtweiger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins.";
RL Ciba Found. Symp. 145:102-118(1989).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
DR GO; GO:0005737; Cytoplasm; NAS.
KW Glycoprotein.
FT NON TER 1 1
FT CARBOHYD 2 2 O-LINKED (GLCNAC).
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1300 MW; D0B873344C61A776 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 6 QP 7

RESULT 44
FARB ASCSU STANDARD; PRT; 13 AA.
ID FARB ASCSU
AC P43173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF11.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

```



```

CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D6886B05 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 6 SE 7

RESULT 45
PEDI_HYDAT
ID PEDI_HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroidea; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RX MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris."
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 12 SE 13

RESULT 46
PSAE_PEA
ID PSAE_PEA STANDARD; PRT; 13 AA.
AC P20118;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit IV (PSI-E) (Photosystem I 13 kDa
DE protein) (Fragment).
DE PSAE.
GN Pisum
CN Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE.
RX MEDLINE=88137587; PubMed=3277857;
RA Dunn P.P.J., Packman L.C., Pappin D., Gray J.C.;
RT "N-terminal amino acid sequence analysis of the subunits of pea
RT photosystem I."
RL FEBS Lett. 228:157-161(1988).
CC -!- FUNCTION: Stabilizes the interaction between psaC and the PSI
CC core, assists the docking of the ferredoxin to PSI and interacts
CC with ferredoxin-NADP oxidoreductase (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.

```

```

CC -!- SIMILARITY: BELONGS TO THE PSAE FAMILY.
DR PIR; S00316; S00316.
KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1190 MW; D895A63A52D8DB1D CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 47
UHA3_CANFA
ID UHA3_CANFA STANDARD; PRT; 13 AA.
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX TISSUE=Heart;
CC MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins."
RL Electrophoresis 18:2795-2802(1997).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.9, ITS MW IS: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 50.0%; Score 2; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 12 SE 13

RESULT 48
ATP6_SPIOL
ID ATP6_SPIOL STANDARD; PRT; 14 AA.
AC P80086;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP synthase A chain (BC 3.6.3.14) (Protein 6) (Fragment).
GN ATP6.
CN Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX STRAIN=cv. Medania; TISSUE=Leaf mesophyll;
RA MEDLINE=92209531; PubMed=1313368;
RA Hamasur B., Glaser E.;
RT "Plant mitochondrial POF1 ATP synthase. Identification of the
RT individual subunits and properties of the purified spinach leaf
RT mitochondrial ATP synthase."

```

```

RL Eur. J. Biochem. 205:409-416(1992).
CC -1- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A
CC DIRECT ROLE IN THE TRANSLLOCATION OF PROTONS ACROSS THE MEMBRANE.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS. CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
DR PIR; S21247; S21247.
DR InterPro; IPR000568; ATPsynt_Asub.
DR PROSITE; PS00449; ATPASE_A; PARTIAL.
KW Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.
FT NON TER 14
FT SEQUENCE 14 AA; 1619 MW; 9F1D60181FC1PF45 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 4 EQ 5

RESULT 49
MARI ALTSP
ID MARI ALTSP STANDARD; PRT; 14 AA.
AC P2939;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Marinosstatin C-2 [Marinosstatin C-1; Marinosstatin D].
OS Alteromonas sp. (strain B-10-31).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadales; Alteromonas.
OX NCBI_TaxID=29456;
RN [1]
RP SEQUENCE, AND ACTIVE SITE.
RX MEDLINE=92176155; PubMed=1794974;
RA Takano R., Imada C., Kamei K., Hara S.;
RT "The reactive site of marinosstatin, a proteinase inhibitor from
RT marine Alteromonas sp. B-10-31."
RN J. Biochem. 110:856-858(1991).
CC -1- FUNCTION: INHIBITS SUBTILISIN, CHYMOTRYPSIN, AND ELASTASE, BUT
CC NOT TRYPSIN.
KW Serine protease inhibitor; Pyrrolidone carboxylic acid.
FT PEPTIDE 1 14
FT PEPTIDE 3 14 MARINOSTATIN C-2.
FT PEPTIDE 4 14 MARINOSTATIN D.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT SITE 6 7 REACTIVE BOND.
FT SEQUENCE 14 AA; 1644 MW; 6E7CEE92EF32E44 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 13 SE 14

RESULT 50
NSK2_SARBU
ID NSK2_SARBU STANDARD; PRT; 14 AA.
AC P41493;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-FEB-1996 (Rel. 33, Last annotation update)
DE Neosulfakinin-II (NEB-SK-II).

```

```

OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata."
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: MYOTROPIC PEPTIDE.
CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A56632; A56632.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN_1.
KW Neuropeptide; Amidation; Sulfation.
FT MOD RES 9 9 SULFATION (POTENTIAL).
FT MOD RES 14 14 AMIDATION (POTENTIAL).
FT SEQUENCE 14 AA; 1794 MW; 8B4E06D5B61C62AA CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 4 EQ 5

RESULT 51
PPK6_PERAM
ID PPK6_PERAM STANDARD; PRT; 14 AA.
AC P82693;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-6 (Pea-PK-6) (FXPRIL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRILamides in the nervous system of
RT the American cockroach."
RN J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.
CC -1- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN
CC ABDOMINAL PERISYPHATHETIC ORGANS.
CC -1- MASS SPECTROMETRY: MW=1590.8; METHOD=NALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro; IPR001484; Pyrokinnin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Amidation; Pyrokinnin.
FT MOD RES 14 14 AMIDATION.
FT SEQUENCE 14 AA; 1592 MW; 3966CC3FF384A998 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 1 SE 2

```

```
RESULT 52
TAT_HV1W2      STANDARD;      PRT;      14 AA.
ID  P12509;
AC
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
RT at risk for AIDS."
RL Science 232:1548-1553(1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12507; AAB12991.1; -
DR HIV; M12507; TAT5WMJ2
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BF6F67AA8 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 4 QP 5

RESULT 53
TAT_HV1W2      STANDARD;      PRT;      14 AA.
ID  P12511;
AC
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11681;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86281278; PubMed=3395517;
RA Yorno J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1."
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M12507; AAB12991.1; -
DR HIV; M12507; TAT5WMJ2
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1467 MW; 37CC737BF6F67AA8 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 4 QP 5

RESULT 54
APP3_MALPA     STANDARD;      PRT;      15 AA.
ID  P83137;
AC
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 3 (CW-3) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed.
RX MEDLINE=21199399; PubMed=11302747;
RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT "Purification and characterization of three antifungal proteins from
RT Cheeseweed (Malva parviflora).";
RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not F.graminearum.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
CC GO; GO:0003799; F:antifungal peptide activity; IDA.
CC GO; GO:0007275; P:development; NAS.
CC Fungicide; Antibiotic.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 11 EQ 12
```

```
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J03653; AAA44685.1; -
DR HIV; J03653; TAT$JVI1.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 4 QP 5

RESULT 54
APP3_MALPA     STANDARD;      PRT;      15 AA.
ID  P83137;
AC
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 3 (CW-3) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed.
RX MEDLINE=21199399; PubMed=11302747;
RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT "Purification and characterization of three antifungal proteins from
RT Cheeseweed (Malva parviflora).";
RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not F.graminearum.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
CC GO; GO:0003799; F:antifungal peptide activity; IDA.
CC GO; GO:0007275; P:development; NAS.
CC Fungicide; Antibiotic.
FT NON TER 15 15
SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 11 EQ 12
```

```

RESULT 55
ARCA_STRPS
ID ARCA_STRP5 STANDARD; PRT; 15 AA.
AC P58827;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD)
DE (Streptococcus acid glycoprotein) (Fragment).
GN ARCA OR SAGP.
OS Streptococcus pyogenes (serotype M5).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=160491;
RN [1]
RP SEQUENCE AND CHARACTERIZATION.
RC STRAIN=Manfredo / Serotype M5;
RX MEDLINE=98298018; PubMed=9632565;
RA Degan B.A., Palmer J.M., Robson T., Jones C.E.D., Fischer M.,
RA Glanville M., Mellor G.D., Diamond A.G., Kehoe M.A., Goodacre J.A.;
RT "Inhibition of human peripheral blood mononuclear cell proliferation
RT by Streptococcus pyogenes cell extract is associated with arginine
RT deiminase activity";
RL Infect. Immun. 66:3050-3058(1998).
CC -!- FUNCTION: Antitumor protein. Has a powerful and dose-dependent
CC inhibitory effect on antigen, superantigen, or mitogen-stimulated
CC human peripheral blood mononuclear cell (PBMC) proliferation. It
CC may inhibit cell proliferation by arresting cell cycle and
CC inducing apoptosis.
CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the arginine deiminase family.
DR HAMAP: MF_00242; -; 1.
KW Hydrolase; Arginine metabolism; Glycoprotein.
FT INIT MET 0
FT NON TER 15
SQ SEQUENCE 15 AA; 1657 MW; D21150201B00EE46 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 10 SE 11

RESULT 56
CHIL_PEA
ID CHIL_PEA STANDARD; PRT; 15 AA.
AC P21225;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endochitinase A1 (EC 3.2.1.14) (Fragment).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Birte; TISSUE=Leaf;
RA Vad K., Mikkelsen J.D., Collinge D.B.;
RT "Induction, purification and characterization of chitinase isolated
RT from pea leaves inoculated with Ascochyta pisi.";
RL Planta 184:24-29(1991).
CC -!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CC CONTAINING FUNGAL PATHOGENS.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-

```

```

CC acetyl-D-glucosamine polymers of chitin.
CC -!- INDUCTION: By infection with the fungal pathogen Ascochyta pisi.
CC -!- SIMILARITY: BELONGS TO CHITINASE CLASS 1A WHICH IS SIMILAR TO
CC CLASS 1B IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CC CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
CC HYDROLASES).
DR InterPro; IPR001002; Chitin_binding_1.
DR InterPro; IPR000726; Glyco_Hydro_19.
DR PROSITE; PS00026; CHITIN BINDING; PARTIAL.
DR PROSITE; PS00773; CHITINASE 19.1; PARTIAL.
DR PROSITE; PS00774; CHITINASE 19.2; PARTIAL.
KW Hydrolase; Glycosidase; Chitin degradation; Chitin-binding;
KW Multigene family.
FT NON TER 15
SQ SEQUENCE 15 AA; 1438 MW; 23355ED6B11E869 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 1 EQ 2

RESULT 57
IRBP_CRISP
ID IRBP_CRISP STANDARD; PRT; 15 AA.
AC P12665;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
DE retinol-binding protein) (Fragment).
DR RBP3.
OS Cricetidae sp. (Hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae.
OX NCBI_TaxID=36483;
RN [1]
RP SEQUENCE.
RX MEDLINE=86301171; PubMed=3743780;
RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
RA Bridges C.D.B.;
RT "N-terminal sequence homologies in interstitial retinol-binding
RT proteins from 10 vertebrate species.";
RL FEBS Lett. 205:309-312(1986).
CC -!- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOLIDS BETWEEN
CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
CC -!- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
CC EPITHELIUM CELLS.
DR PIR; G24417; G24417.
KW Vitamin A; Transport.
FT NON TER 15
SQ SEQUENCE 15 AA; 1752 MW; C51A8780C85DEC1E CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 8 QP 9

RESULT 58
LEC2_PSOSC
ID LEC2_PSOSC STANDARD; PRT; 15 AA.
AC P22585;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)

```

```

DE 01-OCT-1994 (Rel. 30, Last annotation update)
DE Basic lectin B2 (Fragment).
OC Psophocarpus scandens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Euposids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3890;
RN [1]
RP SEQUENCE
RC TISSUE=Seed;
RA Kortt A.A.;
RT "Isolation and characterization of the lectins from the seeds of
RT Psophocarpus scandens.";
RL Phytochemistry 27:2847-2855(1988).
CC -!- SUBUNIT: DIMER OF TWO IDENTICAL OR NEARLY IDENTICAL SUBUNITS OF
CC -!- ABOUT 32000 APPARENT MW.
CC -!- PTM: CONTAINS ABOUT 9% CARBOHYDRATE. HETEROGENEITY IN CARBOHYDRATE
CC COMPOSITION MAY RESULT IN DIFFERENT ISOLECTIN FORMS.
CC -!- SIMILARITY: WITH P.TETRAONOLOBUS BASIC LECTINS IN N-TERMINAL
CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.
DR PIR: PA0008; PA0008.
KW Lectin; Glycoprotein.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1847 MW; D194CE400C832796 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 12 EQ 13

RESULT 59
MM01 RAT STANDARD; PRT; 15 AA.
AC P81563;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)
DE (MMP-1) (Fibroblast collagenase) (Myocardial collagenase) (Fragment).
GN MMP1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=96201136; PubMed=8605638;
RA Tyagi S.C., Cleutjens J.P.M.;
RT "Myocardial collagenase: purification and structural
RT characterization.";
RL Can. J. Cardiol. 12:165-171(1996).
CC -!- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X. MAY
CC PLAY A ROLE IN THE DETERIORATION OF THE HEART WALL EXTRACELLULAR
CC MATRIX PROTEINS DURING THE ONSET OF DILATED CARDIOMYOPATHY.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -!- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
CC ACTIVATION PEPTIDE.
CC -!- PTM: THE N-TERMINAL IS BLOCKED.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
KW Hydrolase; Metalloprotease; Zinc; Calcium; Collagen degradation;

```

```

KW Extracellular matrix.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 5 SE 6

RESULT 60
PGKH PHYPA STANDARD; PRT; 15 AA.
ID PGKH PHYPA
AC P80659;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase, chloroplast (EC 2.7.2.3) (Fragment).
DE Physcomitrella patens (Moss).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes.";
RL Planta 201:261-272(1997).
CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -!- PATHWAY: Calvin cycle.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
DR InterPro; IPR001576; PGK.
DR PROSITE; PS00111; PGLYCERATE KINASE; PARTIAL.
KW Transferase; Kinase; Multigene family; Calvin cycle; Chloroplast.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1531 MW; 56A5ECC1F677EEC6 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 4 EQ 5

RESULT 61
PGTS PELAC STANDARD; PRT; 15 AA.
ID PGTS PELAC
AC P80564;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pyrogallol hydroxyltransferase small subunit (EC 1.9.7.1.2)
DE (Transhydroxylase) (Fragment).
OS Pelobacter acidgallii.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Pelobacteraceae; Pelobacter.
OX NCBI_TaxID=35816;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 2377 / Braunschweig;
RX MEDLINE=96215436; PubMed=8647079;
RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;

```

RT "One molecule of molybdopterin guanine dinucleotide is associated with each subunit of the heterodimeric Mo-Fe-S protein transhydroxylase of *Pelobacter acidigallici* as determined by SDS/PAGE and mass spectrometry.";

RL Eur. J. Biochem. 237:406-413(1996).

CC -!- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3,5-trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-tetrahydroxybenzene.

CC -!- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).

CC -!- SUBUNIT: Heterodimer of a large and a small subunit.

DR PIR; S65429; S65429.

KW Oxidoreductase; Molybdenum; Iron-sulfur.

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1843 MW; 0567BDD004C28499 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 2 EQ 3

RESULT 62

ID_RBS_PHYPA STANDARD; PRT; 15 AA.

AC P80657;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34; Last sequence update)

DT 15-SEP-2003 (Rel. 42; Last annotation update)

DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO small subunit) (Fragment).

DE small subunit) (Fragment).

GN RBCs.

OS Physcomitrella patens (Moss).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

OX NCBI_TaxID=3218;

RN [1]

RP SEQUENCE.

RC TISSUE=Protonema;

RA Kasten B., Buck F., Nuske J., Reski R.;

RT "Cytokinin affects nuclear- and plastome-encoded energy-converting plastid enzymes.";

RL Planta 201:261-272(1997).

CC -!- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-ribulose 1,5-bisphosphate, the primary event in photosynthetic carbon dioxide fixation, as well as the oxidative fragmentation of the pentose substrate in the photorespiration process. Both reactions occur simultaneously and in competition at the same active site.

CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2 3-phospho-D-glycerate.

CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-phospho-D-glycerate + 2-phosphoglycolate.

CC -!- SUBUNIT: 8 large chains + 8 small chains.

CC -!- SUBCELLULAR LOCATION: Chloroplast.

CC -!- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.

KW Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase; Oxidoreductase; Monooxygenase; Chloroplast.

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1801 MW; 28B9E7AC4AED6CE0 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
Db 9 QP 10

RESULT 63

ID_RS20_BACST STANDARD; PRT; 15 AA.

AC P59681;

DT 15-SEP-2003 (Rel. 42, Created)

DT 15-SEP-2003 (Rel. 42; Last sequence update)

DT 15-SEP-2003 (Rel. 42; Last annotation update)

DE 30S ribosomal protein S20 (BS20) (Fragment).

GN RPST.

OS *Bacillus stearothermophilus*.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Geobacillus*.

OX NCBI_TaxID=1422;

RN [1]

RP SEQUENCE.

RC STRAIN=10;

RA PubMed=4607606;

RA Yaguchi M., Matheson A.T., Visentin L.P.;

RT "Prokaryotic ribosomal proteins: N-terminal sequence homologies and structural correspondence of 30 S ribosomal proteins from *Escherichia coli* and *Bacillus stearothermophilus*.";

RL FEBS Lett. 46:296-300(1974).

CC -!- FUNCTION: Binds directly to 16S ribosomal RNA (By similarity).

CC -!- SIMILARITY: BELONGS TO THE S20P FAMILY OF RIBOSOMAL PROTEINS.

DR HAMAP; MF 00500; -; 1.

KW Ribosomal protein; rRNA-binding.

FT INIT_MET 0 0

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1645 MW; 4E4646265E4C6206 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 13 SE 14

RESULT 64

ID_RT32_BOVIN STANDARD; PRT; 15 AA.

AC P82927;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41; Last sequence update)

DT 28-FEB-2003 (Rel. 41; Last annotation update)

DE Mitochondrial 28S ribosomal protein S32 (S32mt) (MRP-S32) (Fragment).

GN MRPS32.

OS *Bos taurus* (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RC TISSUE=Liver;

RA MEDLINE=21276436; PubMed=11279123;

RA Xoc E.C.; Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;

RT "The small subunit of the mammalian mitochondrial ribosome: identification of the full complement of ribosomal proteins present.";

RL J. Biol. Chem. 276:19363-19374(2001).

CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit (28S) which comprises a 12S rRNA and about 30 distinct proteins.

CC -!- SUBCELLULAR LOCATION: Mitochondrion.

KW Ribosomal protein; Mitochondrion.

FT NON_TER 1 1

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1725 MW; 34E58A79E31DB758 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3

Db 11 EQ 12

RESULT 65

UC13 MAIZE

ID UC13 MAIZE STANDARD; PRT; 15 AA.

AC P80619;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 243)

DE (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE.

RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated

RT genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 6.8, ITS MW IS: 56.9 kDa.

CC -!- SIMILARITY: TO GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASES.

DR Maize-2DPAGE; P80619; COLEOPTILE.

DR MaizeDB; 123946; -- 1

FT NON_TER 1 15

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1739 MW; 02038EE7471AE038 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

13 SE 14

Db

RESULT 66

UC27 MAIZE

ID UC27 MAIZE STANDARD; PRT; 15 AA.

AC P80633;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Unknown protein from 2D-page of etiolated coleoptile (Spot 688)

DE (Fragment).

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE.

RC TISSUE=Coleoptile;

RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,

RA Pernollet J.-C., Zivy M., de Vienne D.;

RT "The maize two dimensional gel protein database: towards an integrated

RT genome analysis program.";

RL Theor. Appl. Genet. 93:997-1005(1996).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 6.4, ITS MW IS: 48.4 kDa.

CC -!- SIMILARITY: TO XENOPUS HISTONE-BINDING PROTEIN N1/N2 AND RABBIT

CC AND HUMAN NUCLEAR AUTOANTIGENIC SPERM PROTEIN.

DR Maize-2DPAGE; P80633; COLEOPTILE.

DR MaizeDB; 123958; -- 1

FT NON_TER 1 1

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1739 MW; 02038EE7471AE038 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

13 SE 14

Db

RESULT 67

UN01 PINPS

ID UN01 PINPS STANDARD; PRT; 15 AA.

AC P81106;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Unknown protein from 2D-page of needles (S1247/S1248) (N150/N151)

DE (fragment).

OS Pinus pinaster (Maritime pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

OX NCBI_TaxID=71647;

RN [1]

RP SEQUENCE.

RC TISSUE=Needle;

RA Plomion C., Costa P., Bahrman N., Frigerio J.M.;

RA "Genetic analysis of needle proteins in maritime pine. 1. Mapping

RT dominant and codominant protein markers assayed on diploid tissue, in

RT a haploid-based genetic map.";

RL Silvae Genet. 46:161-165(1997).

RN [2]

RP SEQUENCE.

RC TISSUE=Needle;

RC MEDLINE=99274088; PubMed=10344291;

RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,

RA Frigerio J.-M., Plomion C.;

RT "Separation and characterization of needle and xylem maritime pine

RT proteins.";

RL Electrophoresis 20:1098-1108(1999).

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.5, ITS MW IS: 62 kDa.

FT NON_TER 1 1

FT NON_TER 15 15

SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3

3 EQ 4

Db

RESULT 68

URE2 MORMO

ID URE2 MORMO STANDARD; PRT; 15 AA.

AC P17338;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Urease beta subunit (EC 3.5.1.5) (15 kDa subunit) (Urea

DE amidohydrolase) (Fragment).

GN UREB.

OS Morganella morganii (Proteus morganii).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Morganella.

OX NCBI_TaxID=582;

RN [1]

RP SEQUENCE.

```

RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RL isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
CC PIR; B35389; B35389.
KW Hydrolase.
DR
KW
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1530 MW; 2D98944F2P20C7E8 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 5 QP 6

RESULT 69
BRB_BASAL STANDARD; PRT; 16 AA.
ID BRB_BASAL
AC P83187;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-basurubin (Fragment)
OS Basella alba (Malabar spinach) (Ceylon spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Basellaceae; Basella.
OX NCBI_TaxID=3589;
RN [1];
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21547763; PubMed=11688973;
RA Wang H., Ng T.B.;
RT "Novel antifungal peptides from ceylon spinach seeds.";
RL Biochem. Biophys. Res. Commun. 288:765-770(2001).
CC -!- FUNCTION: Possesses antifungal activity against B.cinerea,
CC M.arachidicola and F.oxysporum but not C.comatus and R.solani.
CC Inhibits HIV-1 reverse transcriptase and cell-free translation.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IDA.
KW Fungicide.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1952 MW; 28F9FE4FC181682C CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 11 EQ 12

RESULT 70
FIBA_EQUAS STANDARD; PRT; 16 AA.
ID FIBA_EQUAS
AC P14449;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;

```

```

RN [1]
SEQUENCE.
RP Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC Blood coagulation; Plasma.
KW PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1696 MW; 09598EB63C2A5957 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 10 SE 11

RESULT 71
FIBA_MELME STANDARD; PRT; 16 AA.
ID FIBA_MELME
AC P14456;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Meles meles (Eurasian badger).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
OX NCBI_TaxID=9662;
RN [1];
SEQUENCE.
RP Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1708 MW; 09433547919EC7C4 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 6 SE 7

RESULT 72
FIBA_MUSVI STANDARD; PRT; 16 AA.
ID FIBA_MUSVI

```


AC P14458;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mustela.
 OX NCBI_TaxID=9667;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 KW Blood coagulation; Plasma.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT NON_TER 16 16
 FT SEQUENCE 16 AA; 1679 MW; 09432A57919ECF66 CRC64;
 SQ
 Query Match 50.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SE 2
 ||
 DB 6 SE 7

RESULT 73
 HTPG ACICA STANDARD; PRT; 16 AA.
 ID HTPG ACICA STANDARD; PRT; 16 AA.
 AC P81876;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chapterone protein htpg (Heat shock protein htpg) (High temperature
 DE protein G) (Fragment).
 GN HTPG.
 OS Acinetobacter calcoaceticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=471;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=69-V;
 RX MEDLINE=99274045; PubMed=10344248;
 RA Benndorf D., Loffhagen N., Babel W.;
 RT "Induction of heat shock proteins in response to primary alcohols in
 RT Acinetobacter calcoaceticus";
 RL Electrophoresis 20:781-789(1999).
 CC -!- FUNCTION: Molecular chaperone. Has ATPase activity (By
 CC similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- INDUCTION: BY HEAT SHOCK AND PRIMARY ALCOHOLS.
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
 DR HAMAP; MF_00505; -; 1.
 DR InterPro; IPR001404; Hsp90.
 DR PROSITE; PS00298; HSP90; PARTIAL.
 KW Chapterone; ATP-binding; Heat shock.
 FT NON_TER 16 16
 FT SEQUENCE 16 AA; 1769 MW; 316C70D8928CB482 CRC64;
 SQ

Query Match 50.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SE 2
 ||
 DB 1 SE 2

RESULT 74
 IBP4_PIG STANDARD; PRT; 16 AA.
 ID IBP4_PIG STANDARD; PRT; 16 AA.
 AC P24854;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
 DE (IGF-binding protein 4) (Fragment).
 GN IGFBP4.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92109718; PubMed=1722398;
 RA Coleman M.E., Pan Y.-C.E., Ethernon T.D.;
 RT "Identification and NH2-terminal amino acid sequence of three
 RT insulin-like growth factor-binding proteins in porcine serum.";
 RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
 CC -!- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFS
 CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
 CC PROMOTING EFFECTS OF THE IGFS ON CELL CULTURE. THEY ALTER THE
 CC INTERACTION OF IGFS WITH THEIR CELL SURFACE RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 IGFBP domain.
 CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
 DR PIR; JH0517; JH0517.
 DR InterPro; IPR000867; Insl_gro_fac.pr.
 DR InterPro; IPR000716; Thyroglobulin_1.
 DR PROSITE; PS00222; IGF BINDING; PARTIAL.
 DR PROSITE; PS00484; THYROGLOBULIN_1; PARTIAL.
 KW Growth factor binding.
 FT NON_TER 16 16
 FT SEQUENCE 16 AA; 1799 MW; 40988840096655E2 CRC64;
 SQ
 Query Match 50.0%; Score 2; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SE 2
 ||
 DB 10 SE 11

RESULT 75
 LPK1_LOCM1 STANDARD; PRT; 16 AA.
 ID LPK1_LOCM1 STANDARD; PRT; 16 AA.
 AC P20404;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Locustapyrrolin 1 (LOM-PK-1).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=91224474; PubMed=2026322;
 SQ

RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Isolation, primary structure, and synthesis of locustapyrokinin: a
RL myotropic peptide of Locusta migratoria.";
RL Gen. Comp. Endocrinol. 81:97-104(1991).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR PIR; A49761; A49761.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 50.0%; Score 2; DB 1; Length 16;
Best Local Similarity 100.0%; Pred.No. 4.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QP 4
|
|
Db 10 QP 11

Search completed: November 25, 2003, 18:17:30
Job time : 2.93617 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:03:34 ; Search time 9.6383 Seconds
(without alignment)
107.095 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_virus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	100.0	18	4	Q9UCF4
2	3	75.0	9	8	Q8WFT4
3	3	75.0	10	8	Q8WFT6
4	3	75.0	10	8	Q8WFT5
5	3	75.0	14	10	P82332
6	3	75.0	16	2	P82597
7	3	75.0	17	4	Q9UCT3
8	3	75.0	17	5	Q9TWI6
9	3	75.0	18	6	Q9TOR0
10	3	75.0	18	11	Q99MD5
11	3	75.0	18	12	Q9DS59
12	3	75.0	20	10	Q9SM31
13	3	75.0	20	12	Q8UXT4
14	3	75.0	20	12	Q8UXS4
15	3	75.0	20	12	Q8UXT3
16	3	75.0	20	12	Q8UXS2

17	3	75.0	20	12	Q8UXTO
18	3	75.0	20	12	Q8UXS5
19	3	75.0	20	12	Q8UXT1
20	3	75.0	20	12	Q8UXS6
21	3	75.0	20	12	Q8UXS9
22	3	75.0	20	12	Q8UXS3
23	3	75.0	20	12	Q8UXT2
24	3	75.0	20	12	Q8UXS1
25	2	50.0	8	2	Q8RSR3
26	2	50.0	8	2	Q47273
27	2	50.0	8	4	Q16428
28	2	50.0	8	4	Q9P285
29	2	50.0	8	5	Q8MUN6
30	2	50.0	8	6	Q9MYL5
31	2	50.0	8	11	Q99NX9
32	2	50.0	8	11	Q62721
33	2	50.0	8	12	Q9WJ33
34	2	50.0	9	2	P72345
35	2	50.0	9	2	Q53914
36	2	50.0	9	2	Q47063
37	2	50.0	9	6	Q9XSL0
38	2	50.0	9	6	Q9TRX0
39	2	50.0	9	8	Q8W875
40	2	50.0	9	9	Q8H921
41	2	50.0	9	10	P82429
42	2	50.0	9	10	P82440
43	2	50.0	9	11	Q9QWG2
44	2	50.0	9	11	O08979
45	2	50.0	9	12	Q82622
46	2	50.0	9	12	Q83622
47	2	50.0	9	13	Q8AYL5
48	2	50.0	9	13	Q8AUM7
49	2	50.0	9	15	Q8AEW8
50	2	50.0	9	16	Q935G1
51	2	50.0	10	2	Q9ZIB1
52	2	50.0	10	2	P82588
53	2	50.0	10	4	Q8NER0
54	2	50.0	10	4	O00493
55	2	50.0	10	4	Q96QT9
56	2	50.0	10	5	Q8MUP1
57	2	50.0	10	5	Q8WPL6
58	2	50.0	10	5	Q8MUN7
59	2	50.0	10	5	P82217
60	2	50.0	10	6	Q8MU52
61	2	50.0	10	6	P83205
62	2	50.0	10	8	Q8WBR7
63	2	50.0	10	8	Q96041
64	2	50.0	10	8	Q8SHA8
65	2	50.0	10	10	Q8LLJ0
66	2	50.0	10	10	Q8GUV6
67	2	50.0	10	11	Q91WZ3
68	2	50.0	10	11	Q9QVE8
69	2	50.0	10	11	Q9QVF0
70	2	50.0	10	11	Q9QVF1
71	2	50.0	10	11	Q9QVE7
72	2	50.0	10	11	Q8CJE0
73	2	50.0	10	12	P90391
74	2	50.0	10	12	Q86580
75	2	50.0	10	15	Q86324
76	2	50.0	10	15	Q86325
77	2	50.0	10	15	Q86326
78	2	50.0	11	2	Q52526
79	2	50.0	11	3	Q9HFN8
80	2	50.0	11	4	Q16427
81	2	50.0	11	4	Q9UBM2
82	2	50.0	11	4	Q9UCF1
83	2	50.0	11	4	Q16217
84	2	50.0	11	5	Q25916
85	2	50.0	11	5	Q8MM58
86	2	50.0	11	6	Q9XSP7
87	2	50.0	11	6	Q9XSP2
88	2	50.0	11	6	Q9XSP5
89	2	50.0	11	6	Q9XSP8

Q8uxto	hepatitis c
Q8uxs5	hepatitis c
Q8uxt1	hepatitis c
Q8uxs6	hepatitis c
Q8uxs9	hepatitis c
Q8uxs3	hepatitis c
Q8uxt2	hepatitis c
Q8uxs1	hepatitis c
Q8rsr3	lactobacilli
Q47273	escherichia
Q16428	homo sapien
Q9p285	homo sapien
Q8mun6	helicobacter
Q9myl5	pongo pygma
Q99nx9	hydrochoer
Q62721	rattus norv
Q9wj33	pseudorabie
P72345	pseudomonas
Q53914	streptomyce
Q47063	escherichia
Q9xsl0	capra hircu
Q9trx0	oryctolagus
Q8w875	bostrixychia
Q8h921	cyanophaga
P82429	nicotiana t
P82440	nicotiana t
Q9qwg2	mus musculu
O08979	mus musculu
Q82622	avian infec
Q83622	murray vall
Q8ayl5	carassius a
Q8aum7	carassius a
Q8aeu8	human immun
Q935g1	salmonella
Q9zib1	clostridium
P82588	streptococc
Q8ner0	homo sapien
O00493	homo sapien
Q96qt9	homo sapien
Q8mup1	helicobacter
Q8wpl6	gikopleura
Q8mun7	helicobacter
P82217	bombyx mori
Q8mj52	equus cabal
P83205	ovis aries
Q8wbr7	chaitophoru
Q96041	oenothera b
Q8sha8	rampholeon
Q8llj0	oryza sativ
Q8guv6	capsella ru
Q91wz3	rattus sp.
Q9qve8	mus sp. pro
Q9qvfo	mus sp. pro
Q9qvfi	mus sp. pro
Q9qve7	mus sp. pro
Q8cje0	rattus norv
P90391	tomato yell
Q86580	simian para
Q86324	rous sar-com
Q86325	rous sarcom
Q86326	rous sarcom
Q52526	rhizobium s
Q9hfn8	candida rug
Q16427	homo sapien
Q9ubm2	homo sapien
Q9ucr1	homo sapien
Q16217	homo sapien
Q25916	plasmodium
Q8mm58	helicobacter
Q9xsp7	pygathrix n
Q9xsp2	hylobates s
Q9xsp5	pan troglod
Q9xsp8	presbytis j

```
90 Q9XSP6 2 50.0 11 6 Q9XSP6
91 Q9XSQ4 2 50.0 11 6 Q9XSQ4
92 Q77885 2 50.0 11 7 Q77885
93 Q77884 2 50.0 11 7 Q77884
94 O19718 2 50.0 11 7 O19718
95 Q77913 2 50.0 11 7 Q77913
96 Q32704 2 50.0 11 8 Q32704
97 Q8RV30 2 50.0 11 10 Q8RV30
98 P82336 2 50.0 11 10 P82336
99 Q9QVH3 2 50.0 11 11 Q9QVH3
100 Q9R0K9 2 50.0 11 11 Q9R0K9
```

ALIGNMENTS

```
RESULT 1
Q9UCF4 Q9UCF4 PRELIMINARY; PRT; 18 AA.
AC Q9UCF4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Chymotrypsinogen homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Diarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE.
RX MEDLINE=93285747; PubMed=8509158;
RA Kim Y.J., Zhou Z., Hurtado J., Wood D.L., Choi A.S., Pescovitz M.D.,
RA Warfel K.A., Vandagriff J., Davis J.K., Kwon B.S.;
RT "IDDM patients' sera recognize a novel 30-kD pancreatic autoantigen
RT related to chymotrypsinogen.";
RL Immunol. Invest. 22:219-227(1993).
SQ SEQUENCE 18 AA; 1826 MW; 38105D1037CA6837 CRC64;
```

```
Query Match 100.0%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 SEQP 4
Db 14 SEQP 17
```

```
RESULT 2
Q8WFT4 Q8WFT4 PRELIMINARY; PRT; 9 AA.
AC Q8WFT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diademataceae; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]_
RP SEQUENCE FROM N.A.
RX STRAIN=DCA3.
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]_
RP SEQUENCE FROM N.A.
RX STRAIN=DCA3;
```

```
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL: AY012858; AAL33832.2; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;

Query Match 75.0%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 EQP 4
```

```
Db 7 EQP 9
```

```
RESULT 3
Q8WFT6 Q8WFT6 PRELIMINARY; PRT; 10 AA.
AC Q8WFT6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diademataceae; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]_
RP SEQUENCE FROM N.A.
RX STRAIN=DCA1;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]_
RP SEQUENCE FROM N.A.
RX STRAIN=DCA1;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL: AY012856; AAL33830.2; -.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 10 AA; 1301 MW; EDEB101B173B46CA CRC64;
```

```
Query Match 75.0%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 EQP 4
Db 8 EQP 10
```

```
RESULT 4
Q8WFT5 Q8WFT5 PRELIMINARY; PRT; 10 AA.
AC Q8WFT5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
```

OS Diadema antillarum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;
OC Diadema.
OX NCBI_TaxID=105359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DCA2;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
phylogeography of the sea urchin *Diadema*.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DCA2;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of *Diadema antillarum*, a keystone herbivore on
Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012857; AAL33831.2; -.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1262 MW; COBB101B173B46DD CRC64;
Query Match 75.0%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 EOP 4
Db 8 EOP 10
RESULT 5
P82332 PRELIMINARY; PRT; 14 AA.
ID P82332
AC P82332;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page of thylakoid (SP01115) (Fragments).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
RC STRAIN=cv. DE GRACE; TISSUE=LEAF;
RX MEDLINE=20181728; PubMed=10715320;
RA Petitier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
RA Adamska I., van Wijk K.J.;
RT "Proteomics of the chloroplast: systematic identification and
targeting analysis of luminal and peripheral thylakoid proteins.";
RL Plant Cell 12:319-341(2000).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
PERIPHERY.
CC -!- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.5, ITS MW IS: 27.4 KDA.
KW Chloroplast; Thylakoid membrane.
FT NON TER 1 1
FT NON TER 6 7
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1461 MW; 0803373C9C937AAB CRC64;
Query Match 75.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EOP 4
Db 4 EOP 6
RESULT 6
P82597 PRELIMINARY; PRT; 16 AA.
ID P82597
AC P82597;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Thermotable monoacylglycerol lipase (MGLP) (24 kDa) (EC 3.1.1.23)
DE (Fragment).
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE.
RC STRAIN=H-257;
RX MEDLINE=20198254; PubMed=10731713;
RA Imamura S., Kitaura S.;
RT "Purification and characterization of a monoacylglycerol lipase from
the moderately thermophilic *Bacillus* sp. H-257.";
RL J. Biochem. 127:419-425(2000).
CC -!- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY
OCCURRING WITH 1-MONOLAURYLGLYCEROL.
CC -!- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY
INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM
TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.
CC -!- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS
OTHER BACTERIAL LIPASES.
KW Hydrolase.
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;
Query Match 75.0%; Score 3; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEQ 3
Db 1 SEQ 3
RESULT 7
Q9UCT3 PRELIMINARY; PRT; 17 AA.
ID Q9UCT3
AC Q9UCT3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE ALZHEIMER'S beta-amyloid precursor protein, kunitz-type protease
inhibitor, neutrophil elastase inhibitor, P1-VAL-APP-KD
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92041969; PubMed=1939150;
RA Sinha S., Knops J., Esch F., Moyer E.D., Oltersdorf T.;
RT "Conversion of the Alzheimer's beta-amyloid precursor protein (APP)
Kunitz domain into a potent human neutrophil elastase inhibitor.";
RL J. Biol. Chem. 266:21011-21013(1991).
FT NON TER 1 1
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1778 MW; F0CCDC28D6712BA CRC64;
Query Match 75.0%; Score 3; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 1 SEQ 3
|||
Db 5 SEQ 7

RESULT 8

Q9TW16 ID Q9TW16 PRELIMINARY; PRT; 17 AA.
AC Q9TW16;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Major cuticular protein (Fragment).
OS Ceratitis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Ceratitis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE.
RX MEDLINE=95279142; PubMed=7759285;
RA Tsiliris A., Koromantzou E., Allen G., Dimitriadis G.;
RT "Partial N-terminal sequences of larval cuticular proteins from the
RL dipteran *Ceratitis capitata*.";
SQ SEQUENCE 17 AA; 1900 MW; 1731EE5C2FB97DA CRC64;

Query Match 75.0%; Score 3; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 9 SEQ 11

RESULT 9

Q9TOR0 ID Q9TOR0 PRELIMINARY; PRT; 18 AA.
AC Q9TOR0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 21, Last annotation update)
DE cAMP-dependent protein kinase subunit CB (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=93094224; PubMed=1460017;
RA Toner-Webb J., van Patten S.M., Walsh D.A., Taylor S.S.;
RT "Autophosphorylation of the catalytic subunit of cAMP-dependent
RT protein kinase.";
RL J. Biol. Chem. 267:25174-25180(1992).
FT NON_TER 1
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 2155 MW; 2A709A3F639968D7 CRC64;

Query Match 75.0%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 2 SEQ 4

RESULT 10

Q99MD5

Q99MD5 PRELIMINARY; PRT; 18 AA.

AC Q99MD5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Killer cell lectin-like receptor 7 (Fragment).
GN KLR47.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6;
RX MEDLINE=21291699; PubMed=11398966;
RA Wilhelm B.T., McQueen K.L., Freeman J.D., Takei F., Mager D.L.;
RT "Comparative analysis of the promoter regions and transcriptional
RT start sites of mouse *Ly49* genes.";
RL Immunogenetics 53:215-224(2001).
DR EMBL; AF349732; AAK19750.1; -.
KW Lectin; Receptor.
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 2173 MW; A99F15B657328112 CRC64;

Query Match 75.0%; Score 3; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 1 SEQ 3
|||
Db 2 SEQ 4

RESULT 11

Q9DSS9 ID Q9DSS9 PRELIMINARY; PRT; 18 AA.
AC Q9DSS9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE P23 protease (Fragment).
GN P23.
OS Human adenovirus type 4.
OC Viruses; GSDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z-G T95-873;
RX MEDLINE=99175282; PubMed=10074533;
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
RT respiratory disease.";
RL J. Clin. Microbiol. 37:1107-1112(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Z-G T95-873;
RA Crawford-Miksza L.K.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065064; AAD03661.3; -.
DR HSSP; P03252; 1AVP.
KW Protease.
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 1917 MW; 12FCE2715E7FB445 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 3 SEQ 5

RESULT 12

Q9SM31 ID Q9SM31 PRELIMINARY; PRT; 20 AA.
 AC Q9SM31;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Putative sucrose synthase (Fragment).
 GN SSI.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chinese spring;
 RA Helguera M., Khan I.A., Dubcovsky J.;
 RT "Development of PCR markers for wheat leaf rust resistance gene
 Lr47.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ249623; CAB61261.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 20 AA; 2298 MW; CC4FE0F3877CCDC CRC64;

Query Match 75.0%; Score 3; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
 Db 15 EQP 17

RESULT 13

Q8UXT4 ID Q8UXT4 PRELIMINARY; PRT; 20 AA.
 AC Q8UXT4; 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Genome polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
 RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
 RT "Genetic heterogeneity of the envelope 2 gene and eradication of
 RT hepatitis c virus after a second course of alpha interferon.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF466512; AAL70092.1; -.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
 Db 7 SEQ 9

RESULT 14

Q8UXS4 ID Q8UXS4 PRELIMINARY; PRT; 20 AA.

Q8UXS4 ID Q8UXS4 PRELIMINARY; PRT; 20 AA.
 AC Q8UXS4;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Genome polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
 RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
 RT "Genetic heterogeneity of the envelope 2 gene and eradication of
 RT hepatitis c virus after a second course of alpha interferon.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF466522; AAL70102.1; -.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
 Db 7 SEQ 9

RESULT 15

Q8UXT3 ID Q8UXT3 PRELIMINARY; PRT; 20 AA.
 AC Q8UXT3;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Genome polyprotein (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
 RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
 RT "Genetic heterogeneity of the envelope 2 gene and eradication of
 RT hepatitis c virus after a second course of alpha interferon.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF466513; AAL70093.1; -.
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
 Db 7 SEQ 9

RESULT 16

Q8UXT3 ID Q8UXT3 PRELIMINARY; PRT; 20 AA.

```
Q8UXS2
ID Q8UXS2; PRELIMINARY; PRT; 20 AA.
AC Q8UXS2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT Hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF46524; AAL70104.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db |||
7 SEQ 9

RESULT 17
Q8UXT0
ID Q8UXT0; PRELIMINARY; PRT; 20 AA.
AC Q8UXT0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT Hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF46516; AAL70096.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db |||
7 SEQ 9

RESULT 18
Q8UXS5
ID Q8UXS5; PRELIMINARY; PRT; 20 AA.
AC Q8UXS5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT Hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF46521; AAL70101.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db |||
7 SEQ 9

RESULT 19
Q8UXT1
ID Q8UXT1; PRELIMINARY; PRT; 20 AA.
AC Q8UXT1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT Hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF46515; AAL70095.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db |||
7 SEQ 9
```



```
RESULT 20
Q8UXS6 PRELIMINARY; PRT; 20 AA.
ID Q8UXS6
AC Q8UXS6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis c virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466520; AAL70100.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;
Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEQ 3
Db |||
7 SEQ 9

RESULT 21
Q8UXS9 PRELIMINARY; PRT; 20 AA.
ID Q8UXS9
AC Q8UXS9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis c virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466517; AAL70097.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;
Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEQ 3
Db |||
7 SEQ 9
```

```
RESULT 22
Q8UXS3 PRELIMINARY; PRT; 20 AA.
ID Q8UXS3
AC Q8UXS3;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis c virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466523; AAL70103.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;
Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEQ 3
Db |||
7 SEQ 9

RESULT 23
Q8UXT2 PRELIMINARY; PRT; 20 AA.
ID Q8UXT2
AC Q8UXT2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulestin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Puel J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis c virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466514; AAL70094.1; -.
DR InterPro; IPR002531; HCV_NSI.
DR Pfam; PF01560; HCV_NSI.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;
Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEQ 3
Db |||
7 SEQ 9
```

```
Db 7 SEQ 9

RESULT 24
Q8UXS1
ID Q8UXS1 PRELIMINARY; PRT; 20 AA.
AC Q8UXS1
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RA Boulesin A., Sandres-Saune K., Payen J.-L., Alric L., Dubois M.,
RA Pasquier C., Vinel J.-P., Pascal J.-P., Fael J., Izopet J.;
RT "Genetic heterogeneity of the envelope 2 gene and eradication of
RT hepatitis C virus after a second course of alpha interferon.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF466525; AAL70105.1; -.
DR InterPro: IPR002531; HCV NS1.
DR Pfam; PF01560; HCV NS1; I.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2347 MW; 468241FEDD122929 CRC64;

Query Match 75.0%; Score 3; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 7 SEQ 9

RESULT 25
Q8RSR3
ID Q8RSR3 PRELIMINARY; PRT; 8 AA.
AC Q8RSR3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PduG protein (Fragment).
GN PDUg.
OS Lactobacillus collinoides.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33960;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMG 18050;
RA Sauvageot N., Gouffi K., Laplace J.M., Auffray Y.;
RT "Characterisation of the diol dehydratase pdu operon of Lactobacillus
RT collinoides.";
RL FEMS Microbiol. Lett. 0:0-0(0).
DR EMBL; AJ297723; CAD01093.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 882 MW; ECA40B05B5BDD6 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 5 SE 6
```

```
RESULT 26
Q47273
ID Q47273 PRELIMINARY; PRT; 8 AA.
AC Q47273
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Orf33, orf151, orf56, orf96, rus, orf45, orf127, and mmpC
DE genes.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=96196428; PubMed=8648624;
RA Mahdi A.A., Sharples G.J., Mandal T.N., Lloyd R.G.;
RT "Holiday Junction Resolvases encoded by homologous rusa genes in
RT Escherichia coli K-12 and Phage 32.";
RL J. Mol. Biol. 257:561-573(1996).
DR EMBL; X92587; CAA63323.1; -.
SQ SEQUENCE 8 AA; 935 MW; FD4041A05B05B336 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 3 SE 4

RESULT 27
Q16428
ID Q16428 PRELIMINARY; PRT; 8 AA.
AC Q16428
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Dystrophin protein (Fragment).
GN DYSTROPHIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163501; PubMed=8566960;
RA Holder E., Maeda M., Bies R.D.;
RT "Expression and regulation of the dystrophin Purkinje promoter in
RT human skeletal muscle, heart, and brain.";
RL Hum. Genet. 97:232-239(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; S81419; AAD14363.1; -.
DR EMBL; AB037493; BAA90413.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;

Query Match 50.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 28
```

Q9P285
ID Q9P285 PRELIMINARY; PRT; 8 AA.
AC Q9P285;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Clotting factor VIII (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Shibata M., Shima M., Morichika S., Yoshiola A.;
RT "Human clotting factor VIII gene, junction regions of the deletion of
RT exon 4 through 7.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB040872; BAA94312.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 866 MW; 1C15987AAB05BDD3 CRC64;
Query Match 50.0%; Score 2; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SE 2
DB 3 SE 4
RESULT 29
Q8MUN6
ID Q8MUN6 PRELIMINARY; PRT; 8 AA.
AC Q8MUN6;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN MPI.
OS Heliconius melpomene melpomene.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
OX NCBI_TaxID=171917;
RN [1]
RP SEQUENCE FROM N.A.
RA Bull V., Beltran M., Birmingham E., Jiggins C., McMillan O.,
RA Mallet J.;
RT "Molecular evidence for gene flow between species of Heliconius.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF516247; AAM61933.1; -.
KW isomerase.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 977 MW; 16E736DB1DD1EAA3 CRC64;
Query Match 50.0%; Score 2; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EQ 3
DB 5 EQ 6
RESULT 30
Q9MYL5
ID Q9MYL5 PRELIMINARY; PRT; 8 AA.
AC Q9MYL5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Dystrophin.
OS Pongo pygmaeus (Orangutan),
OS Pan troglodytes (Chimpanzee), and
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600, 9598, 9593;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=P.pygmaeus, P.troglodytes, and G.gorilla;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project";
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB037496; BAA90419.1; -.
DR EMBL; AB037494; BAA90415.1; -.
DR EMBL; AB037495; BAA90417.1; -.
SQ SEQUENCE 8 AA; 825 MW; F21865A5A2CB05B6 CRC64;
Query Match 50.0%; Score 2; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SE 2
DB 2 SE 3
RESULT 31
Q99NX9
ID Q99NX9 PRELIMINARY; PRT; 8 AA.
AC Q99NX9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Amyloid beta protein (Fragment).
GN APP.
OS Eukaryotes hydrochaeris (Capybara) (Carpincho).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;
OC Hydrochaeris.
OX NCBI_TaxID=10149;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011342; AAG47377.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 1071 MW; 1356D686DB19C9C3 CRC64;
Query Match 50.0%; Score 2; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EQ 3
DB 4 EQ 5
RESULT 32
Q62721
ID Q62721 PRELIMINARY; PRT; 8 AA.
AC Q62721;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Prohibitin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

```

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher;
RX MEDLINE=95331633; PubMed=7607556;
RA Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA McClung J.K.;
RT "Regions of evolutionary conservation between the rat and human
RT prohibitin-encoding genes.";
RL Gene 158:291-294(1995).
DR EMBL; U17178; AAA86692.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match 50.0%; Score 2; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 4 SE 5

RESULT 33
Q9WJ33
ID Q9WJ33 PRELIMINARY; PRT; 8 AA.
AC Q9WJ33;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Suid herpesvirus 1 putative UL47 and UL46 genes and partial gb
DE (Fragment).
GN GB.
OS Pseudorabies virus (strain Kaplan) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=33703;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kaplan;
RX MEDLINE=99239778; PubMed=10225272;
RA Bras F., Dezelee S., Simonet B., Nguyen X., Vende P., Flamand A.,
RA Masse M.J.;
RT "The left border of the genomic inversion of pseudorabies virus
RT contains genes homologous to the UL46 and UL47 genes of Herpes Simplex
RT Virus type 1, but no UL45 gene.";
RL Virus Res. 60:29-40(1999).
DR EMBL; AJ010303; CAA09075.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 875 MW; 262DDAB76AAB05BB CRC64;

Query Match 50.0%; Score 2; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 34
P72345
ID P72345 PRELIMINARY; PRT; 9 AA.
AC P72345;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE TabA (Fragment).
GN TABA.
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.

```

```

OX NCBI_TaxID=317;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BR2R;
RX MEDLINE=93167809; PubMed=7679566;
RA Barta T.M., Kinscherf T.G., Uchytel T.F., Willis D.K.;
RT "DNA sequence and transcriptional analysis of the tbla gene required
RT for tabtoxin biosynthesis by Pseudomonas syringae.";
RL Appl. Environ. Microbiol. 59:458-466(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BR2R;
RA Kinscherf T.G., Willis D.K.;
RT "Sequence analysis of the tabtoxin biosynthetic region.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF519896; AAB25381.2; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1037 MW; 2B34D9D5BB05B047 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 4 SE 5

RESULT 35
Q53914
ID Q53914 PRELIMINARY; PRT; 9 AA.
AC Q53914;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Curd protein (Fragment).
OS Streptomyces cyaneus (Streptomyces curacoi).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1904;
RN [1]
RP SEQUENCE FROM N.A.
RA Bergh S.T., Uhlen M.;
RT "Cloning, analysis and heterologous expression of the polyketides
RT synthetis genes of Streptomyces curacoi.";
RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; M33704; AAA26724.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1027 MW; 995BDDDDC4140AB1 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 8 QP 9

RESULT 36
Q47063
ID Q47063 PRELIMINARY; PRT; 9 AA.
AC Q47063;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE URF 1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=W;
RX MEDLINE=85215599; PubMed=2987841;
RA Takagi J.S., Ida N., Tokushige M., Sakamoto H., Shimura Y.;
RT "Cloning and nucleotide sequence of the aspartase gene of Escherichia
RT coli W.";
RL Nucleic Acids Res. 13:2063-2074 (1985).
DR EMBL: X02307; CAA26175.1; -.
SQ SEQUENCE 9 AA; 1061 MW; 9DE21EASB9C72EA1 CRC64;

Query Match          50.0%; Score 2; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 8 EQ 9

RESULT 37
Q9XSLO PRELIMINARY; PRT; 9 AA.
AC Q9XSLO;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Alpha s2-casein (Fragment).
GN CSNIS2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=21313038; PubMed=11419340;
RA Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,
RA Cosenza G., Mariani P., Pastore N., Masina P.;
RT "An allele associated with a non detectable amount of as2 casein in
RT goat milk.";
RL Anim. Genet. 32:19-26 (2001).
DR EMBL: AJ238475; CAB44298.1; -.
FT NON_TER 1 1 I -> V.
FT VARIANT 5 5
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1047 MW; AAA2A5A5B051EB16 CRC64;

Query Match          50.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 8 SE 9

RESULT 38
Q9TRSO PRELIMINARY; PRT; 9 AA.
AC Q9TRSO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calcyclin-associated protein, CAP50=CA2+/phospholipid-binding protein
DE L-7 fragment (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=92250478; PubMed=1533622;
RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;

```

```

RT "A calcyclin-associated protein is a newly identified member of the
RT CA2+/phospholipid-binding proteins, annexin family.";
RL J. Biol. Chem. 267:8919-8924 (1992).
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;

Query Match          50.0%; Score 2; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 1 SE 2

RESULT 39
Q8W875 PRELIMINARY; PRT; 9 AA.
AC Q8W875;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ribulose-1,5-bisphosphate large subunit (Fragment).
GN RBCL.
OS Bostrychia calliptera.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomelaceae;
OC Bostrychia.
OX NCBI_TaxID=161377;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P.E350.PA, and P3999.NT;
RA Zuccarello G.C., West J.A.;
RT "Phylogeography of the Bostrychia calliptera/B. pinnata complex
RT (Rhodomeleaceae, Rhodophyta) and divergence rates based on nuclear,
RT mitochondrial and plastid DNA markers.";
DR EMBL: AF382914; AAL67249.1; -.
DR EMBL: AF382916; AAL67253.1; -.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 981 MW; 93B94DC1B771AB05 CRC64;

Query Match          50.0%; Score 2; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 2 SE 3

RESULT 40
Q8H9Z1 PRELIMINARY; PRT; 9 AA.
AC Q8H9Z1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Capsid protein.
GN G20.
OS Cyanophaga S-KM1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=187678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S-KM1;
RA Okunishi S., Maeda H.;
RT "Cyanophage in Kagoshima Bay.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB080247; BAC54112.1; -.
SQ SEQUENCE 9 AA; 1167 MW; DB9205AB59DB42D6 CRC64;

```

```

Query Match          50.0%; Score 2; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
   ||
Db 7 SE 8

RESULT 41
P82429 PRELIMINARY; PRT; 9 AA.
AC P82429;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 44 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_TaxID=4097;
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER
SQ SEQUENCE 9 AA; 986 MW; C22CCADC6C77776 CRC64;

Query Match          50.0%; Score 2; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
   ||
Db 2 QP 3

RESULT 42
P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 42 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]_TaxID=4097;
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2D5BB1B07 CRC64;

Query Match          50.0%; Score 2; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
   ||
Db 7 SE 8

RESULT 43
P82429 PRELIMINARY; PRT; 9 AA.
AC P82429;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Protein G beta-2 subunit (Fragment).
GN GNB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
EX MEDLINE=98030528; PubMed=9365246;
RA Chretien S., Duprez V., Maouche L., Gisselbrecht S., Mayeux P.,
RA Lacombe C.;
RT "Abnormal erythropoietin (Epo) gene expression in the murine
RT erythroleukemia IW32 cells is issued from a rearrangement between the
RT G-protein b2 gene subunit and the Epo genes.";
RL Oncogene 15:1995-1999(1997).
DR EMBL; Y11970; CAA72706.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 1133 MW; 86FD0736DB172B05 CRC64;

Query Match          50.0%; Score 2; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
   ||
Db 2 SE 3

RESULT 44
P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AML1 protein (Fragment).
GN AML1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Tumor;
RX MEDLINE=97332339; PubMed=9188573;
RA Antoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
RA Pedersen F.S.;
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas
RT induced by attenuated SL3-3 murine leukemia virus mutants.";
RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Query Match          50.0%; Score 2; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
   ||
Db 2 SE 3

RESULT 45
P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AML1 protein (Fragment).
GN AML1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Tumor;
RX MEDLINE=97332339; PubMed=9188573;
RA Antoft H.W., Sorensen A.B., Bareil C., Schmidt J., Luz A.,
RA Pedersen F.S.;
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas
RT induced by attenuated SL3-3 murine leukemia virus mutants.";
RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

```

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

Db 3 QP 4

RESULT 45

Q82622 ID Q82622 PRELIMINARY; PRT; 9 AA.
 AC Q82622;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ORF A (Fragment).
 OS Avian infectious bronchitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 RN NCBI_TaxID=11120;
 RX MEDLINE=86010264; PubMed=2995560;
 RA Bourns M.E., Binns M.M., Brown T.D.K.;
 RT "Sequencing of coronavirus IBV genomic RNA: Three open reading frames
 in the 5' 'unique' region of mRNA D.";
 RL J. Gen. Virol. 66:2253-2258(1985).
 DR EMBL; M29338; AAA46234.1; -.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1134 MW; D2C4B3327741B46 CRC64;

Query Match 50.0%; Score 2; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3

Db 1 EQ 2

RESULT 46

Q83622 ID Q83622 PRELIMINARY; PRT; 9 AA.
 AC Q83622;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 1.1 kDa protein (Fragment).
 OS Murray valley encephalitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 RN NCBI_TaxID=11079;
 RX MEDLINE=88119912; PubMed=2828633;
 RA Hahn C.S., Hahn Y.S., Rice C.M., Lee E., Dalgarno L., Strauss E.G.,
 RA Strauss J.H.;
 RT "Conserved elements in the 3' untranslated region of flavivirus RNAs
 and potential cyclization sequences.";
 RL J. Mol. Biol. 198:33-41(1987).
 DR EMBL; M35172; AAA66627.1; -.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 1055 MW; FF36D40AAB05A2C1 CRC64;

Query Match 50.0%; Score 2; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2

Db 4 SE 5

RESULT 47

Q8AYL5 ID Q8AYL5 PRELIMINARY; PRT; 9 AA.
 AC Q8AYL5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome P450 aromatase (Fragment).
 GN CYP19A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 RN NCBI_TaxID=7957;
 RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 in the brain and ovary of teleost fish.";
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324897; AAN32618.1; -.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 1060 MW; C49E76D7272B040D CRC64;

Query Match 50.0%; Score 2; DB 13; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

Db 7 QP 8

RESULT 48

Q8AUM7 ID Q8AUM7 PRELIMINARY; PRT; 9 AA.
 AC Q8AUM7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cytochrome P450 aromatase (Fragment).
 GN CYP19A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Catassius.
 RN NCBI_TaxID=7957;
 RP SEQUENCE FROM N.A.
 RA Tchoudakova A.V., Kishida M., Wood E., Callard G.V.;
 RT "Promoter characteristics of two CYP19 genes differentially expressed
 in the brain and ovary of teleost fish.";
 RL J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
 DR EMBL; AF324895; AAN32616.1; -.
 DR EMBL; AF324896; AAN32617.1; -.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;

Query Match 50.0%; Score 2; DB 13; Length 9;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4

Db 7 QP 8

RESULT 49

Q8AEW8 ID Q8AEW8 PRELIMINARY; PRT; 9 AA.
 AC Q8AEW8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

```
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (Fragment).
GN Human immunodeficiency virus 1.
OS Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HAART patient 26;
RA Saurya S.;
RT "Characterization of HIV-1 genes from AIDS patients on combination
RT therapy with discordance between viral load and CD4+ T cell counts.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ496724; CAD43154.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1020 MW; 9D2A4411ADC1AB05 CRC64;

Query Match 50.0%; Score 2; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 2 SE 3

RESULT 50
Q935G1 PRELIMINARY; PRT; 9 AA.
AC Q935G1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative membrane protein (fragment).
GN HCM1_01C.
OS Salmonella typhi.
OG Plasmid pHCM1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Churcher C., Mungall K.L., Bentley S.D., Chillingworth T., Connor P.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
DR EMBL; AL513383; CAD09867.1; -.
KW Plasmid; Complete proteome.
FT NON_TER 9
SQ SEQUENCE 9 AA; 904 MW; 5FDC77776D86767 CRC64;

Query Match 50.0%; Score 2; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 5 QP 6

RESULT 51
Q9ZIB1 PRELIMINARY; PRT; 10 AA.
ID Q9ZIB1
AC Q9ZIB1;
```

```
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Toxin B (Fragment).
GN TOXB.
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1496;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8864;
RA Dodson A.P., Borriello S.P.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035716; AAD02038.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1120 MW; 913DA042C736DDC1 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 9 SE 10

RESULT 52
P82588 PRELIMINARY; PRT; 10 AA.
ID P82588
AC P82588;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Unknown protein from 2D-page (fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=13114;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=JRS4;
RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
RA VanBogelen R.A.;
RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes
RT proteins.";
RL Submitted (MAY-2000) to the SWISS-PROT data bank.
CC -1- MASS SPECTROMETRY: MW=23573.25; METHOD=ELECTROSPRAY.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1134 MW; 4D5A1DCB105685B7 CRC64;

Query Match 50.0%; Score 2; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 1 SE 2

RESULT 53
Q8NER0 PRELIMINARY; PRT; 10 AA.
ID Q8NER0
AC Q8NER0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ahi-1 isoform I (fragment).
GN AHI-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```



```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12186888;
RA Jiang X., Hanna Z., Kaouass M., Girard L., Jolicoeur P.;
RT "Ahi-1, a Novel Gene Encoding a Modular Protein with WD40-Repeat and
RT SH3 Domains, Is Targeted by the Ahi-1 and Mis-2 Provirus
RT Integrations.";
RL J. Virol. 76:9046-9059(2002).
DR EMBL; AY133243; AAM94177.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1062 MW; 838C04D505BB1DC1 CRC64;

Query Match 50.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 6 SE 7

RESULT 54
O00493 PRELIMINARY; PRT; 10 AA.
ID O00493
AC O00493;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MJD1 alt MS (Fragment).
GN MJD1 INC 45.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Leukocyte;
RA Sugawara M., Toyoshima I., Takeda S., Imota T., Kato K., Wada C.,
RT "Genomic DNA containing the insertion that is seen in the alternative
RT transcript of MJD1.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003802; BAA20388.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1161 MW; 9A6E507B1AB2CB05 CRC64;

Query Match 50.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SE 2
Db 3 SE 4

RESULT 55
Q96QT9 PRELIMINARY; PRT; 10 AA.
ID Q96QT9
AC Q96QT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Protein tyrosine phosphatase 1B (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21326081; PubMed=11316810;
RA Fukada T., Tonks N.K.;
RT "The Reciprocal Role of Egr-1 and Sp Family Proteins in Regulation of

```

```

RT the PTP1B Promoter in Response to the p210 Bcr-Abl Oncoprotein-
RT tyrosine Kinase.";
RL J. Biol. Chem. 276:25512-25519(2001).
DR EMBL; AY029236; AAK31734.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1314 MW; AC08E219CB133B16 CRC64;

Query Match 50.0%; Score 2; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 8 EQ 9

RESULT 56
Q8MUP1 PRELIMINARY; PRT; 10 AA.
ID Q8MUP1
AC Q8MUP1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN MPI.
OS Heliconius cydno chioneus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
OX NCBI_TaxID=171915;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-STRI-B-569-Mpi-1;
RA Bull V., Beltran M., Birmingham E., Jiggins C., McMillan O.,
RA Mallet J.;
RT "Molecular evidence for gene flow between species of Heliconius.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516213; AAM61899.1; -.
KW Isomerase.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1175 MW; 56A626DB1DD1EAA3 CRC64;

Query Match 50.0%; Score 2; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQ 3
Db 7 EQ 8

RESULT 57
Q8WPL6 PRELIMINARY; PRT; 10 AA.
ID Q8WPL6
AC Q8WPL6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to wasp protein (Fragment).
GN BAC001.19.
OS Oikopleura dioica.
OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
OC Oikopleuridae; Oikopleura.
OX NCBI_TaxID=34765;
RN [1]
RP SEQUENCE FROM N.A.
RA Seo H.C., Kube M., Edvardsen R.B., Jensen M.F., Beck A., Spriet E.,
RA Gorsky G., Thompson E.M., Lehrach H., Reinhardt R., Chourrout D.;
RT "The marine chordate Oikopleura dioica has a miniature genome.";
RL Science 0:0-0(2001).
DR EMBL; AF374376; AAL56467.1; -.
FT NON_TER 10

```

```

SQ SEQUENCE 10 AA; 1079 MW; 7C9F8A3DDB05A40B CRC64;
  Query Match 50.0%; Score 2; DB 5; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.8e+04;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 5 SE 6

RESULT 58
QBMUN7 PRELIMINARY; PRT; 10 AA.
AC Q8MUN7;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN MPI.
OS Heliconius melpomene rosina.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconius.
OX NCBI_TaxID=171916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-STRI-B-548-Mpi-1;
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
RA Mallet J.;
RT "Molecular evidence for gene flow between species of Heliconius.";
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516237; AAM61923.1; -.
KW Isomerase.
FT NON_TER 1 10
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1175 MW; 56A626DB1DD1EAA3 CRC64;

  Query Match 50.0%; Score 2; DB 5; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.8e+04;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 7 EQ 8

RESULT 59
P82217 PRELIMINARY; PRT; 10 AA.
AC P82217;
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RA MDLINE=21177481; PubMed=11280994;
RX Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
RT silkworm.";
RL I Chuan Hsueh Pao 28:217-224 (2001).
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1148 MW; DC779AB32AE451A9 CRC64;

  Query Match 50.0%; Score 2; DB 5; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.8e+04;

SQ SEQUENCE 10 AA; 1256 MW; 13A904D1B6DB173B CRC64;

  Query Match 50.0%; Score 2; DB 6; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.8e+04;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 5 EQ 6

RESULT 61
P83205 PRELIMINARY; PRT; 10 AA.
AC P83205;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Placenta;
RA El Amir B., Remy B., Sousa N.M., Beckers J.-F.M.P.;
RT "Isolation and characterization of pregnancy-associated glycoproteins
RT extracted from sheep (Ovis aries) placentas.";
RL Mol. Reprod. Dev. 0:0-0(2002).
CC -!- FUNCTION: THIOLESTERASE WHICH IS BELIEVED TO PARTICIPATE IN
CC INTRACELLULAR DEGRADATION AND TURNOVER OF PROTEINS. HAS ALSO BEEN
CC IMPLICATED IN TUMOR INVASION AND METASTASIS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: HYDROLYZES PROTEINS, WITH A SPECIFICITY
CC RESEMBLING THAT OF PAPAIN.
CC -!- SUBUNIT: DIMER OF A HEAVY CHAIN AND A LIGHT CHAIN CROSS-LINKED BY
CC A DISULFIDE BOND (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: LYSOSOMAL (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro; IPR000169; Stprot acsite.
DR PROSITE; PS00640; THIOLESTERASE ASN; PARTIAL.
DR PROSITE; PS00139; THIOLESTERASE_CYS; PARTIAL.

```

DR PROSITE; PS00639; THIOLE PROTEASE HIS; PARTIAL.
 KW Hydrolase; Thiol protease; Lysosome.
 FT CHAIN 1 >10 CAIHEPSIN B LIGHT CHAIN.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;
 Query Match 50.0%; Score 2; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 EQ 3
 Db 9 EQ 10

RESULT 62

Q8WB7 PRELIMINARY; PRT; 10 AA.
 AC Q8WB7; 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DE Cytochrome oxidase subunit I (Fragment).
 GN COI.
 OS Chaitophorus leucomelas.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 OC Aphidoidea; Drepanosiphidae; Chaitophorus.
 OX NCBI_TaxID=136351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shingleton A.W., Stern D.L.;
 RT "Molecular phylogenetic evidence for multiple origins of ant mutualism within the aphid genus Chaitophorus."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF444288; AAL38565.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;
 Query Match 50.0%; Score 2; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SE 2
 Db 2 SE 3

RESULT 63

Q96041 PRELIMINARY; PRT; 10 AA.
 AC Q96041; 02, Created)
 DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)
 DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)
 DE NADH-ubiquinone oxidoreductase subunit 3 (Fragment).
 GN NAD3.
 OS Oenothera bertiana (Bertero's evening primrose).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Myrtales; Onagraceae; Oenothera.
 OX NCBI_TaxID=3950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schuster W.;
 RT "Ribosomal protein gene rpl5 is cotranscribed with the nad3 gene in Oenothera mitochondria."
 RL Mol. Gen. Genet. 240:445-449 (1993).
 DR EMBL; X69553; CAA49285.1; -.

KW Mitochondrion; Ubiquinone.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1097 MW; 723067B0476DD9CB CRC64;
 Query Match 50.0%; Score 2; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SE 2
 Db 2 SE 3

RESULT 64

Q8SHA8 PRELIMINARY; PRT; 10 AA.
 AC Q8SHA8; 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DE Cytochrome c oxidase subunit I (fragment).
 GN COI.
 OS Rhampholeon spectrum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
 OC Rhampholeon.
 OX NCBI_TaxID=179929;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Townsend T.M., Larson A.L.;
 RT "Molecular Phylogenetics and Mitochondrial Genomic Evolution in the Chamaeleonidae (Reptilia, Squamata)."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF448772; AAL90598.1; -.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1279 MW; 35BF8E27336409D7 CRC64;
 Query Match 50.0%; Score 2; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 OP 4
 Db 2 QP 3

RESULT 65

Q8LLJ0 PRELIMINARY; PRT; 10 AA.
 AC Q8LLJ0; 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DE Cytochrome C (Fragment).
 GN CCI.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22167279; PubMed=12177461;
 RA Jang I.-C., Choi W.-B., Lee K.-H., Song S.-I., Nahm B.H., Kim J.-K.;
 RT "High-Level and Ubiquitous Expression of the Rice Cytochrome c Gene OsCci and Its Promoter Activity in Transgenic Plants Provides a Useful Plant Promoter for Transgenesis of Monocots."
 RL Plant Physiol. 129:1473-1481 (2002).
 DR EMBL; AF399666; AAM95337.1; -.
 DR Gramene; Q8LLJ0; -.
 FT NON_TER 10 10

SQ SEQUENCE 10 AA; 993 MW; 973D4B6GDB05B9D5 CRC64;

Query Match
Best Local Similarity 50.0%; Score 2; DB 10; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 5 SE 6

RESULT 66

Q8GUV6 PRELIMINARY; PRT; 10 AA.

AC Q8GUV6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative receptor-like kinase (Fragment).
GN RLK1.
OS Capsella rubella.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosid II; Brassicales; Brassicaceae; Capsella.
OX NCBI_TaxID=81985;
RN [1]
RP SEQUENCE FROM N.A.
RA Wanke D., Gielkowski I., Spitzer C., Mukhtar M.S., Bollenbach L.,
RA Bruemmer J., Deslandes L., Seki H., Turck F., Zhou A., Uelker B.,
RA Smessich I.;
RT "Structure and evolution of stress related proteins."
RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY167750; AA012512.1; --
KW Receptor; Kinase.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1010 MW; 6C9C7DC455A1ADDB CRC64;

Query Match
Best Local Similarity 50.0%; Score 2; DB 10; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 2 SE 3

RESULT 67

Q91WZ3 PRELIMINARY; PRT; 10 AA.

AC Q91WZ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Lutetizing hormone/chorionic gonadotropin receptor homolog (Fragment).
DE Rattus sp.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96147985; PubMed=8571710;
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl O.P.;
RT "[Cloning and overexpression of rat ovary LH/hCG receptor cDNA in insect cells].";
RL Shih Yen Sheng Wu Hsueh Pao 28:283-290(1995).
DR EMBL; S80660; AAB50710.1; --
KW Chorion; Receptor.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1129 MW; 09A5F22DC4177760 CRC64;

Query Match
Best Local Similarity 50.0%; Score 2; DB 11; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
DB 1 QP 2

RESULT 68

Q9QVE8 PRELIMINARY; PRT; 10 AA.

AC Q9QVE8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/16 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the processing of mouse protamine P2 precursor."
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
SQ SEQUENCE 10 AA; 1224 MW; D4050B040B1EAB6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2; DB 11; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
DB 9 EQ 10

RESULT 69

Q9QVF0 PRELIMINARY; PRT; 10 AA.

AC Q9QVF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/5 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the processing of mouse protamine P2 precursor."
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 10
SQ SEQUENCE 10 AA; 1125 MW; 9E14CE687B05A775 CRC64;

Query Match
Best Local Similarity 100.0%; Score 2; DB 11; Length 10;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
DB 5 SE 6

RESULT 70

Q9QVF1

```

ID Q9QVF1 PRELIMINARY; PRT; 10 AA.
AC Q9QVF1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinge A., Debarie M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
RT processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1280 MW; 01DD2975A406841B CRC64;

Query Match 50.0%; Score 2; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SE 2
Db 9 SE 10

RESULT 71
Q9QVE7 PRELIMINARY; PRT; 10 AA.
ID Q9QVE7;
AC Q9QVE7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/20 (fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinge A., Debarie M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
RT processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1197 MW; 79920ED866DB1B04 CRC64;

Query Match 50.0%; Score 2; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQ 3
Db 5 EQ 6

RESULT 72
Q8CJEO PRELIMINARY; PRT; 10 AA.
ID Q8CJEO;
AC Q8CJEO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Resistin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

```

```

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Nohira T., Hisatomi H.;
RT "Rattus norvegicus resistin DNA, intron2.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB093559; BAC21195.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1079 MW; 34EA46D326DDC777 CRC64;

Query Match 50.0%; Score 2; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 9 QP 10

RESULT 73
P90391 PRELIMINARY; PRT; 10 AA.
ID P90391;
AC P90391;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C2 protein (Fragment).
OS Tomato yellow leaf curl virus (TYLCV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10832;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TYLCV-Is;
RA Wernecke M.E., Roye M.E., McLaughlin W.A., Nakhla M.K., Maxwell D.P.;
RT "Identification of tomato yellow leaf curl geminivirus (TYLCV-Is) in
RT tomatoes and peppers in Jamaica.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U84397; AAB47965.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1058 MW; 25FF98B5A775A5A7 CRC64;

Query Match 50.0%; Score 2; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QP 4
Db 2 QP 3

RESULT 74
Q86580 PRELIMINARY; PRT; 10 AA.
ID Q86580;
AC Q86580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Large protein (Fragment).
OS Simian parainfluenza virus 5.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulaviruses.
OX NCBI_TaxID=11207;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93224905; PubMed=8385701;
RA Higuchi Y., Miyahara Y., Kawano M., Tsurudome M., Matsumura H.,
RA Kusagawa S., Komada H., Nishio M., Ito Y.;
RT "Sequence analysis of the large (L) protein of simian virus 5.";
RL J. Gen. Virol. 74:789-789(1993).
DR EMBL; S57860; AAB26118.1; -.
FT NON_TER 1 1

```

SQ SEQUENCE 10 AA; 1144 MW; 0C25A0D9C86776D4 CRC64;
Query Match 50.0%; Score 2; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QP 4
Db 4 QP 5
RESULT 75
Q86324
ID Q86324 PRELIMINARY; PET; 10 AA.
AC Q86324;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gp37 (Fragment).
GN ENV.
OS Rous sarcoma virus.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11886;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Schmidt-Ruppin subgroup A;
RX MEDLINE=98083689; PubMed=9421881;
RA Hara H., Kaji A.;
RT "the U3 region of the long terminal repeat of a subgroup A
RT transformation-defective Rous sarcoma virus (tdpH2010) converts a
RL noncytopathic virus to a cytopathic virus."
RL Virus Genes 15:171-180(1997).
DR EMBL; U41726; AAB60580.1; -.
FT NON TER 1
SQ SEQUENCE 10 AA; 1119 MW; 27ED4115BB0776D8 CRC64;
Query Match 50.0%; Score 2; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 QP 4
Db 4 QP 5

Search completed: November 25, 2003, 18:25:30
Job time : 11.6883 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:01:38 ; Search time 12.9574 Seconds
(without alignments)
48.999 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4	100.0	4	22	Colostrin derive
2	4	100.0	4	22	Colostrin peptid
3	4	100.0	4	22	Colostrin peptid
4	4	100.0	4	22	Ewe colostrin pe
5	4	100.0	4	23	Colostrin consti
6	4	100.0	4	23	Colostrin consti
7	4	100.0	4	23	Neural cell regula
8	4	100.0	8	22	Ewe colostrin pe
9	4	100.0	10	22	Human peptide #165

10	4	100.0	13	18	AAW38008	WW domain binding
11	4	100.0	15	19	AAW21371	Human HUPF-1 mutan
12	4	100.0	17	20	AAW81031	Melanoma associate
13	4	100.0	18	21	AAW23520	Human negative elo
14	4	100.0	20	21	AAW03800	Human III activity i
15	3	75.0	3	22	AAW91032	Thyrotropin releas
16	3	75.0	5	21	AAW29539	Alpha-helical link
17	3	75.0	5	22	AAW07152	Substituted phenan
18	3	75.0	6	16	AAW83516	Peptide mimetic of
19	3	75.0	6	19	AAW61750	Peptide mimetic of
20	3	75.0	6	20	AAW97058	Peptidomimetic cap
21	3	75.0	6	20	AAW94750	Mutant H protein a
22	3	75.0	6	20	AAW84413	HIV-1 nucleic acid
23	3	75.0	6	22	AAW86473	Human gliadin pept
24	3	75.0	6	22	AAW86474	Human gliadin pept
25	3	75.0	6	22	AAW86481	Human gliadin pept
26	3	75.0	6	22	AAW86486	Human gliadin pept
27	3	75.0	6	22	AAW86487	Human gliadin pept
28	3	75.0	6	22	AAW86494	Human gliadin pept
29	3	75.0	6	22	AAW86497	Human gliadin pept
30	3	75.0	6	22	AAE05001	Synthetic peptide
31	3	75.0	6	22	AAW60618	Stp100 thrombospon
32	3	75.0	6	24	ABP70731	Phosphorylation si
33	3	75.0	7	20	AAW50012	Thermus thermophil
34	3	75.0	7	20	AAW48764	Membrane dipeptid
35	3	75.0	7	22	AAW44117	H11 binding site c
36	3	75.0	7	22	AAW44119	H11 binding site c
37	3	75.0	7	22	AAW44154	H11 binding site c
38	3	75.0	7	22	AAW44232	H11 binding site c
39	3	75.0	7	22	AAW44237	H11 binding site c
40	3	75.0	7	22	AAW44242	H11 binding site c
41	3	75.0	7	22	AAW44247	H11 binding site c
42	3	75.0	7	22	AAW44252	H11 binding site c
43	3	75.0	7	22	AAW44257	H11 binding site c
44	3	75.0	7	22	AAW46757	H11 binding site c
45	3	75.0	7	22	AAW68700	Cleavage signal pe
46	3	75.0	8	5	AAW40188	Hexapeptide coded
47	3	75.0	8	7	AAW60137	Sequence of prefer
48	3	75.0	8	14	AAW35925	Hepatitis C virus
49	3	75.0	8	15	AAW59433	Gp2b(896-903) pept
50	3	75.0	8	15	AAW48371	Peptide fragment w
51	3	75.0	8	15	AAW58622	G2b residues 996-
52	3	75.0	8	15	AAW586119	Peptide derived fr
53	3	75.0	8	18	AAW33664	Poliovirus type 3
54	3	75.0	8	19	AAW79269	Bovine glucuronyl
55	3	75.0	8	19	AAW45999	Peptide #24 based
56	3	75.0	8	19	AAW46001	Peptide #27 based
57	3	75.0	8	22	ABP21164	HIV A03 motif pol
58	3	75.0	8	22	ABP21201	HIV A03 motif pol
59	3	75.0	8	22	ABP23175	HIV A11 motif pol
60	3	75.0	8	22	ABW52109	Human API-73 trypt
61	3	75.0	8	23	AAO15739	Haemophilus influe
62	3	75.0	8	23	ABG31180	Rat delta PKC regi
63	3	75.0	8	23	ABG50428	Selective targetin
64	3	75.0	8	24	ABJ38203	Human cytomagalovi
65	3	75.0	9	13	AAW26441	N-terminal auxilia
66	3	75.0	9	16	AAW87291	Plasmodium falcipa
67	3	75.0	9	17	AAW49287	Human leucocyte an
68	3	75.0	9	17	AAW07112	Synthetic peptide
69	3	75.0	9	18	AAW29260	Soybean hydrolysat
70	3	75.0	9	20	AAW53335	Bcr-Abl epitope (a
71	3	75.0	9	20	AAW40157	Amino acid sequenc
72	3	75.0	9	20	AAW26673	BCR-ABL-derived li
73	3	75.0	9	20	AAW74273	HJ loop peptide K1
74	3	75.0	9	20	AAW74285	HJ loop peptide K0
75	3	75.0	9	20	AAW96177	YKK-alpha polypept
76	3	75.0	9	21	AAW56091	LCMW nucleoprotein
77	3	75.0	9	21	AAW44419	HLA-A1 binding orn
78	3	75.0	9	22	ABP21125	HIV A03 motif pol
79	3	75.0	9	22	AAU23816	Human MHC class I
80	3	75.0	9	22	AAU23945	Human MHC class I
81	3	75.0	9	22	AAW07143	N-terminal sequenc
82	3	75.0	9	22	AAW22208	HIV peptide SEQ ID

83 3 75.0 9 22 AAU06538 Human MHC molecule
 84 3 75.0 9 22 AAU06560 Human MHC molecule
 85 3 75.0 9 22 AAU06777 Human MHC molecule
 86 3 75.0 9 22 AAU06901 Human MHC molecule
 87 3 75.0 9 22 AAG99519 PRAME derived HLA-
 88 3 75.0 9 22 AAB76046 Trypanosoma cruzi
 89 3 75.0 9 22 AAB37962 Antithrombin III m
 90 3 75.0 9 23 ABG79105 Human ELF2 class I
 91 3 75.0 9 23 ABG79105 Hepatitis B virus
 92 3 75.0 9 23 ABG32314 HLA-A2 associated
 93 3 75.0 9 23 ABB51670 Human 34P3D7 HLA A
 94 3 75.0 9 23 ABB51848 Human 34P3D7 HLA B
 95 3 75.0 9 23 ABB51967 Human 34P3D7 HLA B
 96 3 75.0 9 24 ABJ38202 Human cytomagalovi
 97 3 75.0 9 24 ABJ38205 Human cytomagalovi
 98 3 75.0 9 24 ABR16023 Human cancer-relat
 99 3 75.0 9 24 ABR16177 Human cancer-relat
 100 3 75.0 9 24 ABR16202 Human cancer-relat

ALIGNMENTS

RESULT 1

AAB72255
 ID AAB72255 standard; peptide; 4 AA.

XX
 AC AAB72255;

DT 14-MAY-2001 (first entry)

XX Colostrinin derived cytokine inducing peptide SEQ ID 10.

XX Colostrinin; immune response; cytokine; blood cell proliferation;
 KW central nervous system disorder; neurological disorder; mental disorder;
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
 KW neurosis; infection.

XX Synthetic.

XX WO200111937-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22818.

XX 17-AUG-1999; 99US-0149311.

XX (TEXA) UNIV TEXAS SYSTEM.

XX (REGS-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX WPI; 2001-202804/20.

XX Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator -

XX Claim 1; Page 34; 50pp; English.

XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The
 CC peptides have immune response modulatory activity, and are capable of
 CC inducing cytokines. Colostrinin and its derived peptides are useful for
 CC inducing cytokine production, for modulating an immunological response
 CC and for inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies.

XX SQ Sequence 4 AA;
 Query Match 100.0%; Score 4; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQP 4

Db 1 SEQP 4

RESULT 2

AAB72509

ID AAB72509 standard; Peptide; 4 AA.

XX AAB72509;

AC AAB72509;

XX 09-MAY-2001 (first entry)

XX Colostrinin peptide #10.

XX Dermatological; oxidative stress regulator; colostrinin.

XX Unidentified.

XX WO200112650-A2.

XX 22-FEB-2001.

XX 17-AUG-2000; 2000WO-US22665.

XX 17-AUG-1999; 99US-0149310.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Stanton GJ, Hughes TK, Boldogh I;

XX WPI; 2001-218342/22.

XX Modulating oxidative stress level in a cell, involves contacting the
 PT cell with an oxidative stress regulator selected from colostrinin, its
 PT constituent peptide, analog or their combinations -

XX Claim 6; Page 25; 48pp; English.

XX The present invention relates to a method for modulating the oxidative
 CC stress level in a cell or a patient, comprising contacting the cell with,
 CC or administering to the patient, an oxidative stress regulator selected
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),
 CC to change the level of an oxidising species in the cell. The method can
 CC be used to treat oxidative damage to skin, by decreasing or preventing an
 CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 4; DB 22; Length 4;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQP 4

Db 1 SEQP 4

RESULT 3

AAB72541

ID AAB72541 standard; Peptide; 4 AA.

XX AAB72541;

XX 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #10.
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX Unidentified.
 OS
 XX WC200112651-A2.
 PN
 XX 22-FEB-2001.
 PD
 XX 17-AUG-2000; 2000WO-US22774.
 PF
 XX 17-AUG-1999; 99US-0149633.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Boldogh I;
 XX
 PI WPI; 2001-226545/23.
 DR
 XX Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating
 PT damaged neural cells in a patient -
 PT
 XX
 PS Claim 6; Page 21; 35pp; English.
 PS
 XX The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.
 CC
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 4; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQP 4
 Db |||||
 1 SEQP 4

RESULT 4
 AAB59314
 ID AAB59314 standard; Peptide; 4 AA.
 XX
 AC AAB59314;
 AC
 DT 21-MAR-2001 (first entry)
 DT
 XX Ewe colostrinin peptide fragment A-5.
 DE
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
 KW
 XX
 OS Ovis sp.
 XX
 PN WO200075173-A2.
 PN
 XX 14-DEC-2000.
 PD
 XX 02-JUN-2000; 2000WO-GB02128.
 PF
 XX 02-JUN-1999; 99GB-0012852.
 PR
 XX (REGE-) REGEN THERAPEUTICS PLC.
 PA
 XX Georgiades JA;
 PI
 XX WPI; 2001-071058/08.
 DR
 XX Peptides having an N-terminal amino acid sequence isolated from

PT colostrinin for treating e.g. disorders of the central nervous system
 PT and immune system, viral and bacterial infections, and diseases
 PT characterized by amyloid plaques -
 XX
 PS Claim 7; Page 27; 63pp; English.
 XX
 XX The present invention provides the sequences of a number of peptides
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
 CC fragment of colostrum. These peptides can be used in the treatment of
 CC central nervous system disorders such as senile dementia, Parkinson's
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system
 CC disorders such as bacterial and viral infections, to improve the
 CC development of a child's immune system, as a dietary supplement, and to
 CC promote the dissolution of beta-amyloid plaques.
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 4; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQP 4
 Db |||||
 1 SEQP 4

RESULT 5
 AAE20237
 ID AAE20237 standard; peptide; 4 AA.
 XX
 AC AAE20237;
 AC
 DT 18-JUN-2002 (first entry)
 DT
 XX Colostrinin constituent peptide #10.
 DE
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnery.
 KW
 XX Unidentified.
 OS
 XX
 PH Key Location/Qualifiers
 FT Modified-site 4 /note= "Optionally C-terminal amide"
 FT
 XX WO200213850-A1.
 PN
 XX 21-FEB-2002.
 PD
 XX 17-AUG-2000; 2000WO-US22776.
 PF
 XX 17-AUG-2000; 2000WO-US22776.
 PR
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA
 XX Stanton GJ, Hughes TK, Boidogh I;
 PI WPI; 2002-269151/31.
 DR
 XX Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog -
 XX
 PS Claim 6; Page 25; 51pp; English.
 PS
 XX The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress
 CC level in a cell e.g. mammalian or human cell present in a cell culture,
 CC tissue, organ, or organism; or for treating oxidative damage to the skin
 CC of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide.

XX Sequence 4 AA;

Query Match 100.0%; Score 4; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQP 4
 ||||
 Db 1 SEQP 4

RESULT 6

AAWS1045
 ID AAMS1045 standard; Peptide; 4 AA.

AC AAMS1045;

DT 30-MAY-2002 (first entry)

DE Colostrinin constituent peptide.

KW Colostrinin; colostrum; immunomodulator; cardiovascular;
 KW blood cell regulator; cytokine inducer; human.

XX Homo sapiens.

OS Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "Optional C-terminal amidation"

FN WO200213849-A1.

XX 21-FEB-2002.

PD 17-AUG-2000; 2000WO-US22775.

PF 17-AUG-2000; 2000WO-US22775.

PR (TEXA) UNIV TEXAS SYSTEM.

PA (REGE-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

PI WPI; 2002-269150/31.

DR Modulation of blood cell proliferation in a patient involves use of
 PT blood cell regulator selected from colostrinin, its constituent peptide
 PT and/or analogue

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide
 CC that is used as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. Methods are
 CC claimed for: inducing a cytokine in a cell by contact with an
 CC immunological regulator, where the cell is present in a cell
 CC culture, a tissue, an organ or an organism, and the cell is
 CC mammalian, including human; modulating an immune response in a cell
 CC by contact with the immunological regulator under conditions
 CC effective to induce a cytokine; modulating an immune response in a

CC patient by administering an immunological regulator under conditions
 CC effective to induce a cytokine, where the immunological regulator
 CC is administered topically or as part of a dietary supplement, and
 CC where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation
 CC by contacting blood cells with a blood cell regulator, where the
 CC blood cells are present in a cell culture or an organism, are
 CC mammalian or human, and where the blood cells are increased in
 CC number or differentiated; and a method for modulating blood cell
 CC proliferation in a patent. A claimed cytokine-inducing composition
 CC comprises a pharmaceutical carrier and an active agent such as the
 CC present peptide.

XX Sequence 4 AA;

Query Match 100.0%; Score 4; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQP 4
 ||||
 Db 1 SEQP 4

RESULT 7

AAO14586
 ID AAO14586 standard; peptide; 4 AA.

AC AAO14586;

DT 27-MAY-2002 (first entry)

DE Neural cell regulatory colostrinin peptide 10.

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;
 KW neural cell treatment.

XX Unidentified.

OS Key Location/Qualifiers
 FH Modified-site 4
 FT /note= "Optional C-terminal amide"

FN WO200213851-A1.

XX 21-FEB-2002.

PD 17-AUG-2000; 2000WO-US22777.

PF 17-AUG-2000; 2000WO-US22777.

PR (TEXA) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;

PI WPI; 2002-269152/31.

DR Promoting cell differentiation in a patient involves use of blood cell
 PT regulator selected from colostrinin, its constituent peptide and/or
 PT analog

XX Claim 7; Page 21; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.
 CC neural cell differentiation). The method involves contacting cells with a
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich
 CC polypeptide aggregate that is present in colostrum. The method of the
 CC invention is useful for promoting the differentiation of cells and for
 CC treating damaged neural cells in a patient. The present amino acid
 CC sequence represents a specifically claimed colostrinin peptide used in
 CC the method of the invention.

XX SQ Sequence 4 AA;
Query Match 100.0%; Score 4; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEQP 4
Db 1 SEQP 4
RESULT 8
AAB59345
ID AAB59345 standard; Peptide; 8 AA.
AC AAB59345;
XX DT 21-MAR-2001 (first entry)
XX DE Ewe colostrinin peptide fragment derived sequence #5.
XX KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX OS Ovis sp.
XX PN WO200075173-A2.
XX PD 14-DEC-2000.
XX PF 02-JUN-2000; 2000WO-GB02128.
XX PR 02-JUN-1999; 99GB-0012852.
XX PA (REGG-) REGEN THERAPEUTICS PLC.
XX PI Georgiades JA;
XX DR WPI; 2001-071058/08.
XX PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX PS Claim 8; Page 27; 63pp; English.
XX CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX SQ Sequence 8 AA;
Query Match 100.0%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEQP 4
Db 1 SEQP 4
RESULT 9
AAM98380
ID AAM98380 standard; Peptide; 10 AA.
XX AC AAM98380;

XX 24-JAN-2002 (first entry)
XX DE Human peptide #1655 encoded by a SNP oligonucleotide.
XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; histone; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX OS Homo sapiens.
XX PN WO200147944-A2.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000WO-US35498.
XX PR 28-DEC-1999; 99US-0173419.
XX PR 27-DEC-2000; 2000US-0173419.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach M;
XX DR WPI; 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX PS Disclosure; Page 4031; 4143pp; English.
XX CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.
XX SQ Sequence 10 AA;
Query Match 100.0%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SEQP 4
Db 3 SEQP 6
RESULT 10
AAW38008
ID AAW38008 standard; Peptide; 13 AA.
XX AC AAW38008;
XX DT 23-APR-1998 (first entry)
XX

DE WW domain binding clone 4 obtained from a pp library.
 XX
 KW Peptide recognition unit; WW domain; cell signalling; growth regulation;
 KW cytoskeleton organisation; targeted drug screening; modulator;
 KW WW domain interaction.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 6..9
 FT /note= "PPPPY motif"
 XX
 PN WO9737223-A1.
 XX
 PD 09-OCT-1997.
 XX
 PF 03-APR-1997; 97WO-US05547.
 XX
 PR 03-APR-1996; 96US-0630916.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UYNC-) UNIV NORTH CAROLINA.
 XX
 PI Fowlkes DM, Kay BK, Pirozzi G;
 DR WPI; 1997-503234/46.
 XX
 XX Identifying cell signalling and growth regulatory polypeptides by
 PT reaction with multivalent recognition complex - polypeptides are
 PT useful in targetted drug selection
 XX
 PS Claim 92; Fig 27; 220pp; English.
 XX
 CC Peptides AA38005-08 are the sequences of WW domain binding clones
 CC obtained by screening random or biased libraries with the WW domains of
 CC the novel WWP proteins. The present peptide was obtained after screening
 CC with WW domain 1 of WWP1 (WWP1.1). The peptides are peptide recognition
 CC units ("ligands"), and are used for analysing specificities of the WW
 CC domains. The WW domain is a small functional domain. Its name is derived
 CC from the observation that two tryptophan residues, one in the amino
 CC terminal portion of the WW domain and one in the carboxyl terminal
 CC portion, are conserved. Most proteins containing WW domains have a
 CC function involving cell signalling and growth regulation or the
 CC organisation of the cytoskeleton. Polypeptides containing a WW domain
 CC are identified by treating a multivalent recognition unit complex that
 CC has selective binding affinity for a WW domain, with many polypeptides
 CC and identifying those with selective affinity for the complex. Proteins
 CC containing WW domains are used for targeted drug screening, i.e. to
 CC identify potential modulators of specific WW domain interactions.
 CC note: sequence in SEQ ID listing differs from sequence given in figure.
 CC The SEQ ID sequence is as follows: GPSEQPPPEYTVK.
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 4; DB 18; Length 13;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQP 4
 Db 3 SEQP 6
 RESULT 11
 AA2Y21371
 ID AAY21371 standard; Protein; 15 AA.
 XX
 AC AAY21371;
 XX
 DT 22-JUL-1999 (first entry)
 XX
 DE Human HUPF-I mutant protein fragment 23.
 XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 02-APR-1998; 98WO-IB00705.
 XX
 PR 10-APR-1997; 97US-0043163.
 XX
 PA (UYUT-) RIJKSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYKO-) UNIV ROTTERDAM ERASMUS.
 XX
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 DR WPI; 1998-609901/51.
 DR N-PSDB; AAX75768.
 XX
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 PT RNA
 XX
 PS Disclosure; Figure 17; 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC used of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 4; DB 19; Length 15;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQP 4
 Db 1 SEQP 4
 RESULT 12
 AA8W1031
 ID AA8W1031 standard; Peptide; 17 AA.
 XX

XX 05-AUG-1998; 98JP-0232394.
 XX
 XX 05-AUG-1998; 98JP-0232394.
 XX
 XX (SANE-) SANEI TOKA KK.
 XX
 XX WPI; 2000-402976/35.
 XX
 XX Inhibitory peptides of cyclic nucleotide phosphodiesterase III
 PT activity. -
 XX
 XX Claim 1; Page 2; 5pp; Japanese.
 XX
 XX This invention relates to 10 peptide (see AAB03795-B03804) which have
 CC inhibitory action against cyclic nucleotide phosphodiesterase III
 CC (PDEIII) activity. The peptides have use as cardiotoxic and
 CC antithrombotic agents. The present sequence represents peptide C18.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 100.0%; Score 4; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQP 4
 DB 8 SEQP 11
 ||||
 RESULT 15
 AAB91032
 ID AAB91032 standard; Peptide; 3 AA.
 XX
 AC AAB91032;
 XX
 XX 22-JUN-2001 (first entry)
 DT
 DE Thytotropin releasing hormone (THR) related peptide SEQ ID NO:206.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200069900-A2.
 PN
 XX 23-NOV-2000.
 PD
 XX 17-MAY-2000; 2000WO-US13576.
 PF
 XX 17-MAY-1999; 99US-0134406.
 PR
 XX 10-SEP-1999; 99US-0153406.
 PR
 XX 15-OCT-1999; 99US-0159783.
 PR
 XX (CONJ-) CONJUCHEM INC.
 PA
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 PI
 XX WPI; 2001-112059/12.
 DR
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 XX
 XX Disclosure; Page 257; 733pp; English.
 PS
 XX The present invention describes a modified therapeutic peptide (I)
 XX comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 3 AA;
 SQ
 Query Match 75.0%; Score 3; DB 22; Length 3;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EQP 4
 DB 1 EQP 3
 ||||
 RESULT 16
 AAB29539
 ID AAB29539 standard; peptide; 5 AA.
 XX
 AC AAB29539;
 XX
 XX 14-FEB-2001 (first entry)
 DT
 DE Alpha-helical linker SEQ ID NO:7 used in IL-6R/IL-6 fusion protein.
 XX
 KW Alpha-helical linker peptide; IL-6R/IL-6 fusion protein;
 KW interleukin-6 receptor; antigenicity; stability; immunostimulant.
 XX
 OS Synthetic.
 OS
 XX JP20000247997-A.
 PN
 XX 12-SEP-2000.
 PD
 XX 23-FEB-1999; 99JP-0044620.
 PF
 XX 23-FEB-1999; 99JP-0044620.
 PR
 XX (TOXJ) TOSOH CORP.
 PA
 XX WPI; 2000-675256/66.
 DR
 XX A fusion protein comprising interleukin-6 (IL-6) receptor and IL-6
 PT useful as drug for stimulating immune system, comprises IL-6 coupled to
 PT its receptor through a peptide linker of alpha helix type -
 XX
 PS Claim 3; Page 8; 17pp; Japanese.
 XX
 XX The invention relates to a fusion protein comprising, N to C-terminally,
 CC an interleukin-6 receptor (IL-6R), an alpha-helical linker peptide
 CC (AAB29535-B29541), and IL-6. The fusion protein has immunostimulant
 CC activity, and may be useful in compositions to stimulate the immune
 CC system. The alpha-helical linker peptides are less antigenic than
 CC conventional linker peptides, and also increase the stability of the
 CC fusion protein. The present sequence represents an alpha-helical
 CC linker peptide used in the IL-6R/IL-6 fusion protein of the invention.
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 75.0%; Score 3; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 2 SEQ 4

RESULT 17

AAU07152
ID AAU07152 standard; peptide; 5 AA.

XX AC AAU07152;
XX DT 24-OCT-2001 (first entry)

XX DE Substituted Phenanthrene-9,10-dione R3 peptide group #3.

XX XX Phenanthrene-9,10-dione; T-cell mediated disorder; autoimmune disease;
KW organ graft rejection; immunosuppressive; CD45 inhibitor; R3 peptide.

XX OS Synthetic.
XX XX WO200146125-A2.
XX PN 28-JUN-2001.

XX PF 18-DEC-2000; 2000WO-GB04854.

XX PR 21-DEC-1999; 99US-0172788.

XX PA (ASTR) ASTRAZENECA AB.
XX PA (ASTR) ASTRAZENECA UK LTD.

XX PI Chapdelaine MJ, Knappenberger K, Steelman G, Suchard S, Sygowski L;
PI Urbanek R, Veale CA;
XX DR WPI; 2001-502468/55.

XX PT Method of treating immunologically-related diseases, autoimmune
PT disorders and organ graft rejection comprises administration of
PT substituted phenanthrene-9,10-diones -

XX PS Claim 1; Page 37; 42pp; English.

XX CC The invention relates to a method of treating immunologically-related
CC diseases, autoimmune disorders and organ graft rejection comprises
CC administration of substituted phenanthrene-9,10-diones. The substituted
CC phenanthrene-9,10-diones have been shown to inhibit the phosphatase
CC activity of CD45 (leukocyte common antigen) which leads to
CC proliferation of T-cells. Available treatments for autoimmune disorders
CC and organ graft rejection have therapeutic disadvantages. For example,
CC cyclosporin A, the drug most commonly used at present, has renal and
CC CNS toxicity. The present sequence represents an N-linked peptide forming
CC the R3 group of a substituted phenanthrene-9,10-dione.

XX SQ Sequence 5 AA;

Query Match 75.0%; Score 3; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
|||
Db 1 EQP 3

RESULT 18
AAR83516

XX ID AAR83516 standard; Protein; 6 AA.

XX AC AAR83516;
XX DT 23-APR-1996 (first entry)

XX DE Zif268 zinc finger 1 randomised residues with affinity for HIV-1.

XX

KW zinc finger; variant; randomised; alpha-helical region; Zif268;
KW customised affinity; cancer; therapy; virus infection; HIV-1;
KW human immunodeficiency virus; consensus target sequence;
KW transcription-activator; transcription-inhibitor; plant disease.
XX OS Synthetic.

XX PN WO9519431-Al.
XX PD 20-JUL-1995.

XX PF 18-JAN-1995; 95WO-US00829.

XX PR 28-SEP-1994; 94US-0312604.

XX PR 18-JAN-1994; 94US-0183119.

XX PA (SCRI) SCHIPPS RES INST.

XX PI Barbas CF, Gottesfeld JM, Wright PE;
XX DR WPI; 1995-263862/34.

XX PT New zinc finger-nucleotide binding polypeptide(s) - used for
PT modulating the function of cellular nucleotide sequences, partic.
PT for treating cell proliferative disorders
XX PS Example 10; Fig 9; 135pp; English.

XX CC Regions of the alpha-helix in each of the Zif268 zinc fingers 1,
XX CC 2 and 3 were randomised and selected for binding to particular
XX CC conserved target sequences in HIV-1. In finger 1, the randomised
XX CC residues were at positions -1,2,3,4,5 and 6 in the alpha-helical
XX CC region. The present sequence has affinity for the TGT target
XX CC sequence. Zinc finger proteins are useful for suppressing
XX CC transcription and therefore for treating proliferative disorders.

XX SQ Sequence 6 AA;

Query Match 75.0%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||

Db 1 SEQ 3

RESULT 19
AAW61750

XX ID AAW61750 standard; peptide; 6 AA.

XX AC AAW61750;
XX DT 09-NOV-1998 (first entry)

XX DE Peptide mimetic of cytokine receptor gamma chain 17.

XX KW Peptide mimetic; gamma-chain; cytokine receptor; signal transduction;
KW autoimmune disease; graft vs. host disease; transplant rejection;
KW graft rejection; interleukin; immunosuppressant; T cell; B cell.

XX OS Synthetic.
XX PN WO9834631-Al.

XX PD 13-AUG-1998.

XX PF 06-FEB-1998; 98WO-US02339.

XX PR 07-FEB-1997; 97US-0036941.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX Korngold R, Townsend RM;
 XX WPI; 1998-446944/38.
 XX
 XX New peptide(s) mimicking a loop in the gamma chain of cytokine
 PT receptors - inhibit signal transduction through these receptors,
 PT useful as immunosuppressants for treating or preventing e.g.
 PT leukaemia, autoimmune disease, graft rejection
 XX
 XX Claim 2; Page 28; 54pp; English.
 XX
 XX The peptide mimetics AAW61734-W61756 and AAW77001-W77014 mimic a loop on
 CC the gamma-chain of cytokine receptors, and interacts with a cytokine or
 CC a gamma-chain partner receptor chain of a heterodimeric cytokine
 CC receptor. They inhibit signal transduction mediated by cytokine:receptor
 CC binding (of cytokines that bind to receptors with a gamma-chain). They
 CC are used to inhibit or suppress cytokine-mediated immune responses,
 CC growth, proliferation, function and activity of cells. Particularly they
 CC are used for treatment or prevention of lymphoma, leukaemia, allergy
 CC (e.g. asthma), autoimmune disease (e.g. rheumatoid arthritis, lupus,
 CC multiple sclerosis or myasthenia gravis), graft vs. host disease and
 CC transplant or graft rejection. They inhibit function of interleukin
 CC (II)-2, -4, -7, -9, -13 and -15 (the receptors for which include a
 CC common gamma -chain), so function as immunosuppressants by reducing
 CC proliferation of T and B cells.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 75.0%; Score 3; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SEQ 3
 ||||
 Db 3 SEQ 5
 ||||
 RESULT 20
 AAW97058
 ID AAW97058 standard; peptide; 6 AA.
 XX
 XX AAW97058;
 AC
 XX 29-APR-1999 (first entry)
 DT
 XX Peptidomimetic capable of inhabiting CD28 and/or CTLA-4 interactions.
 DE
 XX Peptidomimetic; CD28; CTLA-4; CD80; CD86; B7-1; B7-2; diabetes;
 KW immune system disease; autoimmune disease; psoriasis; multiple sclerosis;
 KW lupus erythematosus; rheumatoid arthritis; transplant rejection; cancer.
 XX
 XX Synthetic.
 OS
 XX WO9856401-Al.
 FN
 XX 17-DEC-1998.
 PD
 XX 11-JUN-1998; 98WO-US12312.
 PF
 XX 12-JUN-1997; 97US-0049470.
 PR
 XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 PA
 XX Blechner S, El Tayar N, Jameson B, Tepper M;
 PI WPI; 1999-080854/07.
 XX
 XX New peptidomimetic compounds - useful in the prophylaxis, diagnosis
 PT and treatment of pathologies and disorders, which are improved by
 PT inhibition of CD28 and/or CTLA-4 interaction with CD80 (B7-1) and
 PT CD86 (B7-2)
 XX

PS Disclosure; Page 9; 62pp; English.
 XX
 CC AAW97053-82 represent peptidomimetic compounds that inhibit CD28 and/or
 CC CTLA-4 interactions with CD80 and CD86. The peptides are used in
 CC pharmaceutical compositions for the prophylaxis, diagnosis and treatment
 CC of pathologies and disorders, which are improved by inhibition of CD28
 CC and/or CTLA-4 interaction with CD80 (B7-1) and CD86 (B7-2). Disorders
 CC include immune system diseases (e.g. Autoimmune diseases such as
 CC psoriasis, multiple sclerosis, lupus erythematosus, diabetes, rheumatoid
 CC arthritis, and therapy against solid organ/cellular transplant
 CC rejection) and cancer.
 XX
 SQ Sequence 6 AA;
 Query Match 75.0%; Score 3; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 EQP 4
 ||||
 Db 3 EQP 5
 ||||
 RESULT 21
 AAW94750
 ID AAW94750 standard; peptide; 6 AA.
 XX
 XX AAW94750;
 AC
 XX 20-APR-1999 (first entry)
 DT
 XX Mutant H protein antigen (strain CAM-70) fragment (residues 277-282).
 DE
 XX Measles; H protein; F protein; antigen; mutant; vaccine; detection;
 KW diagnostic reagent; attenuated.
 KW
 XX Measles virus.
 OS
 XX WO9855627-Al.
 FN
 XX 10-DEC-1998.
 PD
 XX 04-JUN-1998; 98WO-JP02481.
 PF
 XX 04-JUN-1997; 97JP-0184285.
 PR
 XX (OSAU) UNIV OSAKA.
 PA
 XX Kawanishi H, Ueda S, Watanabe M;
 PI WPI; 1999-070272/06.
 XX
 PT Mutant measles virus H and F protein antigens and genes encoding
 PT them - for production of attenuated virus or genetic vaccines and of
 PT diagnostic reagents
 PT
 XX Claim 1; Page 58; 93pp; Japanese.
 PS
 XX Sequences AAW94746-751 represent specifically claimed peptide fragments
 CC of a mutant measles virus H protein antigen isolated from the CAM-70
 CC strain of measles virus. The invention provides mutant measles virus
 CC antigenic proteins such as the H protein from the CAM-70 (attenuated) or
 CC NA (epidemic) strain of measles virus and the F protein from the CAM-70
 CC or NA strain and nucleic acid sequences encoding the proteins. These
 CC antigenic proteins and their fragments are used in the production of
 CC vaccines for measles and the production of diagnostic reagents (e.g.
 CC measles antigens for the detection of specific antibodies in the blood
 CC of patients). The vaccines may be recombinant or other live attenuated
 CC measles virus strains or may be genetic vaccines (e.g. adenovirus
 CC vectors).
 XX
 XX Sequence 6 AA;
 SQ

Query Match 75.0%; Score 3; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
 |||
 Db 1 EQP 3

RESULT 22
 AAW84413
 ID AAW84413 standard; Peptide; 6 AA.
 XX
 AC AAW84413;
 XX
 DT 22-MAR-1999 (first entry)
 XX
 DE HIV-1 nucleic acid binding protein zinc finger 1 peptide.
 XX
 KW zinc finger; nucleotide-binding protein; cell proliferative disorder;
 KW gene therapy; cancer; psoriasis; pemphigus vulgaris; Bechet's syndrome;
 KW lipid histiocytosis; human immune deficiency virus; HIV; viral infection;
 KW transgenic plant.
 XX
 OS Synthetic.
 XX
 PN WC9854311-AL.
 XX
 PD 03-DEC-1998.
 XX
 PF 27-MAY-1998; 98WO-US10801.
 XX
 PR 27-MAY-1997; 97US-0863813.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Gottesfeld JM, Wright PE;
 XX
 DR WPI; 1999-059831/05.
 XX
 CC New zinc finger nucleotide-binding protein variant that modulates
 PT selected nucleotide sequence - used for treatment of proliferative
 PT and viral diseases by gene therapy, and can be made selective for
 PT any target sequence
 XX
 PS Example 10; Fig 9; 158pp; English.

AAW84398-421 represent the peptides obtained from randomised finger 1
 sequences of zinc finger nucleotide-binding proteins that bind to HIV-1
 target sequences. The peptides were produced in the course of the
 invention. The specification describes zinc finger nucleotide-binding
 protein variants with at least two zinc finger modules that bind to a
 cellular nucleotide sequence and modulate its function. Zinc finger
 proteins, and compositions containing them, are used to increase or
 reduce transcription of a gene linked to the cellular nucleotide
 sequence. The proteins are used specifically for treating or preventing
 cell proliferative disorders (in humans, animals or plants, including
 those induced by viruses), particularly where expressed from nucleic
 acid by gene therapy (including ex vivo methods). Typical diseases that
 can be treated are many forms of cancer, psoriasis, pemphigus vulgaris,
 Bechet's syndrome and lipid histiocytosis, also treatment of human
 immune deficiency virus (HIV) and other viral infections, and production
 of transgenic plants resistant to bacterial and viral diseases. The
 present oligonucleotide is used in the course of the invention.

Sequence 6 AA;
 Query Match 75.0%; Score 3; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
 |||

Db 1 SEQ 3

RESULT 23
 AAB86473
 ID AAB86473 standard; peptide; 6 AA.
 XX
 AC AAB86473;
 XX
 DT 29-OCT-2001 (first entry)
 XX
 DE Human gliadin peptide homologue SEQ ID 2.
 XX
 KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;
 KW dermatitis herpetiformis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN DE10005932-AL.
 XX
 PD 23-AUG-2001.
 XX
 PF 10-FEB-2000; 2000DE-1005932.
 XX
 PR 10-FEB-2000; 2000DE-1005932.
 XX
 PA (UYLE) UNIV LEIPZIG.
 XX
 PI Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
 XX
 DR WPI; 2001-503463/56.
 XX
 CC New tripeptide and hexapeptide compounds which are gliadin homologues
 PT useful for the diagnosis of celiac disease and dermatitis herpetiformis
 PT -
 XX
 PS Claim 1; Page 6; 10pp; German.

This invention describes tripeptide and hexapeptide homologues of gliadin
 which are used in a novel method for the diagnosis of celiac disease and
 dermatitis herpetiformis comprising: (a) covalently bonding one of the
 tripeptides or hexapeptides to cellulose membranes via the C-terminus,
 CC washing with methanol, blocking with buffer, washing with TBS-T,
 CC incubating in human serum, washing with anti-human immunoglobulin A or G,
 CC conjugating with peroxide, incubating, washing, measuring the
 CC luminescence and evaluating the data in a known manner; or (b)
 CC biotinylating one of the tripeptides or hexapeptides, synthetically
 CC produced and also containing Lys at the C-terminus, applying the
 CC biotinylated peptide to streptavidin-coated and blocked microtiter plates
 CC in a concentration of 1 micro g/ml, washing, applying patient's serum and
 CC determining the bound immunoglobulins with a second antibody carrying a
 CC marker which can be evaluated. The tripeptides and hexapeptides, which
 CC are cheap to produce and have long term stability in test kits, avoid the
 CC use of gliadin antibodies which is expensive, subjective and
 CC semi-quantitative and of enzyme immunoassays which are associated with
 CC low sensitivity and low specificity. Also, the method can be automated.
 CC AAB86472-AAB86501 represent the gliadin homologues described in the
 CC method of the invention.

Sequence 6 AA;
 Query Match 75.0%; Score 3; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
 |||
 Db 3 EQP 5

RESULT 24
 AAB86474

ID AAB86474 standard; peptide; 6 AA.
 XX AAB86474;
 AC
 XX 29-OCT-2001 (first entry)
 DT
 XX Human gliadin peptide homologue SEQ ID 3.
 DE
 XX Gliadin; antibody; epitope; human; celiac disease; diagnosis;
 KW dermatitis herpetiformis.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX DE10005932-A1.
 PN
 XX 23-AUG-2001.
 PD
 XX 10-FEB-2000; 2000DE-1005932.
 PF
 XX 10-FEB-2000; 2000DE-1005932.
 PR
 XX (UYLE) UNIV LEIPZIG.
 PA
 XX Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
 PI WPI; 2001-503463/56.
 DR
 XX New tripeptide and hexapeptide compounds which are gliadin homologues
 XX useful for the diagnosis of celiac disease and dermatitis herpetiformis
 XX
 XX Claim 1; Page 6; 10pp; German.
 PS
 XX This invention describes tripeptide and hexapeptide homologues of gliadin
 XX which are used in a novel method for the diagnosis of celiac disease and
 CC dermatitis herpetiformis comprising: (a) covalently bonding one of the
 CC tripeptides or hexapeptides to cellulose membranes via the C-terminus,
 CC washing with methanol, blocking with buffer, washing with TBS-T,
 CC incubating in human serum, washing with anti-human immunoglobulin A or G,
 CC conjugating with peroxide, incubating, washing, measuring the
 CC luminescence and evaluating the data in a known manner; or (b)
 CC biotinylating one of the tripeptides or hexapeptides, synthetically
 CC produced and also containing lys at the C-terminus, applying the
 CC biotinylated peptide to streptavidin-coated and blocked microtiter plates
 CC in a concentration of 1 micro g/ml, washing, applying patient's serum and
 CC determining the bound immunoglobulins with a second antibody carrying a
 CC marker which can be evaluated. The tripeptides and hexapeptides, which
 CC are cheap to produce and have long term stability in test kits, avoid the
 CC use of gliadin antibodies which is expensive, subjective and
 CC semi-quantitative and of enzyme immunoassays which are associated with
 CC low sensitivity and low specificity. Also, the method can be automated.
 CC AAB86472-AAB86501 represent the gliadin homologues described in the
 CC method of the invention.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 75.0%; Score 3; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EQP 4
 Db |||
 3 EQP 5
 RESULT 25
 AAB86481
 IJ AAB86481 standard; peptide; 6 AA.
 XX
 AC AAB86481;
 XX
 DT 29-OCT-2001 (first entry)

XX Human gliadin peptide homologue SEQ ID 10.
 DE
 XX Gliadin; antibody; epitope; human; celiac disease; diagnosis;
 KW dermatitis herpetiformis.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX DE10005932-A1.
 PN
 XX 23-AUG-2001.
 PD
 XX 10-FEB-2000; 2000DE-1005932.
 PF
 XX 10-FEB-2000; 2000DE-1005932.
 PR
 XX (UYLE) UNIV LEIPZIG.
 PA
 XX Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
 PI WPI; 2001-503463/56.
 DR
 XX New tripeptide and hexapeptide compounds which are gliadin homologues
 XX useful for the diagnosis of celiac disease and dermatitis herpetiformis
 XX
 XX Claim 1; Page 7; 10pp; German.
 PS
 XX This invention describes tripeptide and hexapeptide homologues of gliadin
 XX which are used in a novel method for the diagnosis of celiac disease and
 CC dermatitis herpetiformis comprising: (a) covalently bonding one of the
 CC tripeptides or hexapeptides to cellulose membranes via the C-terminus,
 CC washing with methanol, blocking with buffer, washing with TBS-T,
 CC incubating in human serum, washing with anti-human immunoglobulin A or G,
 CC conjugating with peroxide, incubating, washing, measuring the
 CC luminescence and evaluating the data in a known manner; or (b)
 CC biotinylating one of the tripeptides or hexapeptides, synthetically
 CC produced and also containing lys at the C-terminus, applying the
 CC biotinylated peptide to streptavidin-coated and blocked microtiter plates
 CC in a concentration of 1 micro g/ml, washing, applying patient's serum and
 CC determining the bound immunoglobulins with a second antibody carrying a
 CC marker which can be evaluated. The tripeptides and hexapeptides, which
 CC are cheap to produce and have long term stability in test kits, avoid the
 CC use of gliadin antibodies which is expensive, subjective and
 CC semi-quantitative and of enzyme immunoassays which are associated with
 CC low sensitivity and low specificity. Also, the method can be automated.
 CC AAB86472-AAB86501 represent the gliadin homologues described in the
 CC method of the invention.
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 75.0%; Score 3; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EQP 4
 Db |||
 3 EQP 5
 RESULT 26
 AAB86486
 ID AAB86486 standard; peptide; 6 AA.
 XX
 AC AAB86486;
 AC
 XX 29-OCT-2001 (first entry)
 DT
 XX Human gliadin peptide homologue SEQ ID 15.
 DE
 XX Gliadin; antibody; epitope; human; celiac disease; diagnosis;
 KW dermatitis herpetiformis.
 KW

XX OS Homo sapiens.
XX OS Synthetic.
XX PN DE10005932-A1.
XX XX
XX PD 23-AUG-2001.
XX XX
XX PF 10-FEB-2000; 2000DE-1005932.
XX XX
XX PR 10-FEB-2000; 2000DE-1005932.
XX XX
XX PA (UYLE) UNIV LEIPZIG.
XX XX
XX PI Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
XX XX
XX DR WPI; 2001-503463/56.
XX XX
XX PT New tripeptide and hexapeptide compounds which are gliadin homologues
XX PT useful for the diagnosis of celiac disease and dermatitis herpetiformis
XX XX
XX PS Claim 2; Page 7; 10pp; German.
XX CC This invention describes tripeptide and hexapeptide homologues of gliadin
XX CC which are used in a novel method for the diagnosis of celiac disease and
XX CC dermatitis herpetiformis comprising: (a) covalently bonding one of the
XX CC tripeptides or hexapeptides to cellulose membranes via the C-terminus,
XX CC washing with methanol, blocking with buffer, washing with TBS-T,
XX CC incubating in human serum, washing with anti-human immunoglobulin A or G,
XX CC conjugating with peroxide, incubating, washing, measuring the
XX CC luminescence and evaluating the data in a known manner; or (b)
XX CC biotinylating one of the tripeptides or hexapeptides, synthetically
XX CC produced and also containing Lys at the C-terminus, applying the
XX CC biotinylated peptide to streptavidin-coated and blocked microtiter plates
XX CC in a concentration of 1 micro g/ml, washing, applying patient's serum and
XX CC determining the bound immunoglobulins with a second antibody carrying a
XX CC marker which can be evaluated. The tripeptides and hexapeptides, which
XX CC are cheap to produce and have long term stability in test kits, avoid the
XX CC use of gliadin antibodies which is expensive, subjective and
XX CC semi-quantitative and of enzyme immunoassays which are associated with
XX CC low sensitivity and low specificity. Also, the method can be automated.
XX CC AAB86472-AAB86501 represent the gliadin homologues described in the
XX CC method of the invention.
XX XX
XX SQ Sequence 6 AA;
Query Match 75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EQP 4
DB 2 EQP 4
RESULT 27
AAB86487
ID AAB86487 standard; peptide; 6 AA.
XX AC AAB86487;
XX XX
XX DT 29-OCT-2001 (first entry)
XX XX
XX DE Human gliadin peptide homologue SEQ ID 16.
XX XX
XX KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;
XX KW dermatitis herpetiformis.
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN DE10005932-A1.

XX PD 23-AUG-2001.
XX XX
XX PF 10-FEB-2000; 2000DE-1005932.
XX XX
XX PR 10-FEB-2000; 2000DE-1005932.
XX XX
XX PA (UYLE) UNIV LEIPZIG.
XX XX
XX PI Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
XX XX
XX DR WPI; 2001-503463/56.
XX XX
XX PT New tripeptide and hexapeptide compounds which are gliadin homologues
XX PT useful for the diagnosis of celiac disease and dermatitis herpetiformis
XX XX
XX PS Claim 2; Page 7; 10pp; German.
XX CC This invention describes tripeptide and hexapeptide homologues of gliadin
XX CC which are used in a novel method for the diagnosis of celiac disease and
XX CC dermatitis herpetiformis comprising: (a) covalently bonding one of the
XX CC tripeptides or hexapeptides to cellulose membranes via the C-terminus,
XX CC washing with methanol, blocking with buffer, washing with TBS-T,
XX CC incubating in human serum, washing with anti-human immunoglobulin A or G,
XX CC conjugating with peroxide, incubating, washing, measuring the
XX CC luminescence and evaluating the data in a known manner; or (b)
XX CC biotinylating one of the tripeptides or hexapeptides, synthetically
XX CC produced and also containing Lys at the C-terminus, applying the
XX CC biotinylated peptide to streptavidin-coated and blocked microtiter plates
XX CC in a concentration of 1 micro g/ml, washing, applying patient's serum and
XX CC determining the bound immunoglobulins with a second antibody carrying a
XX CC marker which can be evaluated. The tripeptides and hexapeptides, which
XX CC are cheap to produce and have long term stability in test kits, avoid the
XX CC use of gliadin antibodies which is expensive, subjective and
XX CC semi-quantitative and of enzyme immunoassays which are associated with
XX CC low sensitivity and low specificity. Also, the method can be automated.
XX CC AAB86472-AAB86501 represent the gliadin homologues described in the
XX CC method of the invention.
XX XX
XX SQ Sequence 6 AA;
Query Match 75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EQP 4
DB 2 EQP 4
RESULT 28
AAB86494
ID AAB86494 standard; peptide; 6 AA.
XX AC AAB86494;
XX XX
XX DT 29-OCT-2001 (first entry)
XX XX
XX DE Human gliadin peptide homologue SEQ ID 23.
XX XX
XX KW Gliadin; antibody; epitope; human; celiac disease; diagnosis;
XX KW dermatitis herpetiformis.
XX OS Homo sapiens.
XX OS Synthetic.
XX XX
XX PN DE10005932-A1.
XX XX
XX PD 23-AUG-2001.
XX XX
XX PF 10-FEB-2000; 2000DE-1005932.

```
PR 10-FEB-2000; 2000DE-1005932.
XX
XX (UYLE ) UNIV LEIPZIG.
XX
XX Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
PI
XX WPI; 2001-503463/56.
XX
XX Claim 2; Page 8; 10pp; German.
XX
XX This invention describes tripeptide and hexapeptide compounds which are gliadin homologues
XX which are used in a novel method for the diagnosis of celiac disease and dermatitis herpetiformis
XX useful for the diagnosis of celiac disease and dermatitis herpetiformis
XX
XX Claim 2; Page 8; 10pp; German.
XX
XX This invention describes tripeptide and hexapeptide compounds which are gliadin homologues of gliadin
XX which are used in a novel method for the diagnosis of celiac disease and
XX dermatitis herpetiformis comprising: (a) covalently bonding one of the
XX tripeptides or hexapeptides to cellulose membranes via the C-terminus,
XX washing with methanol, blocking with buffer, washing with TBS-T,
XX incubating in human serum, washing with anti-human immunoglobulin A or G,
XX conjugating with peroxide, incubating, washing, measuring the
XX luminescence and evaluating the data in a known manner; or (b)
XX biotinylating one of the tripeptides or hexapeptides, synthetically
XX produced and also containing Lys at the C-terminus, applying the
XX biotinylated peptide to streptavidin-coated and blocked microtiter plates
XX in a concentration of 1 micro g/ml, washing, applying patient's serum and
XX determining the bound immunoglobulins with a second antibody carrying a
XX marker which can be evaluated. The tripeptides and hexapeptides, which
XX are cheap to produce and have long term stability in test kits, avoid the
XX use of gliadin antibodies which is expensive, subjective and
XX semi-quantitative and of enzyme immunoassays which are associated with
XX low sensitivity and low specificity. Also, the method can be automated.
XX AAB86472-AAB86501 represent the gliadin homologues described in the
XX method of the invention.
XX
XX Sequence 6 AA;
SQ
Query Match 75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EQP 4
DB 2 EQP 4
RESULT 29
AAB86497
ID AAB86497 standard; peptide; 6 AA.
XX
XX AAB86497;
XX
XX 29-OCT-2001 (first entry)
XX
XX Human gliadin peptide homologue SEQ ID 26.
XX
XX Gliadin; antibody; epitope; human; celiac disease; diagnosis;
XX dermatitis herpetiformis.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX DE10005932-A1.
XX
XX 23-AUG-2001.
XX
XX 10-FEB-2000; 2000DE-1005932.
XX
XX 10-FEB-2000; 2000DE-1005932.
XX
XX (UYLE ) UNIV LEIPZIG.
XX
XX Mothes T, Osman AA, Uhlig HH, Guennel T, Dietl A;
PI
```

```
XX WPI; 2001-503463/56.
XX
XX New tripeptide and hexapeptide compounds which are gliadin homologues
XX useful for the diagnosis of celiac disease and dermatitis herpetiformis
XX
XX Claim 2; Page 8; 10pp; German.
XX
XX This invention describes tripeptide and hexapeptide homologues of gliadin
XX which are used in a novel method for the diagnosis of celiac disease and
XX dermatitis herpetiformis comprising: (a) covalently bonding one of the
XX tripeptides or hexapeptides to cellulose membranes via the C-terminus,
XX washing with methanol, blocking with buffer, washing with TBS-T,
XX incubating in human serum, washing with anti-human immunoglobulin A or G,
XX conjugating with peroxide, incubating, washing, measuring the
XX luminescence and evaluating the data in a known manner; or (b)
XX biotinylating one of the tripeptides or hexapeptides, synthetically
XX produced and also containing Lys at the C-terminus, applying the
XX biotinylated peptide to streptavidin-coated and blocked microtiter plates
XX in a concentration of 1 micro g/ml, washing, applying patient's serum and
XX determining the bound immunoglobulins with a second antibody carrying a
XX marker which can be evaluated. The tripeptides and hexapeptides, which
XX are cheap to produce and have long term stability in test kits, avoid the
XX use of gliadin antibodies which is expensive, subjective and
XX semi-quantitative and of enzyme immunoassays which are associated with
XX low sensitivity and low specificity. Also, the method can be automated.
XX AAB86472-AAB86501 represent the gliadin homologues described in the
XX method of the invention.
XX
XX Sequence 6 AA;
SQ
Query Match 75.0%; Score 3; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 EQP 4
DB 2 EQP 4
RESULT 30
AAB05001
ID AAB05001 standard; peptide; 6 AA.
XX
XX AAB05001;
XX
XX 10-SEP-2001 (first entry)
XX
XX Synthetic peptide #3 analogous to type I repeat of TSP.
XX
XX Thrombospondin; TSP; wound healing; angiogenesis; implant acceptance;
XX anti-platelet aggregation; antimetastatic; therapy; immunosuppressive;
XX sickle cell disease; cytostatic; vulnerary; anti-malaria; anti-sickling;
XX cell adhesion modulator; type I repeat.
XX
XX Synthetic.
XX
XX US6239110-B1.
XX
XX 29-MAY-2001.
XX
XX 07-JUN-1995; 95US-0476134.
XX
XX 01-MAR-1993; 93US-0024436.
XX
XX 24-JAN-1994; 94US-0185614.
XX
XX 22-FEB-1990; 90US-0483527.
XX
XX 24-SEP-1990; 90US-0587197.
XX
XX 25-MAY-1995; 95US-0450738.
XX
XX (GRAC ) GRACE & CO-CONN W R.
XX (MEDI-) MEDICAL COLLEGE PA.
XX
```

PI Eyal J, Hamilton BK, Tuszynski GP;
 DR WPI; 2001-407094/43.
 XX
 PT Method for promoting or inhibiting cell adhesion or thrombospondin-like
 PT activity in a patient, comprises administering polypeptide compounds
 PT that are synthetic analogs of thrombospondin -
 XX
 PS Disclosure; Column 4; 31pp; English.
 XX
 CC The present invention relates to peptide fragments and synthetic
 CC analogues of thrombospondin (TSP) which retain thrombospondin-like
 CC activity. The peptides retain and mimic the bioactivity of TSP as a
 CC potent promoter or inhibitor of cell adhesion and attachment to
 CC different cell lines. The polypeptide is useful for promoting or
 CC inhibiting cellular attachment to tissue culture flasks, for promoting
 CC wound healing, angiogenesis or implant acceptance, as agents for
 CC anti-platelet aggregation or antineoplastic activity, as agents for
 CC antimetastatic activity, or as diagnostic reagents in different
 CC therapeutic applications. The peptide is useful for treating sickle
 CC cell disease. The present sequence is a synthetic peptide segment,
 CC which is analogous to type I repeat of TSP.
 XX
 SQ Sequence 6 AA;
 Query Match 75.0%; Score 3; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQ 3
 |||
 DB 2 SEQ 4
 |||
 RESULT 31
 AAB60618
 ID AAB60618 standard; peptide; 6 AA.
 XX
 AC AAB60618;
 XX
 DT 27-APR-2001 (first entry)
 XX
 DE Etp100 thrombospondin-like hexapeptide motif #4.
 XX
 KW Thrombospondin-like motif; TSP; inhibitor; potentiator;
 KW platelet aggregation; cell adhesion; cell migration;
 KW angiogenesis; cancer metastasis; tumour growth; antitumour;
 KW atherosclerosis; thrombosis; cardiovascular disorder;
 KW ischaemic disorder; thrombolytic; inflammatory disorder;
 KW rheumatoid arthritis; wound healing; vulneryary;
 KW drug targeting moiety.
 OS Unidentified.
 XX
 XX
 PN EP1069137-A1.
 XX
 PD 17-JAN-2001.
 XX
 PF 20-SEP-1991; 2000EP-0111671.
 XX
 PR 24-SEP-1990; 90US-0587197.
 PR 13-SEP-1991; 91US-0757037.
 PR 20-SEP-1991; 91EP-0250255.
 XX
 PA (GRAC) GRACE & CO-CONN W R.
 PA (MEDI-) MEDICAL COLLEGE PENNSYLVANIA.
 XX
 PI Eyal J, Hamilton BK, Tuszynski GP;
 XX
 DR WPI; 2001-212579/22.
 XX
 XX Use of polypeptides having thrombospondin-like activity for e.g.
 PT treating atherosclerosis, thrombosis, angiogenesis, inflammatory

PT disorders, inhibiting tumor cell metastases and growth, reducing tumor
 PT size and colony number -
 XX
 PS Disclosure; Page 4; 39pp; English.
 XX
 CC The invention relates to the use of a peptide with thrombospondin-
 CC like activity for the preparation of a medicament for treating tumours.
 CC The peptide is of the general formula: R1-X1-X2-X3-X4-X5-R2, where:
 CC R1 is a protected or unprotected terminal amino group including
 CC hydrogen, amino acetyl or one amino acid residue, or its desamino form;
 CC X1 and X5 are independently Arg or Cys;
 CC X2, X3 and X4 are independently Arg, Ser, Thr or Val;
 CC R2 is a protected or unprotected terminal carboxyl group including
 CC carboxyl, carboxyl, amide or one amino acid residue including
 CC carboxyamide or its alkylamide forms.
 CC The structure of the peptide is optionally cyclised via a bond
 CC between X1 and X5, or via a bond between R1 and R2. Particularly
 CC preferred is the peptide ASVTAR (AAB60598). The peptides of the
 CC invention act as potentiators or inhibitors of thrombospondin (TSP)
 CC activity, depending on whether TSP is already present. In the presence
 CC of endogenous TSP, the peptides act to inhibit TSP-mediated platelet
 CC aggregation, cell adhesion, cell migration and angiogenesis, while
 CC in its absence, the peptides potentiate these activities. The peptides
 CC admixed with at least one carrier, are useful in the preparation of a
 CC medicament which inhibits tumour cell metastasis, tumour growth, and
 CC reduces tumour size and tumour colony number. The peptides may be
 CC used to inhibit platelet aggregation for the treatment of
 CC atherosclerosis, thrombosis, and other cardiovascular and ischaemic
 CC disorders. They may also be used to inhibit angiogenesis for the
 CC treatment of diabetic retinopathy, neovascular glaucoma and inflammatory
 CC disorders such as rheumatoid arthritis. They may additionally be used
 CC to prepare antibodies useful as diagnostic or therapeutic agents, to
 CC promote or inhibit cellular attachment to surfaces (e.g., medical
 CC devices), and in wound healing. The peptides may further be used to
 CC treat or prevent conditions where thrombospondin-like activity plays a
 CC role (e.g., cardiovascular or ischaemic disorders); as a targeting
 CC moiety to target toxins, drugs, hormones or imaging agents to metastatic
 CC tumour cells for diagnostic or therapeutic purposes; during surgery on
 CC peripheral arteries, cardiovascular surgery or after angioplasty;
 CC in dialysis applications; for preparing antisera for use in immunoassays;
 CC and to isolate thrombospondin cell surface receptors from extracts of
 CC cells or cell membranes. Sequences AAB60600-AAB60622 represent
 CC thrombospondin-like peptide motifs found in a variety of proteins.
 XX
 SQ Sequence 6 AA;
 Query Match 75.0%; Score 3; DB 22; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQ 3
 |||
 DB 2 SEQ 4
 |||
 RESULT 32
 ABP70731
 ID ABP70731 standard; Peptide; 6 AA.
 XX
 AC ABP70731;
 XX
 DT 22-APR-2003 (first entry)
 XX
 DE Phosphorylation site peptide substrate #16.
 XX
 KW Glycogen synthase kinase-3 beta; protein co-ordinate data;
 KW neurotic; neuroprotective; neuroleptic; antidiabetic; immunosuppressive;
 KW antiinflammatory; cardiovascular; antiallergic; antisthmatic;
 KW antiparkinsonian; anticonvulsant; dermatological; vasotropic; GSK-3;
 KW schizophrenia; Alzheimer's disease; diabetes; autoimmune disease;
 KW inflammatory disease; metabolic; neurological; neurodegenerative;
 KW cardiovascular disease; allergy; asthma; Huntington's disease;
 KW Parkinson's disease; AIDS-related dementia; Lou Gehrig's disease;

KW amyotrophic lateral sclerosis; multiple sclerosis;
 XX cardiomyocyte hypertrophy; reperfusion; ischaemia; baldness.
 OS Unidentified.
 XX WC200288078-A2.
 PN 07-NOV-2002.
 PD
 XX 29-APR-2002; 2002WO-US13511.
 XX 30-APR-2001; 2001US-287366P.
 PR 08-JUN-2001; 2001US-297094P.
 PR 27-FEB-2002; 2002US-361899P.
 XX (VERT-) VERTEX PHARM INC.
 PA Ter Haar E, Swenson L, Green J, Arnost MJ;
 XX WPI; 2003-247844/24.
 DR New pyrazolo(3,4-c)pyridazine derivatives are glucocorticoid synthase kinase
 XX -3 inhibitors useful for treating e.g. schizophrenia, Alzheimer's
 PT disease, diabetes, autoimmune diseases, allergy, asthma, multiple
 PT sclerosis, and baldness -
 XX Disclosure; Page 30; 778pp; English.
 PS The present invention relates to novel pyrazolo(3,4-c)pyridazine
 CC derivatives, which have glucocorticoid synthase kinase-3 (GSK-3) inhibitory
 CC activity. The derivatives are useful for inhibiting beta-catenin
 CC phosphorylation and hyperphosphorylated Tau protein production in a
 CC patient and GSK-3 activity in a patient or in a biological sample. The
 CC derivatives are also useful for treating schizophrenia, Alzheimer's
 CC disease, diabetes, autoimmune diseases, inflammatory diseases, metabolic,
 CC neurological and neurodegenerative diseases, cardiovascular diseases,
 CC allergy, asthma, Huntington's disease, Parkinson's disease, AIDS-related
 CC dementia, amyotrophic lateral sclerosis (Lou Gehrig's disease), multiple
 CC sclerosis, cardiomyocyte hypertrophy, reperfusion/ischaemia and baldness.
 CC The present sequence is an example of a peptide substrate comprising a
 CC phosphorylation sequence.
 XX Sequence 6 AA;
 SQ Query Match 75.0%; Score 3; DB 24; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SEQ 3
 Db 2 SEQ 4
 RESULT 33
 AAY50012
 ID AAY50012 standard; peptide; 7 AA.
 XX AAY50012;
 AC 19-JAN-2000 (first entry)
 XX Thermus thermophilus dnaE inverse PCR primer #1-derived peptide.
 DE DNA polymerase III; dnaE gene; alpha subunit; thermostable;
 XX DNA synthesis; speed; accuracy; processivity; frameshift; holoenzyme;
 KW assembly; exonuclease; proofreading; PCR; primer.
 XX Synthetic.
 OS Thermus thermophilus.
 OS WO9953074-A1.
 PN 21-OCT-1999.
 PD

XX 09-APR-1998; 98WO-US07070.
 XX 09-APR-1998; 98WO-US07070.
 PR (UYRQ) UNIV ROCKEFELLER.
 XX Yurieva O, Kuriyan J, O'Donnell ME, Jeruzalmi D;
 PI WPI; 1999-611306/52.
 XX N-PSDB; AAZ30921.
 DR New isolated thermostable DNA polymerase III-type enzyme, used
 PT particularly for the amplification and sequencing of nucleic acids
 PT Example 10; Page 78; 156pp; English.
 PS This sequence represents a peptide encoded by the complement of Thermus
 XX thermophilus dnaE inverse PCR primer #1. Primer #1 was used with primer
 CC #2 (AAZ30922) to amplify a portion of the Thermus thermophilus dnaE
 CC gene. The dnaE gene encodes the alpha subunit of a novel thermostable
 CC DNA polymerase holoenzyme which corresponds to DNA polymerase
 CC III (Pol III) of E. coli. Pol III-type enzymes have a high
 CC processivity (>50 kb) and rapid rate of synthesis (750 nucleotides/s).
 CC Pol III consists of 18 subunits of 10 different types. The DNA
 CC polymerase core is the catalytic unit and consists of the alpha (DNA
 CC polymerase), epsilon (3'-5' exonuclease) and theta subunits. The beta
 CC subunit ("sliding clamp") is ring-shaped and encircles DNA and slides
 CC along it while tethering the Pol III holoenzyme to the template. It is
 CC the beta subunit which is responsible for the high processivity and
 CC speed. The gamma complex (composed of gamma, delta, chi and psi
 CC subunits) is the "clamp loader" which couples ATP hydrolysis to assembly
 CC of beta clamps around DNA. A dimer of the tau subunit acts as a
 CC "macromolecular organizer", holding together molecules of core
 CC polymerase and one molecule of gamma complex, forming the Pol III*
 CC subassembly. Two beta dimers associate with the two cores within Pol
 CC III* to form the holoenzymes capable of replicating both strands of
 CC duplex DNA simultaneously. The Thermus thermophilus Pol III-type enzyme
 CC can be used in molecular cloning techniques such as PCR (polymerase
 CC chain reaction). The current limitations of enzymes previously used in
 CC PCR are that they are unable to synthesise extended lengths of
 CC nucleotides, and in the instance of Taq (Thermus aquaticus) polymerase,
 CC the lack of 3'-5' exonuclease activity and the subsequent inability to
 CC excise misinserted nucleotides (proofreading).
 XX Sequence 7 AA;
 SQ Query Match 75.0%; Score 3; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SEQ 3
 Db 4 SEQ 6
 RESULT 34
 AAY48764
 ID AAY48764 standard; Peptide; 7 AA.
 XX AAY48764;
 AC 20-MAR-2003 (updated)
 XX 10-DEC-1999 (first entry)
 DT Membrane dipeptidase-binding gut homing peptide #9.
 XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
 KW prostatic; ovary; lymph node; adrenal gland; liver; gut; tumour;
 KW membrane dipeptidase.
 XX Synthetic.
 OS Homo sapiens.
 OS

XX PN WO9946284-A2.
 XX PD 16-SEP-1999.
 XX PF 10-MAR-1999; 99WO-US05284.
 XX PR 13-MAR-1998; 98US-0042107.
 XX PR 26-FEB-1999; 99US-0258754.
 XX PA (BURN-) BURNHAM INST.
 XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
 XX DR WPI; 1999-571717/48.
 XX PT New peptides which selectively home to organs or tissues, used for,
 PT e.g. identifying target ligands and for therapy of pathological
 PT conditions -
 XX PS Example 6; Page 147; 193pp; English.
 XX CC The present invention describes peptides that selectively home to a
 CC tissue or organ. The peptides can be used for identifying an organ
 CC or tissue, for identifying a target molecule expressed by an organ or
 CC tissue or for treating an organ or tissue pathology, where the organ or
 CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,
 CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the
 CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences
 CC which are used in the exemplification of the present invention.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 XX SQ Sequence 7 AA;
 Query Match 75.0%; Score 3; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SEQ 3
 Db 3 SEQ 5
 RESULT 35
 AAM44117
 ID AAM44117 standard; Peptide; 7 AA.
 AC AAM44117;
 XX DT 25-OCT-2001 (first entry)
 DE H11 binding site consensus conforming peptide (CCP) #388.
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytotatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX OS Homo sapiens.
 OS Synthetic.
 XX CA2290722-A1.
 XX PD 08-JUN-2001.
 XX PF 08-DEC-1999; 99CA-2290722.
 XX PR 08-DEC-1999; 99CA-2290722.
 XX PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 XX Entwistle JM, MacDonald GC;
 XX WPI; 2001-425937/46.

PI Entwistle JM, MacDonald GC;
 XX WPI; 2001-425937/46.
 XX PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX PS Example 4; Page 102; 154pp; English.
 XX CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX SQ Sequence 7 AA;
 Query Match 75.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SEQ 3
 Db 5 SEQ 7
 RESULT 36
 AAM44149
 ID AAM44149 standard; Peptide; 7 AA.
 AC AAM44149;
 XX DT 25-OCT-2001 (first entry)
 DE H11 binding site consensus conforming peptide (CCP) #420.
 XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytotatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX OS Homo sapiens.
 OS Synthetic.
 XX CA2290722-A1.
 XX PD 08-JUN-2001.
 XX PF 08-DEC-1999; 99CA-2290722.
 XX PR 08-DEC-1999; 99CA-2290722.
 XX PA (NOVO-) NOVOPHARM BIOTECH INC.
 XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 XX Entwistle JM, MacDonald GC;
 XX WPI; 2001-425937/46.

PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX Example 4; Page 102; 154pp; English.
 XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumors that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEQ 3
 |||
 Db 5 SEQ 7

RESULT 37
 AAM44154
 ID AAM44154 standard; Peptide; 7 AA.

XX AAM44154;
 XX 25-OCT-2001 (first entry)
 DE H11 binding site consensus conforming peptide (CCP) #425.
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX Homo sapiens.
 OS Synthetic.
 PN CA2290722-A1.
 XX 08-JUN-2001.
 XX 08-DEC-1999; 99CA-2290722.
 XX 08-DEC-1999; 99CA-2290722.
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;
 XX WPI; 2001-425937/46.
 XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

XX Example 4; Page 102; 154pp; English.
 XX The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumors that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPPCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPPCs
 CC or a population of different SPPCs consisting of immunogenic cancer cell
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.
 XX Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEQ 3
 |||
 Db 5 SEQ 7

RESULT 38
 AAM44232
 ID AAM44232 standard; Peptide; 7 AA.

XX AAM44232;
 XX 25-OCT-2001 (first entry)
 DE H11 binding site consensus conforming peptide (CCP) #503.
 KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
 XX Homo sapiens.
 OS Synthetic.
 PN CA2290722-A1.
 XX 08-JUN-2001.
 XX 08-DEC-1999; 99CA-2290722.
 XX 08-DEC-1999; 99CA-2290722.
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;
 XX WPI; 2001-425937/46.
 XX Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -
 XX Example 4; Page 102; 154pp; English.
 XX The present invention describes a composition (I) comprising stress

CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPCCs specific to target cancer (TC). (I) Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPCCs
 CC or a population of different SPCCs consisting of immunogenic cancer cell
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
 |||
 Db 5 SEQ 7

RESULT 39

AAM44237
 ID AAM44237 standard; Peptide; 7 AA.

XX AC AAM44237;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #508.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.
 OS Synthetic.

XX FN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

XX PS Example 4; Page 102; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPCCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPCCs

CC or a population of different SPCCs consisting of immunogenic cancer cell
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
 CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
 CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
 CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
 CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
 CC or imaging cancer cells, and to monitor the course of amelioration of
 CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
 CC which are used in the exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
 |||
 Db 5 SEQ 7

RESULT 40

AAM44242
 ID AAM44242 standard; Peptide; 7 AA.

XX AC AAM44242;

XX DT 25-OCT-2001 (first entry)

XX DE H11 binding site consensus conforming peptide (CCP) #513.

XX KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPCC;
 KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
 KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
 KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
 KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.

XX OS Homo sapiens.
 OS Synthetic.

XX PN CA2290722-A1.

XX PD 08-JUN-2001.

XX PF 08-DEC-1999; 99CA-2290722.

XX PR 08-DEC-1999; 99CA-2290722.

XX PA (NOVO-) NOVOPHARM BIOTECH INC.

XX PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
 PI Entwistle JM, MacDonald GC;

XX DR WPI; 2001-425937/46.

XX PT Composition useful for treating and diagnosing cancer, comprises stress
 PT protein-peptide complexes associated with tumor, and isolated
 PT antigen-binding fragments of an antibody that binds specifically to the
 PT complex -

XX PS Example 4; Page 102; 154pp; English.

XX CC The present invention describes a composition (I) comprising stress
 CC protein-peptide complexes (SPPC) associated with tumours that is
 CC specifically immunogenically cross-reactive with cell surface-associated
 CC SPCCs specific to target cancer (TC). Also described is an isolated
 CC antigen-binding fragment of an antibody that binds specifically to SPCCs
 CC or a population of different SPCCs consisting of immunogenic cancer cell
 CC surface-associated SPCC of TC. (I) has cytostatic activity and can be
 CC used in vaccine production and as a tumour-specific immunogenic response
 CC inducer. (I) is useful for treating 71 types of cancers or tumours in a

CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma, oligodendroglioma, ependymoma, medulloblastoma, and primitive neural ectodermal tumour (PNET). (I) is useful as cancer immunogen including vaccines. (I) is useful for diagnostic and palliative use, for detecting CC or imaging cancer cells, and to monitor the course of amelioration of CC malignancy in an individual. AAM43707 to AAM47109 represent peptides CC which are used in the exemplification of the present invention.

XX
SQ Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 5 SEQ 7

RESULT 41
AAM44247
ID AAM44247 standard; Peptide; 7 AA.
XX
AC AAM44247;
XX
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #518.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
DR WPI; 2001-425937/46.
XX
PT Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
PS Example 4; Page 102; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting

CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.

XX
SQ Sequence 7 AA;

Query Match 75.0%; Score 3; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 5 SEQ 7

RESULT 42
AAM44252
ID AAM44252 standard; Peptide; 7 AA.
XX
AC AAM44252;
XX
DT 25-OCT-2001 (first entry)
XX
DE H11 binding site consensus conforming peptide (CCP) #523.
XX
KW Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
KW immunogenically cross-reactive; cancer; immunogenic cancer cell;
KW cytostatic; vaccine; tumour-specific immunogenic response inducer;
KW astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
KW ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN CA2290722-A1.
XX
PD 08-JUN-2001.
XX
PF 08-DEC-1999; 99CA-2290722.
XX
PR 08-DEC-1999; 99CA-2290722.
XX
PA (NOVO-) NOVOPHARM BIOTECH INC.
XX
PI Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
PI Entwistle JM, MacDonald GC;
XX
DR WPI; 2001-425937/46.
XX
PT Composition useful for treating and diagnosing cancer, comprises stress
PT protein-peptide complexes associated with tumor, and isolated
PT antigen-binding fragments of an antibody that binds specifically to the
PT complex -
XX
PS Example 4; Page 102; 154pp; English.
XX
CC The present invention describes a composition (I) comprising stress
CC protein-peptide complexes (SPPC) associated with tumours that is
CC specifically immunogenically cross-reactive with cell surface-associated
CC SPPCs specific to target cancer (TC). Also described is an isolated
CC antigen-binding fragment of an antibody that binds specifically to SPPCs
CC or a population of different SPPCs consisting of immunogenic cancer cell
CC surface-associated SPPC of TC. (I) has cytostatic activity and can be
CC used in vaccine production and as a tumour-specific immunogenic response
CC inducer. (I) is useful for treating 71 types of cancers or tumours in a
CC subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
CC oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
CC ectodermal tumour (PNET). (I) is useful as cancer immunogen including
CC vaccines. (I) is useful for diagnostic and palliative use, for detecting
CC or imaging cancer cells, and to monitor the course of amelioration of
CC malignancy in an individual. AAM43707 to AAM47109 represent peptides
CC which are used in the exemplification of the present invention.

Db 5 SEQ 7

RESULT 45
 AAB68700
 ID AAB68700 standard; peptide; 7 AA.
 XX
 AC AAB68700;
 XX
 DT 03-MAY-2001 (first entry)
 XX
 DE Cleavage signal peptide.
 XX
 KW Cleavage signal; intein cleavage activity; protein purification.
 XX
 OS Unidentified.
 XX
 PN WO200112820-A1.
 XX
 PD 22-FEB-2001.
 XX
 PF 17-AUG-2000; 2000WO-US22581.
 XX
 PR 17-AUG-1999; 99US-0149257.
 XX
 PA (HEAL-) HEALTH RES INST.
 XX
 PI Belfort M, Belfort G, Derbyshire V, Wood D, Wu W;
 XX
 DR WPI; 2001-218352/22.
 XX
 PT Screening enhanced, reduced intein cleavage activity by expressing
 PT randomly mutagenized intein DNA and screening cleavage activity using
 PT varying growth medium and conditions, or by assay with chemical,
 PT respectively -
 XX
 PS Disclosure; Page 6; 103pp; English.
 XX
 CC The present invention relates to a method for screening for enhanced or
 CC reduced intein cleavage activity. The method involves subjecting intein
 CC DNA to random mutagenesis, expressing the intein DNA with a reporter and
 CC screening for elevated or reduced intein cleavage activity using varying
 CC growth medium and conditions, or by an assay with a chemical that plays a
 CC part in a cell metabolic and/or biochemical cycle. The method is useful
 CC for purifying a desired protein from a fusion protein. The present
 CC peptide is a cleavage signal peptide, which can be added to the beginning
 CC of proteins for C-terminal cleavage.
 XX
 SQ Sequence 7 AA;
 Query Match 75.0%; Score 3; DB 22; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
 |||
 Db 3 EQP 5

RESULT 46
 AAP40188
 ID AAP40188 standard; peptide; 8 AA.
 XX
 AC AAP40188;
 XX
 DT 25-MAR-2003 (updated)
 DT 31-JAN-1992 (first entry)
 XX
 DE Hexapeptide coded for by codons 93-98 in the RNA sequence coding for
 DE structural capsid protein VP1 of polio virus type 3 (Sabin strain)
 DE (Leon).
 XX
 KW Structural capsid protein; VP1; poliovirus type 3; vaccine;

KW enterovirus; diagnosis.
 XX
 OS Poliovirus type 3 (Sabin strain) (Leon).
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= H-Glu
 FT Modified-site 8 /label= Gln-OH
 FT
 XX WO8401575-A.
 PN
 XX 26-APR-1984.
 PD
 PF 11-OCT-1983; 83WO-GB00254.
 XX
 PR 24-JUN-1983; 83GB-0017242.
 PR 11-OCT-1982; 82GB-0028976.
 PR 11-OCT-1983; 83GB-0027154.
 XX
 PA (NABI-) NAT BIOL STAN BOARD.
 PA (MINO/) MINOR P D.
 PA (NATR) NAT RES DEV CORP.
 XX
 PI Almond J;
 XX
 DR WPI; 1984-113769/18.
 XX
 PT Antigenic poly-peptide for vaccination against Enterovirus - esp.
 PT polio, and for diagnosis
 XX
 PS Disclosure; Page 7; 56pp; English.
 XX
 CC The inventors claim an antigenic polypeptide for vaccination against
 CC Enterovirus. Pref. equivalents are octapeptides coded for by codons
 CC 93-100 of poliovirus type 3 (Sabin strain) VP1 and oligopeptides
 CC coded by a continuous run of 7-18 codons (including 93-98); starting
 CC no lower than 86 and ending no higher than 103. A pref.
 CC immunological carrier for the peptides is tetanus or diphtheria
 CC toxoid. A typical dose is 0.1-1 mg, opt. given as a priming dose
 CC before vaccination.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 8 AA;
 Query Match 75.0%; Score 3; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
 |||
 Db 1 EQP 3

RESULT 47
 AAP60137
 ID AAP60137 standard; peptide; 8 AA.
 XX
 AC AAP60137;
 XX
 DT 25-MAR-2003 (updated)
 DT 07-JUL-1991 (first entry)
 XX
 DE Sequence of preferred type 3 poliovirus octapeptide according
 DE to GB-A-2 128 621.
 XX
 XX Vaccine; diagnosis; enterovirus disease; poliovirus type 1; type 2;
 KW type 3.
 XX
 OS Poliovirus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 5


```

XX SQ Sequence 8 AA;
    Query Match 75.0%; Score 3; DB 15; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 3 EQP 5

RESULT 50
AAR48371
ID AAR48371 standard; peptide; 8 AA.
XX AC AAR48371;
XX DT 16-SEP-1994 (first entry)
XX DE Peptide fragment which adsorbs to anti-platelet antibody.
XX KW Peptide; fragment; anti-platelet antibody; adsorbent; ITP;
XX KW immune thrombocytopenia purpura.
XX OS Synthetic.
XX PN JP06030989-A.
XX PD 08-FEB-1994.
XX PF 13-JUL-1992; 92JP-0185176.
XX PR 13-JUL-1992; 92JP-0185176.
XX PA (TOYM ) TOYOBO KK.
XX WPI; 1994-079346/10.
XX DT New polypeptide and adsorber of anti-platelet antibody - used to
XX PT purify blood
XX PS Claim 1; Page 2; 8pp; Japanese.
XX CC The peptide is a fragment of a larger polypeptide which is used in
XX CC an adsorbent of anti-platelet antibody. The adsorbent is used for
XX CC the treatment of severe immune thrombocytopenia purpura (ITP)
XX CC patients.
XX SQ Sequence 8 AA;
    Query Match 75.0%; Score 3; DB 15; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 3 EQP 5

RESULT 51
AAR58622
ID AAR58622 standard; peptide; 8 AA.
XX AC AAR58622;
XX DT 25-APR-1995 (first entry)
XX DE GP2b residues 896-903, anti-platelet antibody binding peptide.
XX KW Anti-platelet; antibody; adsorbent; nonwoven; fabric; epoxy group;
XX KW ITP patient; external circulation; plasma.

```

```

OS Homo sapiens.
XX PN JP06218050-A.
XX PD 09-AUG-1994.
XX PF 25-JAN-1993; 93JP-0010065.
XX PR 25-JAN-1993; 93JP-0010065.
XX PA (TOYM ) TOYOBO KK.
XX WPI; 1994-290064/36.
XX PT Anti-platelet antibody adsorbent, useful for external circulation
XX PT therapy - comprises peptide able to bind to antibodies which is
XX PT immobilised on nonwoven fabric having epoxy gps
XX PS Disclosure; Page 4; 11pp; Japanese.
XX CC The sequences given in AAR58615-23 represent peptides which have the
XX CC ability to bind anti-platelet antibodies. These peptides may be
XX CC used in an antibody adsorbent which consists of these peptides,
XX CC which may be opt. modified immobilised on a nonwoven fabric having
XX CC epoxy groups in the surface, and composed of fibre of an average of
XX CC 1-30 microns. The adsorbent binds effectively to anti-platelet
XX CC antibodies and is therefore useful for treating serious ITP patients,
XX CC without side effects. The use of the nonwoven fabric allows full
XX CC external circulation with sepn. of the plasma. Peptides are easily
XX CC introduced through epoxy groups.
XX SQ Sequence 8 AA;
    Query Match 75.0%; Score 3; DB 15; Length 8;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 3 EQP 5

RESULT 52
AAR66119
ID AAR66119 standard; peptide; 8 AA.
XX AC AAR66119;
XX DT 07-JUL-1995 (first entry)
XX DE Peptide derived from platelet GP2b receptor amino acids 896-903.
XX KW Platelet; GP1; GP2b; GP3a; receptor; blood; factor; fibrinogen; plasma;
XX KW von Willebrand factor; immobilisation; adsorbent; autoimmune disease;
XX KW antibody; idiopathic thrombocytopenic purpura; ITP; circulation; ligand.
XX OS Synthetic.
XX PN JP06269498-A.
XX PD 27-SEP-1994.
XX PF 17-MAR-1993; 93JP-0057207.
XX PR 17-MAR-1993; 93JP-0057207.
XX PA (TOYM ) TOYOBO KK.
XX WPI; 1994-346230/43.
XX PT Anti-platelet-antibody adsorbent useful for external circulation
XX PT therapy - consisting of opt. modified peptide(s) having
XX PT binding affinity and immobilised to nonwoven fabric

```

XX Disclosure; Page 3; 11pp; Japanese.

PS

XX A series of peptides (AAR66112-35), optionally modified, derived from

CC GPI alpha-chain, GP2b or GP3a receptors on platelets, which bind blood

CC factors such as fibrinogen and von Willebrand factor. The modified

CC peptides can be immobilised on a non-woven fabric adsorbent. The

CC adsorbent can be used to remove anti-platelet-antibodies useful in

CC treating patients with autoimmune diseases such as severe idiopathic

CC thrombocytopenic purpura (ITP). The use of the non-woven fabric

CC eliminates the need for the separation of the blood plasma and permits

CC external circulation for treatment of the entire blood. The functional

CC groups facilitate the introduction of peptides as ligands.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4

DB 3 EQP 5

RESULT 53

AAW33664

ID AAW33664 standard; peptide; 8 AA.

AC AAW33664;

XX

DT 24-APR-1998 (first entry)

XX

DE Poliovirus type 3 VP1 antigenic epitope.

XX

KW Antigenic epitope; virus like particle; poliovirus type 3; VP1;

XX diagnostic reagent; antibiotic; therapy; food supplement; VLP;

KW vaccination; herbicide resistance; industrial enzyme.

XX

OS Poliovirus.

XX

PN WO9739134-A1.

XX

PD 23-OCT-1997.

XX

PF 17-APR-1997; 97WO-GB01065.

XX

PR 17-APR-1996; 96GB-0007899.

XX

PA (SCCR-) SCOTTISH CROP RES INST.

XX

PI Chapman SN, Wilson TMA;

XX

DR WPI; 1997-526468/48.

XX

PT Production of virus like particles - using a nucleic acid sequence

PT capable of assembly with a protein having a first viral portion and

PT second non-viral portion

XX

PS Example 1; Page 9; 33pp; English.

XX

CC This is antigenic epitope from VP1 of poliovirus type 3. This was fused

CC to the 3' end of a synthetic gene coding for the tobacco mosaic virus

CC (TMV) coat protein by PCR amplification with mutagenic primers. This is

CC used in a novel method for producing a protein having a first (viral)

CC portion and a second (non-viral) portion. The method comprises

CC expressing the protein in a cell, providing a nucleic acid sequence

CC capable of assembly with the protein into a virus-like particle (VLP),

CC and permitting in vivo assembly of the protein and nucleic acid into

CC VLPs. The VLPs can be used for the production of proteins such as

CC diagnostic reagents, antibiotics, therapeutic agents or food supplements.

CC They can be used for e.g. expression of metabolic enzymes for pathway

CC engineering, nutritional supplements, anti-potato cyst nematode lectins,

CC gut protease inhibitors, anti-botrytis agents, PGIBs, anti-insect

CC Bacillus thuringiensis toxin and herbicide resistance agents, industrial

CC enzymes, pharmaceuticals, therapeutic proteins, and nucleic acids, and as

CC bioreactors. They can also be used intact for presentation of peptide

CC epitopes for vaccination of animals, the production of therapeutic or

CC industrial proteins and polypeptides and/or the delivery of therapeutic

CC nucleic acid molecules.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 18; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4

DB 1 EQP 3

RESULT 54

AAW79269

ID AAW79269 standard; Peptide; 8 AA.

XX

AC AAW79269;

XX

DT 15-FEB-1999 (first entry)

XX

DE Bovine glucuronyl C5-epimerase internal peptide.

XX

KW Glucuronyl C5-epimerase; cattle; D-glucuronic acid;

XX L-iduronic acid; heparin; heparan sulphate.

XX

OS Bos taurus.

XX

PN WO9848006-A1.

XX

PD 29-OCT-1998.

XX

PF 17-APR-1998; 98WO-SE00703.

XX

PR 18-APR-1997; 97SE-0001454.

XX

PA (LIJ/J) LI J.

XX (LIND/J) LINDAHL U.

PI Li J, Lindahl U;

XX

DR WPI; 1998-583655/49.

XX

PT DNA sequence coding for mammalian glucuronyl C5-epimerase and

PT functional derivatives - capable of converting D-glucuronic acid to

PT L-iduronic acid in the synthesis of heparin and heparan sulphate

XX

PS Disclosure; Page 16; 26pp; English.

XX

CC This is an internal peptide of a glucuronyl C5-epimerase purified

CC from bovine liver. It corresponds to amino acid residues 306-313.

CC of the deduced amino acid sequence (see AAW79263) of the epimerase.

CC N-terminal and internal peptides (see AAW79264-70) of the epimerase

CC were produced by digestion of the purified epimerase using a

CC lysine-specific protease. PCR primers (see AAV62689-91) based on one

CC of these peptides (see AAW79270) were used to generate a probe that

CC was utilised in the isolation of glucuronyl C5-epimerase cDNA (see

CC AAV62688) from a bovine lung cDNA library. The invention relates to

CC isolated or recombinant DNA sequences for a mammalian (including

CC human) glucuronyl C5-epimerase or its functional derivative. These

CC can be used for the recombinant production of the enzyme, which is

CC useful for converting D-glucuronic acid to L-iduronic acid in the

CC biosynthesis of heparin and heparan sulphate.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 19; Length 8;

```

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
   |||
Db 3 SEQ 5

RESULT 55
AAW45999
ID AAW45999 standard; peptide; 8 AA.
AC AAW45999;
XX
XX
DT 03-JUL-1998 (first entry)
XX
DE Peptide #24 based on mouse SST2 2 (residues 1-8).
XX
XX Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;
KW insulin-like growth factor binding protein; IGFBP; SST2; diabetes;
KW somatostatin receptor; insulin-like growth factor.
XX
XX Synthetic.
OS Mus sp.
XX
XX WO9744352-A1.
PN
XX
PD 27-NOV-1997.
XX
XX 22-MAY-1997; 97WO-AU00312.
XX
XX 22-MAY-1996; 96AU-000990.
XX
XX (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.
PA
XX Gerraty NL, Kingston DJ, Westbrook SL;
PI
XX WPI; 1998-018427/02.
DR
XX New non-naturally occurring peptide(s) - which are based on portions
PT of somatostatin, somatostatin receptors and insulin-like growth
PT factor binding protein
XX
XX Example 11; Page 9; 136pp; English.
PS
XX
XX Peptides AAW45983-W456025 are based on portions of somatostatin,
CC somatostatin receptors (SSTR) and insulin-like growth factor binding
CC proteins (IGFBP). They are capable of increasing weight gain, birth
CC weight, growth rates, milk production, levels of circulating insulin,
CC IGF-I and IGF-III, fibre production and muscle weight. They may be used
CC to modulate carbohydrate metabolism and in treatment of diabetes. The
CC oil carrier may be used for delivery of the peptides.
XX
XX Sequence 8 AA;
SQ
Query Match 75.0%; Score 3; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
   |||
Db 5 SEQ 7

RESULT 56
AAW46001
ID AAW46001 standard; peptide; 8 AA.
XX
XX AAW46001;
AC
XX
XX 03-JUL-1998 (first entry)
DT
XX
XX Peptide #27 based on rat SST2 2 (residues 1-8).
DE

```

```

XX Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;
KW insulin-like growth factor binding protein; IGFBP; SST2; diabetes;
KW somatostatin receptor; insulin-like growth factor.
XX
XX Synthetic.
OS Rattus sp.
XX
XX WO9744352-A1.
PN
XX
XX 27-NOV-1997.
XX
XX 22-MAY-1997; 97WO-AU00312.
XX
XX 22-MAY-1996; 96AU-000990.
XX
XX (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.
PA
XX Gerraty NL, Kingston DJ, Westbrook SL;
PI
XX WPI; 1998-018427/02.
DR
XX New non-naturally occurring peptide(s) - which are based on portions
PT of somatostatin, somatostatin receptors and insulin-like growth
PT factor binding protein
XX
XX Example 11; Page 9; 136pp; English.
PS
XX
XX Peptides AAW45983-W456025 are based on portions of somatostatin,
CC somatostatin receptors (SSTR) and insulin-like growth factor binding
CC proteins (IGFBP). They are capable of increasing weight gain, birth
CC weight, growth rates, milk production, levels of circulating insulin,
CC IGF-I and IGF-III, fibre production and muscle weight. They may be used
CC to modulate carbohydrate metabolism and in treatment of diabetes. The
CC oil carrier may be used for delivery of the peptides.
XX
XX Sequence 8 AA;
SQ
Query Match 75.0%; Score 3; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
   |||
Db 5 SEQ 7

RESULT 57
ABP21164
ID ABP21164 standard; Peptide; 8 AA.
XX
XX ABP21164;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX HIV A03 motif pol peptide #159.
DE
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
OS
XX
XX WO200124810-A1.
PN
XX
XX 12-APR-2001.
PD
XX
XX 05-OCT-2000; 2000WO-US27766.
PF
XX
XX 05-OCT-1999; 99US-0412863.
PR
XX
XX (EPIM-) EPIMUNE INC.
PA
XX

```


PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX Claim 32; Page 303; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX SQ Sequence 8 AA;
 XX Query Match 75.0%; Score 3; DB 22; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQ 3
 Db 4 SEQ 6
 RESULT 58
 ABP21201
 ID ABP21201 standard; Peptide; 8 AA.
 AC ABP21201;
 DT 15-JUL-2002 (first entry)
 DE HIV A03 motif pol peptide #196.
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 OS WO200124810-A1.
 XX 12-APR-2001.
 XX 05-OCT-2000; 2000WO-US27766.
 PF 05-OCT-1999; 99US-0412863.
 PR (EPTM-) EPIMUNE INC.
 PA Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

DR WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX Claim 32; Page 304; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX SQ Sequence 8 AA;
 XX Query Match 75.0%; Score 3; DB 22; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQ 3
 Db 3 SEQ 5
 RESULT 59
 ABP23175
 ID ABP23175 standard; Peptide; 8 AA.
 AC ABP23175;
 DT 15-JUL-2002 (first entry)
 DE HIV A11 motif pol peptide #117.
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 OS WO200124810-A1.
 XX 12-APR-2001.
 XX 05-OCT-2000; 2000WO-US27766.
 PF 05-OCT-1999; 99US-0412863.
 PR (EPTM-) EPIMUNE INC.
 PA Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -

PS Claim 32; Page 343; 448pp; English.

XX

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC AB25397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumor-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP1501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention.

XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
|||

Db 4 SEQ 6
|||

RESULT 60

ABBS2109

ID ABB52109 standard; Peptide; 8 AA.

XX AC ABB52109;

XX DT 08-FEB-2002 (first entry)

XX DE Human API-73 tryptic digest peptide #2.

XX KW Human; neuroprotective; nootropic; gene therapy; vaccine;

XX KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;

XX KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;

XX KW Expression Reference Protein Isoform; ERPI; proteolysis.

XX OS Homo sapiens.

XX PN WO200175454-A2.

XX PD 11-OCT-2001.

XX PF 03-APR-2001; 2001WO-US10908.

XX PR 03-APR-2000; 2000US-194504P.

XX PR 28-NOV-2000; 2000US-253647P.

XX PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.

XX PA (PFIZ) PFIZER INC.

XX PI Durham KL, Friedman DL, Herath HMAAC, Kimmel LH, Parekh RB;

XX PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;

XX PI Townsend RR, White F, Williams SA;

XX DR WPI; 2001-639384/73.

XX

PT Screening for Alzheimer's disease in a mammal, by making

PT two-dimensional array of a feature whose relative abundance correlates

PT with disease, and comparing with abundance of the feature in samples of

PT healthy persons -

XX Example; Page 28; 162pp; English.

XX

XX The invention relates to methods for the screening, diagnosis and

CC prognosis of Alzheimer's disease. The methods involve the detection

CC of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's

CC Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid,

CC serum or plasma. The abundance of the AFs and APIs is then

CC normalised to an Expression Reference Protein Isoform (ERPI) in

CC order to determine whether a patient is suffering from, or has

CC a predisposition to, Alzheimer's Disease. The relative abundance of

CC the AFs and APIs correlates with the severity of Alzheimer's Disease.

CC The present sequence is a peptide produced from an API by proteolysis.

XX SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4

|||

Db 1 EQP 3

RESULT 61

AAO15739

ID AAO15739 standard; Peptide; 8 AA.

XX AC AAO15739;

XX DT 14-NOV-2002 (first entry)

XX DE Haemophilus influenzae BASB213 protein potential B-cell epitope 2.

XX KW BASB213; gene therapy; vaccine; otitis media; pneumonia;

XX KW Haemophilus influenzae infection; sinusitis; nosocomial infection;

XX KW invasive disease; B-cell epitope.

XX OS Haemophilus influenzae.

XX PN WO200266503-A2.

XX PD 29-AUG-2002.

XX PF 15-FEB-2002; 2002WO-EP01650.

XX PR 16-FEB-2001; 2001GB-0003866.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Thonard J;

XX DR WPI; 2002-674912/72.

XX PT New BASB213 polypeptide and polynucleotide, useful for the preparation

XX PT of a medicament used in generating an immune response in an animal, and

XX PT for diagnosing, preventing and/or treating microbial diseases with H.

XX PT influenza infection -

XX PS Example 13; Page 69; 87pp; English.

XX

XX The invention comprises the amino acid and coding sequences of

CC Haemophilus influenzae BASB213 proteins. The BASB213 DNA and protein

CC sequences of the invention are useful for generating an immune response

CC in an animal. In particular, the BASB213 DNA and protein sequences are

CC useful for diagnosing, preventing and/or treating microbial diseases with

CC H. influenzae infection (e.g. otitis media, pneumonia, sinusitis,

CC nosocomial infections and invasive diseases). The present amino acid

CC sequence represents a potential B-cell epitope from a H. influenzae
 CC BASB213 protein.
 XX
 SQ Sequence 8 AA;
 Query Match 75.0%; Score 3; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
 ||||
 Db 1 SEQ 3

RESULT 62
 ID ABG31180 standard; Peptide; 8 AA.
 XX
 AC ABG31180;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Rat delta PKC region, pseudo-delta RACK, modified peptide, #20.
 XX
 KW Rat; delta protein kinase C; deltaPKC; V1 domain; vasotropic;
 KW cerebroprotective; deltaV1-1; deltaV1-2; RACK; pseudo-delta RACK;
 KW pseudo-delta receptor for activated C-kinase; deltaV1-5; PKC;
 KW protein kinase C; signal transduction; cell growth; gene expression;
 KW ion channel activity; translocation; hypoxia; stroke; ischaemic damage;
 KW creatine kinase; antagonist; agonist; mutant; mutein.
 XX
 OS Rattus norvegicus.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 6 /note= "Wild-type Asp substituted by Gln"
 FT
 XX WO200257413-A2.
 XX
 XX 25-JUL-2002.
 XX
 XX 09-NOV-2001; 2001WO-US47556.
 XX
 XX 18-JAN-2001; 2001US-262060P.
 XX
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Mochly-Rosen D;
 XX
 XX WPI; 2002-599715/64.
 XX
 XX New delta protein kinase C peptide for reducing or enhancing damage to
 PT cells or tissues exposed to ischemic or hypoxic event caused by stroke,
 PT or for protecting tissue from damage due to ischemia -
 XX
 XX Claim 4; Page 21; 65pp; English.
 XX
 XX The invention discloses peptides comprising deltaV1-1, deltaV1-2,
 CC pseudo-delta receptors for activated C-kinase (RACK), deltaV1-5 or their
 CC derivatives or fragments. Protein kinase C (PKC) is a key enzyme in
 CC signal transduction involved in a variety of cellular functions including
 CC cell growth, regulation of gene expression and ion channel activity. The
 CC localisation of different PKC isozymes to different areas of the cell in
 CC turn appears due to binding of the activated isozymes to the specific
 CC anchoring molecules (RACKs). Peptides that mimic either the PKC-binding
 CC site on RACKs or the RACK-binding site on PKC are isozyme specific
 CC translocation inhibitors of PKC. The disclosed peptides are useful in
 CC activating or inhibiting translocation or function of deltaPKC. The
 CC deltaPKC agonists or antagonists are useful in reducing, enhancing or
 CC protecting against damage to cells or tissues due to ischaemic or hypoxic
 CC event caused by stroke. Acute administration of the peptides, conjugated
 CC to a carrier peptide or a Tat-derived peptide, protected hearts against

CC ischaemic damage as shown by decreased release of creatine kinase. The
 CC data indicate that in an intact heart, inhibition of deltaPKC conferred
 CC greater than 50% protection against ischaemic damage. The peptides
 CC in ABG31159-ABG31219 are the deltaV1-1, deltaV1-2, pseudo-delta RACK,
 CC deltaV1-5 (or their derivatives or fragments) agonists or antagonists to
 XX the rat delta protein kinase C (PKC).
 SQ Sequence 8 AA;
 Query Match 75.0%; Score 3; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
 ||||
 Db 5 EQP 7

RESULT 63
 ID ABG60428 standard; Peptide; 8 AA.
 XX
 AC ABG60428;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Selective targeting peptide #103.
 XX
 KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;
 KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;
 KW viral infection; cardiovascular disease; degenerative disease; ischaemia;
 KW inflammation; macular degeneration; antiinflammatory; antidiabetic;
 KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic.
 KW gene therapy.
 XX
 OS Synthetic.
 XX
 XX WO200220769-A1.
 XX
 XX 14-MAR-2002.
 XX
 XX 07-SEP-2001; 2001WO-US27692.
 XX
 XX 08-SEP-2000; 2000US-231266P.
 XX
 XX 17-JAN-2001; 2001US-0765101.
 XX
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX
 XX Arap W, Pasqualini R;
 XX
 XX WPI; 2002-415731/44.
 XX
 XX Targeting peptides identified by phage display, useful for targeting
 PT delivery to an organ or tissue, particularly for treating a disease,
 PT e.g. cancer, inflammatory or autoimmune diseases, infections or
 PT cardiovascular disease -
 XX
 XX Claim 22; Page 90; 317pp; English.
 XX
 XX The invention relates to an isolated peptide of 100 amino acids or less
 CC in size useful for targeting delivery to an organ or tissue, particularly
 CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory
 CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral
 CC infection, cardiovascular disease or degenerative disease. The peptide is
 CC also useful for inducing apoptosis, particularly to a subject with
 CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,
 CC inflammation or macular degeneration. Furthermore, the peptide is useful
 CC for diagnosing the diseases cited above. Targeting peptides of the
 CC invention can also be used to deliver an agent to a foetus, by attaching
 CC a peptide to the agent and administering the peptide to a pregnant
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting
 CC peptides of the invention.
 XX

SQ Sequence 8 AA;

Query Match 75.0%; Score 3; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 5 SEQ 7

RESULT 64

ABU38203
ID ABU38203 standard; Peptide; 8 AA.

AC ABU38203;

DT 22-MAY-2003 (first entry)

XX Human cytomegalovirus CTL epitope peptide SEQ ID No 261.

KW Virucide; immunostimulant; cytotoxic T-lymphocyte; CTL; epitope; antigen;
KW human cytomegalovirus; HCMV; pp28; pp50; pp65; pp71; pp150; gB; gH; IE-1;
KW IE-2; US2; US3; US6; US11; UL18; cytomegalovirus infection; pregnancy;
KW transplantation.

XX Human cytomegalovirus.

XX WO2003000720-A1.

XX 03-JAN-2003.

XX 26-JUN-2002; 2002WO-AU00829.

XX 26-JUN-2001; 2001AU-0005931.

XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

PI Khanna R, Elkington RA, Walker SJ;

DR WPI; 2003-300379/29.

XX New human cytomegalovirus (HCMV) cytotoxic T-cell epitope peptide,
PT useful for diagnosing, preventing or treating CMV infection, comprises
PT pp28, pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11
PT or UL18 -

XX Claim 70; Page 124; 308pp; English.

CC The invention relates to a novel isolated peptide comprising one or more
CC cytotoxic T-lymphocyte (CTL) epitope(s) of the same or different antigen
CC of a human cytomegalovirus (HCMV). The HCMV antigens can comprise pp28,
CC pp50, pp65, pp71, pp150, gB, gH, IE-1, IE-2, US2, US3, US6, US11 or UL18.
CC The peptide comprises a sequence of about 9-20 contiguous amino acids of
CC the antigen. The peptide epitopes are useful in diagnosing, preventing or
CC treating cytomegalovirus infection in humans, and in monitoring immune
CC responses in various clinical settings (e.g. transplantation or
CC pregnancy). This sequence represents a human cytomegalovirus CTL epitope
CC peptide of the invention.

XX Sequence 8 AA;

Query Match 75.0%; Score 3; DB 24; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
|||
Db 2 EQP 4

RESULT 65

AAR26441

ID AAR26441 standard; peptide; 9 AA.

XX AAR26441;

DT 25-MAR-2003 (updated)

DT 08-FEB-1993 (first entry)

XX N-terminal auxiliary sequence.

XX Negative hydrophobicity; increased renaturation yield.

XX Synthetic.

XX EP500108-A2.

XX 26-AUG-1992.

XX 20-FEB-1992; 92EP-0102864.

XX 21-FEB-1991; 91DE-4105480.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Ambrosius D, Dony C, Rudolph R;

XX WPI; 1992-286227/35.

XX Increasing renaturation yield of recombinant protein from
PT prokaryotic host - by expressing it with terminal hydrophilic
PT aminoacid sequence attached, pref. detachable at specific
PT cleavage site

XX Claim 11; Page 14; 18pp; German.

CC The peptide is used as an auxiliary sequence which can be added to
CC the N and/or C-terminus of recombinant proteins which exist in at
CC least partially inactive form and are activated by solubilisation
CC and/or renaturation techniques. The auxiliary sequence has a ratio
CC of relative hydrophobicity:number of amino acids of -2.0 kcal/mole
CC or smaller. Incorporation of the auxiliary sequence increases the
CC yield during the renaturation process. This method is applied to
CC recombinant proteins produced in prokaryotic organisms, especially
CC E. coli. A specific application is production of recombinant
CC granulocyte-colony stimulating factor (GM-CSF) or its derivatives.
CC See also AAR26436-R26444.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 75.0%; Score 3; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
|||
Db 6 EQP 8

RESULT 66

AAR87291
ID AAR87291 standard; peptide; 9 AA.

XX AAR87291;

DT 16-MAY-1996 (first entry)

XX Plasmodium falciparum HLA-B17 epitope ls42.

XX Liver stage antigen; ISA-1; human leucocyte antigen; HLA; class 1;
KW HLA-B17; epitope; malaria; vaccine; CTL induction;
KW cytotoxic T lymphocyte.

XX Plasmodium falciparum.

XX WO9526982-A2.
 XX
 PD 12-OCT-1995.
 XX
 XX 31-MAR-1995; 95WO-GB00737.
 XX PF
 XX 31-MAR-1994; 94GB-0006492.
 PR
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX Aidoo M, Allsopp CEM, Hill AVS, Lalvani A, Piebanski M;
 PI Whittle HC;
 PI
 XX WPI; 1995-358584/46.
 DR
 XX Plasmodium falciparum peptide(s) - useful in vaccine compositions
 PT for immunising against malaria
 PT
 XX Claim 1; Page 19; 23pp; English.
 PS
 XX Cytotoxic T lymphocytes from malaria-exposed Gambian individuals
 CC with HLA-B17 showed significant lysis of a large pool of peptides
 CC (AAR87287-R87299) derived from Plasmodium falciparum liver stage
 CC antigen-1. These peptides will be useful in a malaria vaccine.
 CC
 XX
 SQ Sequence 9 AA;
 Query Match 75.0%; Score 3; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQ 3
 DB 4 SEQ 6
 RESULT 67
 AAW49287
 ID AAW49287 standard; peptide; 9 AA.
 XX
 AC AAW49287;
 XX
 DT 05-JUN-1998 (first entry)
 XX
 DE Human leucocyte antigen DQ4 binding peptide #178.
 XX
 XX Human leucocyte antigen; HLA-DQ4; combinatorial library;
 KW autoimmune disease; chronic articular rheumatism.
 KW
 XX Synthetic.
 XX
 PN JF08151396-A.
 XX
 PD 11-JUN-1996.
 XX
 XX 28-NOV-1994; 94JP-0292657.
 PF
 XX 28-NOV-1994; 94JP-0292657.
 PR
 XX (TEIJ) TEIJIN LTD.
 PA
 XX WPI; 1996-329479/33.
 DR
 XX HLA-binding oligopeptide and an immuno:regulator contg it - used in
 PT the treatment of auto:immune disease
 PT
 XX Claim 4; Page 27; 61pp; Japanese.
 PS
 XX This peptide is an example of a peptide which binds to a human leucocyte
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
 CC combinatorial library comprising the sequence AAV05953, by screening
 CC with an HLA-DQ4 molecule. The peptide is used for the treatment of

CC autoimmune disease, or especially for treatment of viral diseases.
 XX
 SQ Sequence 9 AA;
 Query Match 75.0%; Score 3; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQ 3
 DB 6 SEQ 8
 RESULT 68
 AAW07112
 ID AAW07112 standard; peptide; 9 AA.
 XX
 AC AAW07112;
 XX
 DT 23-JAN-1997 (first entry)
 XX
 DE Synthetic peptide used in GalNac-transferase activity SPA.
 XX
 XX SPA; scintillation proximity assay; antigen; bead coating; capture;
 KW antibody; N-acetyl-galactosamine transferase; GalNac transferase;
 KW activity; enzyme; O-linked glycosylation.
 KW
 XX Synthetic.
 OS
 XX WO9615258-A1.
 PN
 XX 23-MAY-1996.
 PD
 XX 08-NOV-1995; 95WO-US13483.
 PF
 XX 16-NOV-1994; 94US-0340283.
 PR
 XX (UPJO) UPJOHN CO.
 PA
 XX Elhammer AP;
 PI
 XX WPI; 1996-268220/27.
 DR
 XX Scintillation proximity assay for N-acetyl:galactosaminyl activity
 PT - esp. for large scale screening of cpds. for their effect on enzyme
 PT activity
 PT
 XX Claim 14; Page 17; 29pp; English.
 PS
 XX AAW06985-W07180 are antigenic peptides derived from either the
 CC product of the human c-myc oncogene or the FLAG peptide (DYKDDDK).
 CC The peptides are useful for coating beads used in a scintillation
 CC proximity assay for N-acetyl:galactosamine (GalNac)-transferase (GNT)
 CC activity. The assay involves fewer steps than known assays and is
 CC quicker, producing excellent signal-to-noise ratios. The
 CC assay is capable of screening large numbers of cpds. for their
 CC ability to affect GNT activity and is thus useful for identifying
 CC inhibitors and promoters of glycosylation (in partic. O-linked
 CC glycosylation).
 CC
 XX
 SQ Sequence 9 AA;
 Query Match 75.0%; Score 3; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 EQP 4
 DB 1 EQP 3
 RESULT 69
 AAW29260

PT cancer or virus infection
 XX Disclosure; Page 33; 53pp; French.
 XX
 CC AAY40123-Y40379 represent epitopes that are able to activate cytotoxic
 CC T lymphocytes (CD8+ epitopes), T helper cells (CD4+ epitopes), or
 CC B epitopes recognized by corresponding antibodies. The epitopes may be
 CC used in the composition of the invention. The specification describes a
 CC lipopeptide that has a peptide part derived from mammalian interferon
 CC gamma (IFN γ) and one or more lipophilic parts comprising a linear or
 CC branched, (un)saturated 4-20C hydrocarbyl chain or a steroid. The
 CC lipopeptide mimics the activity of IFN γ . Compositions comprising the
 CC lipopeptide are used to treat or prevent any condition that responds
 CC to IFN γ , and as adjuvant for vaccines (particularly those directed
 CC against tumors, viral or parasitic infections), to stimulate or
 CC (re)orient the immune response between types 1 and 2 cytokine profiles.
 CC Particular applications are treatment of infections (particularly
 CC viral, e.g. acquired immune deficiency syndrome, papilloma (cancer) and
 CC hepatitis, but also bacterial, fungal, parasitic or helminth); cancers
 CC (particularly of kidney, cutaneous T cells or ovary, chronic
 CC myelogenous leukemia or mesothelioma), allergy; and autoimmune
 CC diseases.
 XX
 SQ Sequence 9 AA;
 Query Match 75.0%; Score 3; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQ 3
 Db 3 SEQ 5
 RESULT 72
 AAY26673
 ID AAY26673 standard; peptide; 9 AA.
 XX
 AC AAY26673;
 XX
 DT 14-SEP-1999 (first entry)
 DE BCR-ABL-derived lipopeptide epitope (aa817-825) for mixed micelles.
 XX
 KW Micelle; microaggregate; induction; immune response; lipopeptide; CTL;
 KW cytotoxic T-lymphocyte; epitope; lipid; helper T-lymphocyte; HTL; HBV;
 KW tetanus; toxin; vaccine; HIV; hepatitis B virus; papilloma virus; p53;
 KW melanoma; Plasmodium falciparum; malaria.
 XX
 OS Synthetic.
 OS Abelson murine leukemia virus.
 XX
 PN FR2771640-A1.
 XX
 PD 04-JUN-1999.
 XX
 PF 03-DEC-1997; 97FR-0015246.
 XX
 PR 03-DEC-1997; 97FR-0015246.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 PA (INSERM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (INSP) INST PASTEUR LILLE.
 XX
 PI Bossus M, Bourgault VI, Gras-Masse H, Guillet JG, Lippens G;
 PI Tartar A, Wieruszski JM;
 XX
 DR WPI; 1999-349509/30.
 XX
 PT Immunogenic lipopeptide micelles - comprising lipopeptides
 PT containing cytotoxic and helper T-lymphocyte epitopes
 XX
 PS Disclosure; Page 30; 60pp; French.

XX The invention relates to the generation of mixed micelles or
 CC microaggregates for inducing an immune response comprise: (a) a first
 CC lipopeptide comprising at least one CTL (cytotoxic T-lymphocyte) epitope
 CC and at least one lipid unit; and (b) a second lipopeptide comprising at
 CC least one HTL (helper T-lymphocyte) epitope and at least one lipid unit
 CC different from that of the first lipopeptide. This peptide represents
 CC an example of a lipopeptide epitope used in the invention and is derived
 CC from the BCR protein of the Abelson murine leukemia virus. The
 CC immunogenic lipopeptide micelles are used in vaccines, especially against
 CC HIV, hepatitis B virus (HBV), papilloma viruses, p53, melanoma or
 CC Plasmodium falciparum malaria.
 XX
 SQ Sequence 9 AA;
 Query Match 75.0%; Score 3; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEQ 3
 Db 3 SEQ 5
 RESULT 73
 AAW74273
 ID AAW74273 standard; peptide; 9 AA.
 XX
 AC AAW74273;
 XX
 DT 05-MAY-1999 (first entry)
 DE HJ loop peptide K105H103.
 XX
 KW HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 9 /note= "Mystyl-Gly"
 FT Modified-site 9 /note= "amidated"
 XX
 PN WO9853051-A1.
 XX
 PD 26-NOV-1998.
 XX
 PF 20-MAY-1998; 98WO-US10321.
 XX
 PR 21-MAY-1997; 97US-0861153.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Ben-Sasson SA;
 XX
 DR WPI; 1999-070143/06.
 XX
 PT New peptide derivatives for modulating protein tyrosine kinase
 PT activity - comprise a sequence corresponding to the HJ loop of a
 PT protein tyrosine kinase, used for treating cancers or immune
 PT disorders
 XX
 PS Disclosure; Fig 7; 79pp; English.
 XX
 CC This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,

CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

XX Sequence 9 AA;
 SQ

Query Match 75.0%; Score 3; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
 Db 6 EQP 8

RESULT 74
 AAW74285
 ID AAW74285 standard; peptide; 9 AA.
 AC AAW74285;
 XX

DT 05-MAY-1999 (first entry)

DE HJ loop peptide K094H101.

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;
 KW inflammatory disorder; central nervous system disease; septic shock;
 KW Parkinson's disease; hypertension.

XX Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "Myristyl-Gly"

FT Modified-site 9 /note= "amidated"

XX WO9853051-A1.

XX 26-NOV-1998.

XX 20-MAY-1999; 98WO-US10321.

XX 21-MAY-1997; 97US-0861153.

XX (CHL-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

XX WPI; 1999-070143/06.

XX New peptide derivatives for modulating protein tyrosine kinase
 PT activity - comprise a sequence corresponding to the HJ loop of a
 PT protein tyrosine kinase, used for treating cancers or immune
 PT disorders

XX Disclosure; Fig 7; 79pp; English.

XX This sequence represents a peptide of the invention, and is a derivative
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be
 CC used for the treatment of disorders caused by overactivity or
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and

CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's
 CC disease, stroke and trauma), septic shock, Parkinson's disease or
 CC hypertension. The peptides can also be used to produce antibodies which
 CC can be used to identify cells expressing the STK and to study the
 CC intracellular distribution of the STK. In addition, the peptides can be
 CC used to identify and quantitate ligands which bind the HJ loop of the STK
 CC from which the peptide was derived.

XX Sequence 9 AA;
 SQ

Query Match 75.0%; Score 3; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
 Db 5 EQP 7

RESULT 75
 AAW96177
 ID AAW96177 standard; peptide; 9 AA.
 XX
 AC AAW96177;
 XX

DT 27-APR-1999 (first entry)

DE IKK-alpha polypeptide with binding activity.

XX I-kappa-B kinase; IKK-alpha; gene expression; modulation;
 KW suppression; activation; tumour necrosis factor; TNF; interleukin-1;
 KW IL-1; TNF receptor associated factor; TRAF.

OS Homo sapiens.

XX WO9901541-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98WO-US13782.

XX 10-JUL-1997; 97US-0890854.

XX 01-JUL-1997; 97US-0887115.

XX (TULA-) TULARIK INC.

XX Cao Z, Regnier C, Rothe M;

XX WPI; 1999-106044/09.

XX Newly isolated human kinase I-kappaB Kinase (IKK- α) polypeptides -
 PT useful in screening for agents that modulate the interaction of an
 PT IKK polypeptide to a binding target and for modulating signal
 PT transduction involving I-kappaB in a cell

XX Disclosure; Page -; 32pp; English.

XX I-kappa-B kinase (AAW96158), deletion mutants of it retaining
 CC I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a
 CC six residue domain of I-kappa-B containing one of Ser32 and Ser36,
 CC and a candidate agent) can be used to screen for agents that
 CC modulate the interaction of an IKK polypeptide to a binding target.
 CC The modulation of the kinase activity of IKK-alpha forms a method
 CC for modulating signal transduction involving I-kappa-B in a cell.
 CC The IKK-alpha polypeptides are useful for generating oligonucleotide
 CC primers and probes for use in the isolation of natural
 CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as
 CC translatable transcripts, hybridization probes, polymerase chain
 CC reaction (PCR) probes and primers. Their diagnostic applications
 CC include IKK-alpha hybridization probes for identifying wild-type and

CC mutant IKK-alpha alleles in clinical and laboratory samples.
CC Therapeutic application includes the use of IKK- alpha nucleic acids
CC for modulating cellular expression or intracellular
CC concentration/availability of active IKK-alpha.
CC Catalytically inactive IKK-alpha mutants suppress NF-kappa-B
CC activation induced by tissue necrosis factor (TNF), interleukin-1
CC (IL-1) stimulation, TNF receptor-associated factor (TRAF) and
CC NF-kappa-B-inducing kinase (NIK) overexpression. Polypeptides of
CC IKK-alpha showing exemplary binding activity are described in
CC AAW96165-W96182. These peptides all comprise one of Cys30, Glu543,
CC Leu604, Thr679, Ser680, Pro684, Thr686 or Ser687 of the full length
CC IKK-alpha described in AAW96157. Deletion mutants of the invention
CC comprise at least one of these regions.
CC N.B. The present sequence is not given in the present specification
CC but is derived from the sequence given in AAW96157 as specified.
XX
SQ Sequence 9 AA;

Query Match 75.0%; Score 3; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 1 SEQ 3

Search completed: November 25, 2003, 18:15:53
Job time : 14.9574 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:34:25 ; Search time 7.95745 Seconds
(without alignments)
92.715 Million cell updates/sec

Title: US-09-641-801-10
Perfect score: 4
Sequence: 1 SEQP 4

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	100.0	4	15	US-10-281-652-10
2	4	100.0	14	12	US-10-234-816-40
3	4	100.0	14	15	US-10-185-050-190
4	3	75.0	5	12	US-10-168-758-3
5	3	75.0	5	15	US-10-043-487-493
6	3	75.0	6	10	US-09-873-233A-7
7	3	75.0	6	11	US-09-500-700-88
8	3	75.0	7	12	US-10-192-381-53
9	3	75.0	7	15	US-10-155-922-14
10	3	75.0	7	15	US-10-155-922-97
11	3	75.0	7	15	US-10-155-922-99
12	3	75.0	7	15	US-10-155-922-99
13	3	75.0	7	15	US-10-155-922-101
14	3	75.0	8	10	US-09-758-128-24
15	3	75.0	8	10	US-09-758-128-27
16	3	75.0	8	10	US-09-758-128-27
17	3	75.0	8	10	US-09-758-128-27
18	3	75.0	8	10	US-09-758-128-27
19	3	75.0	8	10	US-09-758-128-27
20	3	75.0	8	10	US-09-758-128-27
21	3	75.0	8	10	US-09-758-128-27
22	3	75.0	8	10	US-09-758-128-27
23	3	75.0	8	10	US-09-758-128-27
24	3	75.0	8	10	US-09-758-128-27
25	3	75.0	8	10	US-09-758-128-27
26	3	75.0	8	10	US-09-758-128-27
27	3	75.0	8	10	US-09-758-128-27
28	3	75.0	8	10	US-09-758-128-27
29	3	75.0	8	10	US-09-758-128-27
30	3	75.0	8	10	US-09-758-128-27
31	3	75.0	8	10	US-09-758-128-27
32	3	75.0	8	10	US-09-758-128-27
33	3	75.0	8	10	US-09-758-128-27
34	3	75.0	8	10	US-09-758-128-27
35	3	75.0	8	10	US-09-758-128-27
36	3	75.0	8	10	US-09-758-128-27
37	3	75.0	8	10	US-09-758-128-27
38	3	75.0	8	10	US-09-758-128-27
39	3	75.0	8	10	US-09-758-128-27
40	3	75.0	8	10	US-09-758-128-27
41	3	75.0	8	10	US-09-758-128-27
42	3	75.0	8	10	US-09-758-128-27
43	3	75.0	8	10	US-09-758-128-27
44	3	75.0	8	10	US-09-758-128-27
45	3	75.0	8	10	US-09-758-128-27
46	3	75.0	8	10	US-09-758-128-27
47	3	75.0	8	10	US-09-758-128-27
48	3	75.0	8	10	US-09-758-128-27
49	3	75.0	8	10	US-09-758-128-27
50	3	75.0	8	10	US-09-758-128-27
51	3	75.0	8	10	US-09-758-128-27
52	3	75.0	8	10	US-09-758-128-27
53	3	75.0	8	10	US-09-758-128-27
54	3	75.0	8	10	US-09-758-128-27
55	3	75.0	8	10	US-09-758-128-27
56	3	75.0	8	10	US-09-758-128-27
57	3	75.0	8	10	US-09-758-128-27
58	3	75.0	8	10	US-09-758-128-27
59	3	75.0	8	10	US-09-758-128-27
60	3	75.0	8	10	US-09-758-128-27
61	3	75.0	8	10	US-09-758-128-27
62	3	75.0	8	10	US-09-758-128-27
63	3	75.0	8	10	US-09-758-128-27
64	3	75.0	8	10	US-09-758-128-27
65	3	75.0	8	10	US-09-758-128-27
66	3	75.0	8	10	US-09-758-128-27
67	3	75.0	8	10	US-09-758-128-27
68	3	75.0	8	10	US-09-758-128-27
69	3	75.0	8	10	US-09-758-128-27
70	3	75.0	8	10	US-09-758-128-27
71	3	75.0	8	10	US-09-758-128-27
72	3	75.0	8	10	US-09-758-128-27
73	3	75.0	8	10	US-09-758-128-27
74	3	75.0	8	10	US-09-758-128-27
75	3	75.0	8	10	US-09-758-128-27
76	3	75.0	8	10	US-09-758-128-27
77	3	75.0	8	10	US-09-758-128-27
78	3	75.0	8	10	US-09-758-128-27
79	3	75.0	8	10	US-09-758-128-27
80	3	75.0	8	10	US-09-758-128-27
81	3	75.0	8	10	US-09-758-128-27
82	3	75.0	8	10	US-09-758-128-27
83	3	75.0	8	10	US-09-758-128-27
84	3	75.0	8	10	US-09-758-128-27
85	3	75.0	8	10	US-09-758-128-27
86	3	75.0	8	10	US-09-758-128-27
87	3	75.0	8	10	US-09-758-128-27
88	3	75.0	8	10	US-09-758-128-27

Sequence 124, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 24, Appl
Sequence 27, Appl
Sequence 32, Appl
Sequence 401, Appl
Sequence 579, Appl
Sequence 698, Appl
Sequence 15, Appl
Sequence 144, Appl
Sequence 14, Appl
Sequence 22, Appl
Sequence 140, Appl
Sequence 272, Appl
Sequence 281, Appl
Sequence 386, Appl
Sequence 498, Appl
Sequence 660, Appl
Sequence 22, Appl
Sequence 140, Appl
Sequence 272, Appl
Sequence 281, Appl
Sequence 386, Appl
Sequence 498, Appl
Sequence 660, Appl
Sequence 15, Appl
Sequence 144, Appl
Sequence 36, Appl
Sequence 92, Appl
Sequence 26, Appl
Sequence 65, Appl
Sequence 161, Appl
Sequence 565, Appl
Sequence 291, Appl
Sequence 291, Appl
Sequence 1778, Appl
Sequence 553, Appl
Sequence 80, Appl
Sequence 84, Appl
Sequence 306, Appl
Sequence 509, Appl
Sequence 705, Appl
Sequence 97, Appl
Sequence 72, Appl
Sequence 91, Appl
Sequence 160, Appl
Sequence 208, Appl
Sequence 233, Appl
Sequence 306, Appl
Sequence 319, Appl
Sequence 334, Appl
Sequence 72, Appl
Sequence 91, Appl
Sequence 160, Appl
Sequence 208, Appl
Sequence 233, Appl
Sequence 306, Appl
Sequence 319, Appl
Sequence 334, Appl
Sequence 80, Appl
Sequence 84, Appl
Sequence 306, Appl
Sequence 509, Appl
Sequence 705, Appl
Sequence 11, Appl
Sequence 291, Appl
Sequence 19, Appl
Sequence 35, Appl

89 3 75.0 10 15 US-10-155-922-60 Sequence 60, Appl
90 3 75.0 10 15 US-10-155-922-61 Sequence 61, Appl
91 3 75.0 10 15 US-10-155-922-62 Sequence 62, Appl
92 3 75.0 10 15 US-10-155-922-79 Sequence 79, Appl
93 3 75.0 10 15 US-10-133-210-207 Sequence 207, App
94 3 75.0 11 7 US-08-736-019-13 Sequence 13, Appl
95 3 75.0 11 11 US-09-964-923A-33 Sequence 33, Appl
96 3 75.0 11 12 US-10-239-313A-510 Sequence 510, App
97 3 75.0 11 15 US-10-033-741-18 Sequence 18, Appl
98 3 75.0 11 15 US-10-033-662-21 Sequence 21, Appl
99 3 75.0 12 12 US-10-137-867-312 Sequence 312, App
100 3 75.0 13 10 US-09-870-759-148 Sequence 148, App

ALIGNMENTS

RESULT 1
; Sequence 10, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-10

Query Match 100.0%; Score 4; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQP 4
 ||||
Db 1 SEQP 4

RESULT 2
US-10-234-816-40
; Sequence 40, Application US/10234816
; Publication No. US20030157514A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRAIN HOMOLGY DOMAIN AND PR
; FILE REFERENCE: D0117 NP
; CURRENT APPLICATION NUMBER: US/10/234,816
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-234-816-40

Query Match 100.0%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQP 4
 ||||
Db 8 SEQP 11

RESULT 3
US-10-185-050-190
; Sequence 190, Application US/10185050
; Publication No. US20030077577A1
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; Kay, Brian K.
; Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 233
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/185,050
; FILING DATE: 28-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,516
; FILING DATE: 03-Apr-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-208-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 190:

US-10-185-050-190
Query Match 100.0%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQP 4
 ||||
Db 3 SEQP 6

RESULT 4
US-10-168-758-3
; Sequence 3, Application US/10168758
; Publication No. US20030207812A1
; GENERAL INFORMATION:
; APPLICANT: Chapdelaine, Marc J
; APPLICANT: Katherine, Knappenberger

```

; APPLICANT: Steelman, Gary
; APPLICANT: Suchard, Suzanne
; APPLICANT: Sygowski, Linda
; TITLE OF INVENTION: CD45
; FILE REFERENCE: 270624-1P US
; CURRENT APPLICATION NUMBER: US/10/168,758
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-168-758-3

Query Match
Best Local Similarity 75.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
DB 1 EQP 3

RESULT 5
US-10-043-487-493
; Sequence 493, Application US/10043487
; Publication No. US20030055220A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, LEGRAIN
; TITLE OF INVENTION: Protein-protein interactions between Shigella flexneri polypeptides
; TITLE OF INVENTION: mammalian polypeptides
; FILE REFERENCE: B4778A
; CURRENT APPLICATION NUMBER: US/10/043,487
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/261,130
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 561
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 493
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Shigella flexneri
US-10-043-487-493

Query Match
Best Local Similarity 75.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
DB 3 SEQ 5

RESULT 6
US-09-873-233A-7
; Sequence 7, Application US/09873233A
; Patent No. US20020146434A1
; GENERAL INFORMATION:
; APPLICANT: UEDA, Shigeharu
; APPLICANT: WATANABE, Michiko
; APPLICANT: KAWANISHI, Hitomi
; TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN
; FILE REFERENCE: 0216-0451P
; CURRENT APPLICATION NUMBER: US/09/873,233A
; CURRENT FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6

US-09-873-233A-7
; TYPE: PRT
; ORGANISM: Measles virus
; FEATURE:
; OTHER INFORMATION: Attenuated measles virus CAM -70 strain
US-09-873-233A-7

Query Match
Best Local Similarity 75.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
DB 1 EQP 3

RESULT 7
US-09-500-700-88
; Sequence 88, Application US/09500700
; Publication No. US20030059767A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPT1160-4
; CURRENT APPLICATION NUMBER: US/09/500,700
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 1 of zif268
US-09-500-700-88

Query Match
Best Local Similarity 75.0%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
DB 1 SEQ 3

RESULT 8
US-10-192-381-53
; Sequence 53, Application US/10192381
; Publication No. US20030170807A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: WORLEY, Paul
; APPLICANT: TU, Jian
; APPLICANT: XIAO, Bo
; APPLICANT: LEAHY, Daniel
; APPLICANT: BENEKEN, Jutta
; APPLICANT: LANAHAN, Anthony
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
; TITLE OF INVENTION: AMENDED)
; FILE REFERENCE: JHU1580-4
; CURRENT APPLICATION NUMBER: US/10/192,381

```

```

; CURRENT FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: US/09/377,285
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: US 60/138,426
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,493
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/138,494
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/097,334
; PRIOR FILING DATE: 1998-08-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: conserved amino acid sequence
US-10-192-381-53

Query Match 75.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 3 EQP 5

RESULT 9
US-10-155-922-14
; Sequence 14, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tohigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-95

Query Match 75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 2 SEQ 4

RESULT 11
US-10-155-922-97
; Sequence 97, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tohigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903

```

```

Qy 1 SEQ 3
Db 2 SEQ 4

RESULT 10
US-10-155-922-95
; Sequence 95, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tohigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-95

Query Match 75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 2 SEQ 4

RESULT 11
US-10-155-922-97
; Sequence 97, Application US/10155922
; Publication No. US20030086893A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tohigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 467392000220
; CURRENT APPLICATION NUMBER: US/10/155,922
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903

```

```

; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-97

Query Match          75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
      |||
Db      2 SEQ 4

RESULT 12
US-10-155-922-99
; Sequence 99, Application US/10155922
; Publication No. US2003008693A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 46739200220
; CURRENT APPLICATION NUMBER: US/10/155,922
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-101

Query Match          75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
      |||
Db      2 SEQ 4

RESULT 14
US-09-758-128-24
; Sequence 24, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT

```

```

; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-97

Query Match          75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
      |||
Db      2 SEQ 4

RESULT 13
US-10-155-922-101
; Sequence 101, Application US/10155922
; Publication No. US2003008693A1
; GENERAL INFORMATION:
; APPLICANT: Hirai, Yohei
; APPLICANT: Oka, Yumiko
; APPLICANT: Takebe, Kyoko
; APPLICANT: Tsuda, Hokari
; APPLICANT: Tochigi, Keiko
; APPLICANT: Shinagawa, Toko
; APPLICANT: Murakami, Kayoko
; APPLICANT: Koshida, Shogo
; TITLE OF INVENTION: OLIGOPEPTIDES FOR PROMOTING HAIR GROWTH
; FILE REFERENCE: 46739200220
; CURRENT APPLICATION NUMBER: US/10/155,922
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: PCT/JP01/04691
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: JP 2000-166903
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: JP 2001-347340
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-347338
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: JP 2001-371175
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: JP 2001-371366
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 101
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-155-922-101

Query Match          75.0%; Score 3; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
      |||
Db      2 SEQ 4

RESULT 14
US-09-758-128-24
; Sequence 24, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT

```

```
; ORGANISM: Mouse
US-09-758-128-24

Query Match      75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 15
US-09-758-128-27
; Sequence 27, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Simon L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rat
US-09-758-128-27

Query Match      75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 16
US-09-826-290-124
; Sequence 124, Application US/09826290
; Patent No. US2002016468A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyansealage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlff, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647

; ORGANISM: Mouse
US-09-758-128-24

Query Match      75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 17
US-09-758-426-24
; Sequence 24, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Simon L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-426-24

Query Match      75.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 18
US-09-758-426-27
; Sequence 27, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Simon L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
```

```
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-27

Query Match
Best Local Similarity 75.0%; Score 3; DB 10; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 5 SEQ 7

RESULT 19
US-09-758-198-24
; Sequence 24, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Norman L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mouse
US-09-758-198-24

Query Match
Best Local Similarity 75.0%; Score 3; DB 10; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 5 SEQ 7

RESULT 20
US-09-758-198-27
; Sequence 27, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, Norman L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-27

Query Match
Best Local Similarity 75.0%; Score 3; DB 10; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 5 SEQ 7

RESULT 21
US-09-861-661-24
; Sequence 24, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-861-661-24

Query Match
Best Local Similarity 75.0%; Score 3; DB 11; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 5 SEQ 7

RESULT 22
US-09-861-661-27
; Sequence 27, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-861-661-27

Query Match
Best Local Similarity 75.0%; Score 3; DB 11; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Qy 1 SEQ 3
|||
Db 5 SEQ 7

RESULT 23
US-10-007-761-32
; Sequence 32, Application US/10007761
; Publication No. US20020150984A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: Peptides for Activation and Inhibition
; TITLE OF INVENTION: of delta-PKC
; FILE REFERENCE: 58600-8208.US00
; CURRENT APPLICATION NUMBER: US/10/007,761
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/262,060
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-delta RACK peptide
US-10-007-761-32

Query Match 75.0%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
|||
Db 5 EQP 7

RESULT 24
US-09-779-308-401
; Sequence 401, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 401
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-401

Query Match 75.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
|||
Db 4 EQP 6

RESULT 25
US-09-779-308-579
; Sequence 579, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 579
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-579

Query Match 75.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
|||
Db 4 EQP 6

RESULT 26
US-09-779-308-698
; Sequence 698, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 698
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-698

Query Match 75.0%; Score 3; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
|||
Db 4 EQP 6

RESULT 27

Db 3 EQP 5
|||

RESULT 31

```

US-10-062-109A-140
; Sequence 140, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-140

Query Match 75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 2 EQP 4
|||

RESULT 32

```

US-10-062-109A-272
; Sequence 272, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-272

Query Match 75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 2 EQP 4
|||

RESULT 33

```

US-10-062-109A-281
; Sequence 281, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-281

Query Match 75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 2 EQP 4
|||

RESULT 34

```

US-10-062-109A-386
; Sequence 386, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 386
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-386

Query Match 75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```
Db      |||
        6 EQP 8

RESULT 39
US-10-005-480A-272
; Sequence 272, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-272

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        5 EQP 7

RESULT 40
US-10-005-480A-281
; Sequence 281, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-281

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        4 EQP 6

RESULT 41
US-10-005-480A-386
; Sequence 386, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 386
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-386

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        1 EQP 3

RESULT 42
US-10-005-480A-498
; Sequence 498, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 498
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-498

Query Match      75.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      |||
        1 EQP 3

RESULT 43
US-10-005-480A-660
```

Sequence 660, Application US/10005480A
 Publication No. US20030191073A1
 GENERAL INFORMATION:
 APPLICANT: Agensys
 APPLICANT: Challita-Eid, Pia M.
 APPLICANT: Raitano, Arthur B.
 APPLICANT: Paris, Mary
 APPLICANT: Hubert, Rene S.
 APPLICANT: Morrison, Karen Jane Meyrick
 APPLICANT: Jakobovits, Aya
 TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
 TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
 TITLE OF INVENTION: Cancer
 FILE REFERENCE: 51158-20062-00
 CURRENT APPLICATION NUMBER: US/10/005,480A
 CURRENT FILING DATE: 2001-11-07
 NUMBER OF SEQ ID NOS: 765
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 660
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-005-480A-660

Query Match 75.0%; Score 3; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
 |||
 Db 5 EQP 7

RESULT 44
 US-10-283-722-15
 Sequence 15, Application US/10283722
 Publication No. US20030194407A1
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Gazelle S. Rastegar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Mary Faris
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
 FILE REFERENCE: 129.2USU2
 CURRENT APPLICATION NUMBER: US/10/283,722
 CURRENT FILING DATE: 2003-02-03
 PRIOR FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/184,558
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/218,956
 PRIOR FILING DATE: 2000-07-13
 NUMBER OF SEQ ID NOS: 752
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 15
 LENGTH: 9
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-283-722-15

Query Match 75.0%; Score 3; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
 |||
 Db 3 EQP 5

RESULT 45
 US-10-283-722-144
 Sequence 144, Application US/10283722
 Publication No. US20030194407A1
 GENERAL INFORMATION:
 APPLICANT: Arthur B. Raitano
 APPLICANT: Daniel E.H. Afar
 APPLICANT: Gazelle S. Rastegar
 APPLICANT: Steve Chappell Mitchell
 APPLICANT: Rene S. Hubert
 APPLICANT: Pia M. Challita-Eid
 APPLICANT: Mary Paris
 APPLICANT: Aya Jakobovits
 TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
 TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
 FILE REFERENCE: 129.2USU2
 CURRENT APPLICATION NUMBER: US/10/283,722
 CURRENT FILING DATE: 2003-02-03
 PRIOR APPLICATION NUMBER: US/09/793,451
 PRIOR FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/184,558
 PRIOR FILING DATE: 2000-02-24
 PRIOR APPLICATION NUMBER: 60/218,956
 PRIOR FILING DATE: 2000-07-13
 NUMBER OF SEQ ID NOS: 752
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 144
 LENGTH: 9
 TYPE: PRT
 ORGANISM: homo sapiens
 US-10-283-722-144

Query Match 75.0%; Score 3; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
 |||
 Db 2 EQP 4

RESULT 46
 US-10-042-202-36
 Sequence 36, Application US/10042202
 Publication No. US20020136733A1
 GENERAL INFORMATION:
 APPLICANT: Adrian Vivian Sinton Hill, Michael AIDOO
 Catherine Elizabeth Margaret ALLSOOP, Ajit LALVANI, Magdalena
 PLEBANSKI, Hilton Carter WHITTLE,
 TITLE OF INVENTION: MALARIA PEPTIDES
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WENDEROOTH, LIND & PONACK, L.L.P.
 STREET: 2033 K Street,N.W., Suite 800,
 CITY: Washington
 STATE: D.C.,
 COUNTRY: U.S.A.
 ZIP: 20006-1021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPad for Windows 95
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/042,202
 FILING DATE: 11-Jan-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,175
 FILING DATE: 28-JAN-1997
 APPLICATION NUMBER: WO PCT/GB95/26982
 FILING DATE: 30-MAR-1995
 APPLICATION NUMBER: GB 9406492.0

```
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: 2002_0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-721-8200
; TELEFAX: (202)-721-8250
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-042-202-36

Query Match          75.0%; Score 3; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SEQ 3
      |||
Db      4 SEQ 6

RESULT 47
US-10-234-432-92
; Sequence 92, Application US/10234432
; Publication No. US20030091598A1
; GENERAL INFORMATION:
; APPLICANT: Homer, Mary J.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF BABESIA INFECTION
; FILE REFERENCE: 210121.560
; CURRENT APPLICATION NUMBER: US/10/234,432
; CURRENT FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Babesia sp. wal
US-10-234-432-92

Query Match          75.0%; Score 3; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
      |||
Db      5 EQP 7

RESULT 48
US-08-736-019-26
; Sequence 26, Application US/08736019
; Publication No. US20030207799A1
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
```

```
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/736,019
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,833
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-736-019-26

Query Match          75.0%; Score 3; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SEQ 3
      |||
Db      6 SEQ 8

RESULT 49
US-09-779-308-65
; Sequence 65, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
```

```

; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-65

Query Match      75.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred.No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
Db      6 EQP 8

RESULT 50
US-09-779-308-161
; Sequence 161, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-161

Query Match      75.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred.No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
Db      1 EQP 3

RESULT 51
US-09-779-308-565
; Sequence 565, Application US/09779308
; Patent No. US20020150972A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Rene S. Hubert
; APPLICANT: Elana Levin

```

```

; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
; FILE REFERENCE: 129.4USU1
; CURRENT APPLICATION NUMBER: US/09/779,308
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181,020
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 718
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 565
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-779-308-565

Query Match      75.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred.No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 EQP 4
Db      4 EQP 6

RESULT 52
US-09-984-245-291
; Sequence 291, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: PZ004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096

```


; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 291
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-291

Query Match 75.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 6 EQP 8

RESULT 53
US-09-966-262-291
; Sequence 291, Application US/09966262
; Publication No. US20030050461A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/966,262
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: US 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069

; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 291
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-262-291

Query Match 75.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 6 EQP 8

RESULT 54
US-09-983-966-291
; Sequence 291, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/983,966
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099

RESULT 56
US-10-190-082-553
; Sequence 553, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Heid, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 553
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-553

Query Match 75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
|||
Db 1 SEQ 3

RESULT 57

US-09-793-451-80
; Sequence 80, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129,2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-80

Query Match 75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
|||
Db 3 EQP 5

RESULT 58

US-09-572-404B-1778
; Sequence 1778, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1778
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in MTNR1 at 139-148 and may interact with Sequen
; OTHER INFORMATION: in this patent.
US-09-572-404B-1778

Query Match 75.0%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
|||
Db 3 SEQ 5

US-09-793-451-84
; Sequence 84, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-84

Query Match 75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 6 EQP 8

RESULT 59
US-09-793-451-306
; Sequence 306, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-306

Query Match 75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4

Db 6 EQP 8
|||
RESULT 60
US-09-793-451-509
; Sequence 509, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 509
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-509

Query Match 75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 6 EQP 8
|||

RESULT 61
US-09-793-451-705
; Sequence 705, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 705
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-705

```
Query Match      75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      4 EQP 6

RESULT 62
US-10-234-816-97
; Sequence 97, Application US/10234816
; Publication No. US20030157514A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL PLECKSTRIN HOMOMOLOGY DOMAIN AND PR
; FILE REFERENCE: D0117 NP
; CURRENT APPLICATION NUMBER: US/10/234,816
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-234-816-97

Query Match      75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
Db      8 SEQ 10

RESULT 63
US-10-062-109A-72
; Sequence 72, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-72

Query Match      75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      3 EQP 5

RESULT 64
US-10-062-109A-91
; Sequence 91, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-91

Query Match      75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      6 EQP 8

RESULT 65
US-10-062-109A-160
; Sequence 160, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-160

Query Match      75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      7 EQP 9
```

```

Db          6 EQP 8

RESULT 66
US-10-062-109A-208
; Sequence 208, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-208

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
           |||
Db          5 EQP 7

RESULT 67
US-10-062-109A-233
; Sequence 233, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-233

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
           |||
Db          5 EQP 7

RESULT 68
US-10-062-109A-306
; Sequence 306, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-306

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
           |||
Db          6 EQP 8

RESULT 69
US-10-062-109A-319
; Sequence 319, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-319

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
           |||
Db          6 EQP 8

```

```
Db          5 EQP 7
||||
RESULT 70
US-10-062-109A-334
; Sequence 334, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-334

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          1 EQP 3

RESULT 71
US-10-005-480A-72
; Sequence 72, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-72

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          1 EQP 3

RESULT 72
US-10-005-480A-91
; Sequence 91, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-91

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          6 EQP 8

RESULT 73
US-10-005-480A-160
; Sequence 160, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-160

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          7 EQP 9
```

```
Db          3 EQP 5
||||
RESULT 72
US-10-005-480A-91
; Sequence 91, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-91

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          6 EQP 8

RESULT 73
US-10-005-480A-160
; Sequence 160, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161p2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-160

Query Match          75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 EQP 4
||||
Db          7 EQP 9
```

RESULT 74

US-10-005-480A-208
; Sequence 208, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-208

Query Match 75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 5 EQP 7

RESULT 75

US-10-005-480A-233
; Sequence 233, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-233

Query Match 75.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 6 EQP 8

Search completed: November 25, 2003, 20:25:37
Job time :- 8.95745 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 19:27:29 ; Search time 4.3617 Seconds
(without alignments)
38.802 Million cell updates/sec

Title: US-09-641-801-10

Perfect score: 4

Sequence: 1 SEQP 4

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	100.0	4	4	US-09-641-803-10
2	4	100.0	10	1	US-08-328-256-5
3	3	75.0	5	1	US-08-292-045-18
4	3	75.0	5	1	US-08-292-045-19
5	3	75.0	6	1	US-08-483-434A-19
6	3	75.0	6	3	US-08-476-134A-28
7	3	75.0	7	6	US-09-230-944-7
8	3	75.0	6	4	US-09-460-384-6
9	3	75.0	6	6	5190920-24
10	3	75.0	6	6	5508208-26
11	3	75.0	7	3	US-09-258-754-162
12	3	75.0	7	3	US-09-042-107-162
13	3	75.0	8	3	US-08-444-818-409
14	3	75.0	9	1	US-07-779-049-1
15	3	75.0	9	1	US-08-080-240-1
16	3	75.0	9	1	US-08-139-054-7
17	3	75.0	9	2	US-08-340-283-137
18	3	75.0	9	3	US-08-159-339A-915
19	3	75.0	9	3	US-08-159-339A-978
20	3	75.0	9	4	US-09-243-560B-3
21	3	75.0	9	4	US-09-243-560B-4
22	3	75.0	9	4	US-09-243-560B-5
23	3	75.0	9	4	US-09-243-560B-6
24	3	75.0	9	4	US-09-719-140-2
25	3	75.0	10	1	US-08-166-195A-11
26	3	75.0	10	1	US-08-166-195A-12
27	3	75.0	10	1	US-08-036-555B-26

28	3	75.0	10	1	US-08-469-569-26	Sequence 26, Appl
29	3	75.0	10	1	US-08-190-788A-61	Sequence 61, Appl
30	3	75.0	10	1	US-08-190-788A-62	Sequence 62, Appl
31	3	75.0	10	1	US-08-190-788A-64	Sequence 64, Appl
32	3	75.0	10	1	US-08-190-788A-238	Sequence 238, App
33	3	75.0	10	1	US-08-249-322A-26	Sequence 26, Appl
34	3	75.0	10	1	US-08-566-800A-1	Sequence 1, Appl
35	3	75.0	10	1	US-08-383-474B-66	Sequence 66, Appl
36	3	75.0	10	1	US-08-383-474B-67	Sequence 67, Appl
37	3	75.0	10	1	US-08-383-474B-69	Sequence 69, Appl
38	3	75.0	10	1	US-08-383-474B-241	Sequence 241, App
39	3	75.0	10	1	US-08-463-155A-6	Sequence 6, Appl
40	3	75.0	10	1	US-08-463-432B-6	Sequence 6, Appl
41	3	75.0	10	1	US-08-465-391A-61	Sequence 61, Appl
42	3	75.0	10	1	US-08-465-391A-62	Sequence 62, Appl
43	3	75.0	10	1	US-08-465-391A-64	Sequence 64, Appl
44	3	75.0	10	1	US-08-465-391A-238	Sequence 238, App
45	3	75.0	10	1	US-08-469-526A-26	Sequence 26, Appl
46	3	75.0	10	1	US-08-206-310A-6	Sequence 6, Appl
47	3	75.0	10	2	US-08-436-772-11	Sequence 11, Appl
48	3	75.0	10	2	US-08-436-772-12	Sequence 12, Appl
49	3	75.0	10	2	US-08-436-883B-11	Sequence 11, Appl
50	3	75.0	10	2	US-08-436-883B-12	Sequence 12, Appl
51	3	75.0	10	2	US-08-398-010A-6	Sequence 6, Appl
52	3	75.0	10	2	US-08-734-591A-26	Sequence 26, Appl
53	3	75.0	10	2	US-08-464-538B-61	Sequence 61, Appl
54	3	75.0	10	2	US-08-464-538B-62	Sequence 62, Appl
55	3	75.0	10	2	US-08-464-538B-64	Sequence 64, Appl
56	3	75.0	10	2	US-08-398-628A-6	Sequence 6, Appl
57	3	75.0	10	2	US-08-932-589-1	Sequence 1, Appl
58	3	75.0	10	2	US-08-469-660-26	Sequence 26, Appl
59	3	75.0	10	2	US-08-463-078E-105	Sequence 105, App
60	3	75.0	10	2	US-08-463-078E-106	Sequence 106, App
61	3	75.0	10	2	US-08-463-076E-108	Sequence 108, App
62	3	75.0	10	2	US-08-463-076E-290	Sequence 290, App
63	3	75.0	10	2	US-08-399-115A-6	Sequence 6, Appl
64	3	75.0	10	3	US-08-461-384B-9	Sequence 9, Appl
65	3	75.0	10	3	US-08-159-339A-933	Sequence 933, App
66	3	75.0	10	3	US-08-407-207A-6	Sequence 6, Appl
67	3	75.0	10	3	US-08-890-489-3	Sequence 3, Appl
68	3	75.0	10	3	US-08-470-335-26	Sequence 26, Appl
69	3	75.0	10	3	US-09-385-135-3	Sequence 3, Appl
70	3	75.0	10	3	US-08-735-021-26	Sequence 26, Appl
71	3	75.0	10	3	US-08-734-664A-26	Sequence 26, Appl
72	3	75.0	10	3	US-08-470-339-26	Sequence 26, Appl
73	3	75.0	10	3	US-08-467-602-26	Sequence 26, Appl
74	3	75.0	10	4	US-09-106-872A-7	Sequence 7, Appl
75	3	75.0	10	4	US-09-252-404A-10	Sequence 10, Appl
76	3	75.0	10	4	US-09-252-404A-11	Sequence 11, Appl
77	3	75.0	10	4	US-09-797-239A-18	Sequence 18, Appl
78	3	75.0	10	4	PCT-US94-05083C-26	Sequence 26, Appl
79	3	75.0	10	5	PCT-US95-06846A-26	Sequence 26, Appl
80	3	75.0	11	1	US-08-036-555B-13	Sequence 13, Appl
81	3	75.0	11	1	US-08-469-569-13	Sequence 13, Appl
82	3	75.0	11	1	US-08-249-322A-13	Sequence 13, Appl
83	3	75.0	11	1	US-08-469-526A-13	Sequence 13, Appl
84	3	75.0	11	2	US-08-734-591A-13	Sequence 13, Appl
85	3	75.0	11	2	US-08-469-660-13	Sequence 13, Appl
86	3	75.0	11	2	US-08-470-335-13	Sequence 13, Appl
87	3	75.0	11	3	US-08-735-021-13	Sequence 13, Appl
88	3	75.0	11	3	US-08-734-664A-13	Sequence 13, Appl
89	3	75.0	11	3	US-08-470-339-13	Sequence 13, Appl
90	3	75.0	11	4	US-09-347-926-4	Sequence 4, Appl
91	3	75.0	11	4	US-08-467-602-13	Sequence 13, Appl
92	3	75.0	11	4	US-10-006-937-2	Sequence 2, Appl
93	3	75.0	11	5	PCT-US94-05083C-13	Sequence 13, Appl
94	3	75.0	11	5	PCT-US95-06846A-13	Sequence 13, Appl
95	3	75.0	12	1	US-08-190-788A-26	Sequence 26, Appl
96	3	75.0	12	1	US-08-190-788A-59	Sequence 59, Appl
97	3	75.0	12	1	US-08-190-788A-78	Sequence 78, Appl
98	3	75.0	12	1	US-08-190-788A-154	Sequence 154, App
99	3	75.0	12	1	US-08-190-788A-157	Sequence 157, App
100	3	75.0	12	1		

ALIGNMENTS

RESULT 1
US-09-641-803-10
; Sequence 10, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-10

Query Match 100.0%; Score 4; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 4
Db 1 SEQ 4

RESULT 2
US-08-328-256-5
; Sequence 5, Application US/08328256
; Patent No. 5643749
; GENERAL INFORMATION:
; APPLICANT: REVEL, Michel
; APPLICANT: ABRAMOVICH, Carolina
; APPLICANT: RATOVITSKI, Edward
; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/328,256
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 107378
; FILING DATE: 24-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: REVEL=13
; REFERENCE/DOCKET NUMBER: 25,618

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-328-256-5

Query Match 100.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

Qy 1 SEQ 4
Db 5 SEQ 8

RESULT 3
US-08-292-045-18
; Sequence 18, Application US/08292045
; Patent No. 5603005
; GENERAL INFORMATION:
; APPLICANT: HERR, JOHN C.
; TITLE OF INVENTION: PRIMATE INTRA-ACROSOMAL SPERM ANTIGEN
; TITLE OF INVENTION: FOR USE IN A CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,045
; FILING DATE:
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/318,551
; FILING DATE: 03-MAR-1989
; APPLICATION NUMBER: US 07/481,491
; FILING DATE: 16-FEB-1990
; APPLICATION NUMBER: US 07/858,798
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5602005man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 494-109-0 CIP

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-292-045-18

Query Match 75.0%; Score 3; DB 1; Length 5;

```
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	2	EQP	4
Db	3	EOP	5

RESULT 4

```

US-08-292-045-19
; Sequence 19, Application US/08292045
; Patent No. 5602005
; GENERAL INFORMATION:
; APPLICANT: HERR, JOHN C.
; APPLICANT: WRIGHT, RICHARD M.
; TITLE OF INVENTION: PRIMATE INTRA-ACROSOMAL SPERM ANTIGEN
; TITLE OF INVENTION: FOR USE IN A CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

```

Query Match 75.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels

Qy	2	EQP	4
Dp	3	EQP	5

RESULT 5

RESOL 3
US-08-483-434A-19
; Sequence 19, Application US/08483434A
; Patent No. 5648461
; GENERAL INFORMATION:
; APPLICANT: EVAL, Jacob

APPLICANT: HAMILTON, Bruce K.
 APPLICANT: TUSZYNSKI, George P.
 TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and
 TITLE OF INVENTION: Therapeutic Use Thereof
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:

Query Match	75.5.0%	Score 3;	DB 1;	Length 6;
Best Local	Similarity	100.0%;	Pred. NO. 2.5e+05;	
Matches	3:	Conservative	0:	Mismatches 0:
				Indels 0:
				Gaps 0:

Qy	1	SEQ	3
Db	2	SEQ	4

RESULT 6

RESULI 6
US-08-476-134A-28
; Sequence 28, Application US/08476134A
; Patent No. 6239110
; GENERAL INFORMATION:
; APPLICANT: EYAL JACOB
; APPLICANT: HAMILTON, BRUCE K.
; APPLICANT: TUSZYSKI, GEORGE P.
; TITLE OF INVENTION: SYNTHETIC ANALOGS OF THROMBOSPONDIN AND THERAPEUTIC USE THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 07206-0009

```
; CURRENT APPLICATION NUMBER: US/08/476,134A
; CURRENT FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 07/587,197
; PRIOR FILING DATE: 1990-09-24
; PRIOR APPLICATION NUMBER: 07/483,527
; PRIOR FILING DATE: 1990-02-22
; PRIOR APPLICATION NUMBER: 08/450,738
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: 08/185,614
; PRIOR FILING DATE: 1994-01-24
; PRIOR APPLICATION NUMBER: 08/024,436
; PRIOR FILING DATE: 1993-03-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: analog of thrombospondin
US-08-476-134A-28

Query Match          75.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
      |||
DB      2 SEQ 4

RESULT 7
US-09-230-944-7
; Sequence 7, Application US/09230944
; Patent No. 6277380
; GENERAL INFORMATION:
; APPLICANT: UEDA, Shigeharu
; APPLICANT: WATANABE, Michiko
; APPLICANT: KAWANISHI, Hitomi
; TITLE OF INVENTION: Measles Virus Mutant Antigen and Gene Coding for the
; FILE REFERENCE: 0216-0407P
; CURRENT APPLICATION NUMBER: US/09/230,944
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: PCT/JP98/02481
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 9-184285 JAPAN
; EARLIER FILING DATE: 1997-06-04
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Measles virus
; FEATURE:
; OTHER INFORMATION: Attenuated measles virus CAM -70 strain
US-09-230-944-7

Query Match          75.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
      |||
DB      1 EQP 3

RESULT 8
US-09-460-384-6
; Sequence 6, Application US/09460384
; Patent No. 6337316
; GENERAL INFORMATION:
```

```
; APPLICANT: EL TAYAR, Nabil
; BLECHNER, Steven
; JAMESON, Brad
; TEPPER, Mark
; TITLE OF INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
; PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
; SAME
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,384
; FILING DATE: 13-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/12312
; FILING DATE: 11-JUN-1998
; APPLICATION NUMBER: US 60/049,470
; FILING DATE: 12-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: EL TAYAR=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-460-384-6

Query Match          75.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
      |||
DB      3 EQP 5

RESULT 9
5190920-24
; Patent No. 5190920
; APPLICANT: EYAL, JACOB; HAMILTON, BRUCE K.; TUSZYNASKI,
; GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
; OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO:24:
; LENGTH: 6
5190920-24

Query Match          75.0%; Score 3; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 SEQ 3
|||
Db 2 SEQ 4

RESULT 10
US-09-258-754-162
; Patent No. 5506208
; APPLICANT: EYAL, JACOB; HAMILTON, BRUCE K.; TUSZYNSKI,
; GEORGE P.
; TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
; THROMBOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
; NUMBER OF SEQUENCES: 45
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,181
; FILING DATE: 22-MAR-1995
; PRIOR APPLICATION NUMBER: 131,565
; FILING DATE: 04-OCT-1993
; APPLICATION NUMBER: 895,764
; FILING DATE: 09-JUN-1992
; APPLICATION NUMBER: 587,197
; FILING DATE: 24-SEP-1990
; SEQ ID NO: 26:
; LENGTH: 6
5506208-26

Query Match 75.0%; Score 3; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 2 SEQ 4

RESULT 11
US-09-258-754-162
; Sequence 162, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-162

Query Match 75.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 3 SEQ 5

RESULT 12
US-09-042-107-162

; Sequence 162, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-162

Query Match 75.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
|||
Db 3 SEQ 5

RESULT 13
US-08-444-818-409
; Sequence 409, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANEV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 409:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-409

Query Match 75.0%; Score 3; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
 |||
 Db 5 SEQ 7

RESULT 14

US-07-779-049-1
 ; Sequence 1, Application US/07779049
 ; Patent No. 5310659
 ; GENERAL INFORMATION:
 ; APPLICANT: ARAMORI, ICHIRO
 ; APPLICANT: FURAGAWA, MASAO
 ; APPLICANT: ONO, HIROKI
 ; APPLICANT: ISHITANI, YOSUKE
 ; APPLICANT: TSUMURA, MANA
 ; APPLICANT: IWAMI, MORITA
 ; APPLICANT: KOJO, HITOSHI
 ; TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 Jefferson Davis Highway, Fourth Floor
 ; CITY: Arlington
 ; STATE: Virginia
 ; ZIP: 22202

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/779,049
 ; FILING DATE: 19911018
 ; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 ; NAME: Oblon, No. 5310659man F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 18-723-0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)521-4500
 ; TELEFAX: (703)486-2347
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: N-terminal
 ; US-07-779-049-1

Query Match 75.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
 |||
 Db 2 SEQ 4

RESULT 15

US-08-080-240-1
 ; Sequence 1, Application US/08080240
 ; Patent No. 5312750
 ; GENERAL INFORMATION:
 ; APPLICANT: ARAMORI, ICHIRO
 ; APPLICANT: FURAGAWA, MASAO
 ; APPLICANT: ONO, HIROKI

APPLICANT: ISHITANI, YOSUKE
 APPLICANT: TSUMURA, MANA
 APPLICANT: IWAMI, MORITA
 APPLICANT: KOJO, HITOSHI
 TITLE OF INVENTION: NOVEL GL-7ACA ACYLASE
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1755 Jefferson Davis Highway, Fourth Floor
 CITY: Arlington
 STATE: Virginia
 ZIP: 22202
 COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/080,240
 ; FILING DATE: 19930622
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Oblon, No. 5312750man F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 18-803-0 DIV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)413-3000
 ; TELEFAX: (703)413-2220
 ; TELEX: 248855 OPAT UR
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: N-terminal
 ; US-08-080-240-1

Query Match 75.0%; Score 3; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
 |||
 Db 2 SEQ 4

RESULT 16

US-08-139-054-7
 ; Sequence 7, Application US/08139054
 ; Patent No. 5578710
 ; GENERAL INFORMATION:
 ; APPLICANT: Ambrosius, Dorothea
 ; APPLICANT: Dony, Carola
 ; APPLICANT: Rudolph, Rainer
 ; TITLE OF INVENTION: IMPROVED ACTIVATION OF RECOMBINANT
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
 ; STREET: 1725 K. St. N.W. Suite 1000
 ; CITY: Washington, D.C.
 ; COUNTRY: USA
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/139,054
 ; FILING DATE:

```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/837,779
; FILING DATE:
; APPLICATION NUMBER: DE P 41 05 480.6
; FILING DATE: 21-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: 920053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)659-2930
; TELEFAX: (202)887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-139-054-7

Query Match 75.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 2 EXP 4
DB 6 EXP 8

RESULT 17
US-08-340-283-137
; Sequence 137, Application US/08340283
; Patent No. 5861318
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ake P.
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR
; TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY
; NUMBER OF SEQUENCES: 205
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellect. Prop. Law
; ADDRESSEE: (1920-32-1)
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 49001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,283
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Wootton, Thomas A.
; REGISTRATION NUMBER: 35,004
; REFERENCE/DOCKET NUMBER: 4828
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (616) 385-7914
; TELEFAX: (616) 385-6897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO: 137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

```

```

; FRAGMENT TYPE: N-terminal
US-08-340-283-137

Query Match          75.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EQP 4
Db      1 EQP 3

RESULT 18
US-08-159-339A-915
; Sequence 915, Application US/08159339A
; Patent No. 60371135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 915:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-159-339A-915

Query Match          75.0%; Score 3; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SEQ 3
Db      2 SEQ 4

```

```
Query Match          75.0%; Score 3; DB 3; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	SEQ	3
Dy	2	SEQ	4

```
RESULT 19
US-08-159-339A-978
; Sequence 978, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 978:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-978

Query Match 75.0%; Score 3; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 5 SEQ 7

RESULT 20
US-08-243-560B-3
; Sequence 3, Application US/09243560B
; Patent No. 6395882
; GENERAL INFORMATION:
; APPLICANT: Rosen, Steven D.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
; FILE REFERENCE: UCAL097US1
; CURRENT APPLICATION NUMBER: US/09/243,560B
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: US 60/074,389
; CURRENT FILING DATE: 1999-02-03
```

```
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-243-560B-3

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 1 SEQ 3

RESULT 21
US-09-243-560B-4
; Sequence 4, Application US/09243560B
; Patent No. 6395882
; GENERAL INFORMATION:
; APPLICANT: Rosen, Steven D.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
; FILE REFERENCE: UCAL097US1
; CURRENT APPLICATION NUMBER: US/09/243,560B
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: US 60/074,389
; CURRENT FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-243-560B-4

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 1 SEQ 3

RESULT 22
US-09-243-560B-5
; Sequence 5, Application US/09243560B
; Patent No. 6395882
; GENERAL INFORMATION:
; APPLICANT: Rosen, Steven D.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
; FILE REFERENCE: UCAL097US1
; CURRENT APPLICATION NUMBER: US/09/243,560B
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: US 60/074,389
; CURRENT FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-243-560B-5

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 SEQ 3
|||
Db 1 SEQ 3

RESULT 23

US-09-243-560B-6
; Sequence 6, Application US/09243560B
; Patent No. 6395882
; GENERAL INFORMATION:
; APPLICANT: Rosen, Steven D.
; APPLICANT: Sassetti, Christopher M.
; TITLE OF INVENTION: No. 6395882el Selectin Ligands
; FILE REFERENCE: UCAL097US1
; CURRENT APPLICATION NUMBER: US/09/243,560B
; CURRENT FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: US 60/074,389
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rabbit
US-09-243-560B-6

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
|||
Db 1 SEQ 3

RESULT 24

US-09-719-140-2
; Sequence 2, Application US/09719140
; Patent No. 6506555
; GENERAL INFORMATION:
; APPLICANT: ANDRE, PATRICE, ET AL
; TITLE OF INVENTION: NOVEL USE OF HIV PROTEASE INHIBITING COMPOUNDS
; FILE REFERENCE: P06994US00/BAS
; CURRENT APPLICATION NUMBER: US/09/719,140
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: PCT/FR99/01391
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: FR 9807373
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Lymphocytic choriomeningitis virus
US-09-719-140-2

Query Match 75.0%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
|||
Db 1 EQP 3

RESULT 25

US-08-166-195A-11
; Sequence 11, Application US/08166195A
; Patent No. 5480799
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.

; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a
; TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5480799th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,195A
; FILING DATE: 10 DEC 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470/73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-166-195A-11

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
|||
Db 6 EQP 8

RESULT 26

US-08-166-195A-12
; Sequence 12, Application US/08166195A
; Patent No. 5480799
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a
; TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5480799th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/166,195A
; FILING DATE: 10 DEC 1993


```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470/73
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-166-195A-12

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 3 EQP 5

RESULT 27
US-08-036-555B-26
; Sequence 26, Application US/08036555B
; Patent No. 5530109
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,555B
; FILING DATE: 24-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10

; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-036-555B-26

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 28
US-08-469-569-26
; Sequence 26, Application US/08469569
; Patent No. 5606032
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
```


MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.1
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-190-788A-64

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 4 EQP 6

RESULT 32
US-08-190-788A-238
Sequence 238, Application US/08190788A
Patent No. 5608035
GENERAL INFORMATION:
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Barrett, Ronald W.
APPLICANT: Baldwin, David N.
APPLICANT: Jacobs, Jeff W.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 312
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies N.V.
STREET: 4001 Miranda Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,788A
FILING DATE: 02-FEB-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,567
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300

TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-190-788A-238

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 3 EQP 5

RESULT 33
US-08-249-322A-26
Sequence 26, Application US/08249322A
Patent No. 5716930
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Mao Su; Hiles, Ian
TITLE OF INVENTION: Gliat Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pelfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,322A
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LUD 250.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-249-322A-26

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 34
US-08-566-800A-1
; Sequence 1, Application US/08566800A
; Patent No. 5736364
; GENERAL INFORMATION:
; APPLICANT: Kelley, Robert F.
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Lee, Geoffrey F.
; TITLE OF INVENTION: No. 5736364e1 Factor VIIa Inhibitors
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/566,800A
; FILING DATE: 04-Dec-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0958B
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-566-800A-1

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 35
US-08-383-474B-66
; Sequence 66, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.

```

```

; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-66

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 2 EQP 4

RESULT 36
US-08-383-474B-67
; Sequence 67, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-67

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 4 EQP 6

RESULT 37

US-08-383-474B-69
; Sequence 69, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 69:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-69

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 4 EQP 6

RESULT 38

US-08-383-474B-241
; Sequence 241, Application US/08383474B
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 241:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-241

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 3 EQP 5

```
RESULT 39
US-08-463-155A-6
; Sequence 6, Application US/08463155A
; Patent No. 5780265
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,155A
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-155A-6

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 6 SEQ 8
|||

RESULT 40
US-08-463-432B-6
; Sequence 6, Application US/08463432B
; Patent No. 5786328
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; APPLICANT: Lazarus, Robert A.
; TITLE OF INVENTION: KUNITZ TYPE PLASMA KALLIKREIN INHIBITORS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,432B
```

```
; FILING DATE: 05-Jun-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0944-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-463-432B-6

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 6 SEQ 8
|||

RESULT 41
US-08-465-391A-61
; Sequence 61, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 61:
```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-61

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 2 EQP 4

RESULT 42
US-08-465-391A-62
; Sequence 62, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-62

Query Match 75.0%; Score 3; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 4 EQP 6

RESULT 43
US-08-465-391A-64
; Sequence 64, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-64

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 4 EQP 6

RESULT 44

```

US-08-465-391A-238
; Sequence 238, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331v1el, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-238

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EOP 4
Db 3 EOP 5

RESULT 45
US-08-469-526A-26
; Sequence 26, Application US/08469526A
; Patent No. 5792849
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Marchionni, Mark

```

```

; APPLICANT: Chen, Maio Su
; APPLICANT: Hiles, Ian
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,526A
; FILING DATE: 06 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-469-526A-26

Query Match 75.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 6 SEQ 8

RESULT 46
US-08-206-310A-6
; Sequence 6, Application US/08206310A
; Patent No. 5795954
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Robert A.
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ DOMAIN
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California

```



```
;
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/206,310A
; APPLICATION NUMBER: 04-Mar-1994
; FILING DATE: 04-Mar-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Daryl B.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: 882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1249
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-206-310A-6
;
; Query Match 75.0%; Score 3; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.5e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SEQ 3
; Db |||
; 6 SEQ 8
;
; RESULT 47
; US-08-436-772-11
; Sequence 11, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
;
; Query Match 75.0%; Score 3; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.5e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SEQ 3
; Db |||
; 6 SEQ 8
;
; RESULT 47
; US-08-436-772-11
; Sequence 11, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
```

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-436-772-11
;
; Query Match 75.0%; Score 3; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.5e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 EQP 4
; Db |||
; 6 EQP 8
;
; RESULT 48
; US-08-436-772-12
; Sequence 12, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; US-08-436-772-12
;
; Query Match 75.0%; Score 3; DB 2; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.5e+02;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 EQP 4
; Db |||
; 3 EQP 5
;
; RESULT 49
; US-08-436-883B-11
; Sequence 11, Application US/08436883B
```

```
; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5820861th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,883B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73C
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-436-883B-11

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 6 EQP 8

RESULT 50
US-08-436-883B-12
; Sequence 12, Application US/08436883B
; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5820861th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: IBM PC compatible
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,010A
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/206310
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: P0882P1-3
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-010A-6
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,883B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73C
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-436-883B-12

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
Db 3 EQP 5

RESULT 51
US-08-398-010A-6
; Sequence 6, Application US/08398010A
; Patent No. 5834244
; GENERAL INFORMATION:
; APPLICANT: Robert A. Lazarus and Mark S. Dennis
; TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
; TITLE OF INVENTION: DOMAIN PROTEINS
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,010A
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/206310
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: P0882P1-3
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-010A-6
```

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 52
US-08-734-591A-26
; Sequence 26, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Hiles, Ian
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95
; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,591A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4

STRANDEDNESS:
; TOPOLOGY: linear
US-08-734-591A-26

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 53
US-08-464-538B-61
; Sequence 61, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Portorof, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-538B-61

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	2 EQP 4	
RESULT 54	US-08-464-538B-62	
;	Sequence 62, Application US/08464538B	
;	Patent No. 5861476	
;	GENERAL INFORMATION:	
;	APPLICANT: Barrett, Ronald W.	
;	APPLICANT: Yanofsky, Stephen D.	
;	APPLICANT: Baldwin, David	
;	APPLICANT: Jacobs, Jeff W.	
;	APPLICANT: Bovy, Philippe R.	
;	APPLICANT: Leahy, Ellen M.	
;	APPLICANT: Pottorff, Richard S.	
;	TITLE OF INVENTION: Peptides and Compounds That Bind to the	
;	TITLE OF INVENTION: IL-1 Receptor	
;	NUMBER OF SEQUENCES: 402	
;	CORRESPONDENCE ADDRESS:	
;	ADDRESSEE: Townsend and Townsend and Crew LLP	
;	STREET: Two Embarcadero Center, 8th Floor	
;	CITY: San Francisco	
;	STATE: California	
;	COUNTRY: USA	
;	ZIP: 94111	
;	COMPUTER READABLE FORM:	
;	MEDIUM TYPE: Floppy disk	
;	COMPUTER: IBM PC compatible	
;	OPERATING SYSTEM: PC-DOS/MS-DOS	
;	SOFTWARE: PatentIn Release #1.0, Version #1.25	
;	CURRENT APPLICATION DATA:	
;	APPLICATION NUMBER: US/08/464,538B	
;	FILING DATE: 05-JUN-1995	
;	CLASSIFICATION: 514	
;	PRIOR APPLICATION DATA:	
;	APPLICATION NUMBER: US 08/373,474	
;	FILING DATE: 01-FEB-1995	
;	CLASSIFICATION: 514	
;	PRIOR APPLICATION DATA:	
;	APPLICATION NUMBER: US 08/190,788	
;	FILING DATE: 02-FEB-1994	
;	CLASSIFICATION: 514	
;	ATTORNEY/AGENT INFORMATION:	
;	NAME: Smith, William M.	
;	REGISTRATION NUMBER: 30,223	
;	REFERENCE/DOCKET NUMBER: 16528A-001810	
;	TELECOMMUNICATION INFORMATION:	
;	TELEPHONE: 415-326-2400	
;	TELEFAX: 415-326-2422	
;	INFORMATION FOR SEQ ID NO: 62:	
;	SEQUENCE CHARACTERISTICS:	
;	LENGTH: 10 amino acids	
;	TYPE: amino acid	
;	STRANDEDNESS: single	
;	TOPOLOGY: linear	
;	MOLECULE TYPE: peptide	
;	US-08-464-538B-62	
Query Match	75.0%; Score 3; DB 2; Length 10;	
Best Local Similarity	100.0%; Pred. No. 1.5e+02;	
Matches	3; Conservative 0; Mismatches 0; Indels 0;	
QY	2 EQP 4	
Db	4 EQP 6	
RESULT 55	US-08-464-538B-64	
;	Sequence 64, Application US/08464538B	
;	Patent No. 5861476	
;	GENERAL INFORMATION:	
;	APPLICANT: Barrett, Ronald W.	
;	APPLICANT: Yanofsky, Stephen D.	
;	APPLICANT: Baldwin, David	
;	APPLICANT: Jacobs, Jeff W.	
;	APPLICANT: Bovy, Philippe R.	
;	APPLICANT: Leahy, Ellen M.	
;	APPLICANT: Pottorff, Richard S.	
;	TITLE OF INVENTION: Peptides and Compounds That Bind to the	
;	TITLE OF INVENTION: IL-1 Receptor	
;	NUMBER OF SEQUENCES: 402	
;	CORRESPONDENCE ADDRESS:	
;	ADDRESSEE: Townsend and Townsend and Crew LLP	
;	STREET: Two Embarcadero Center, 8th Floor	
;	CITY: San Francisco	
;	STATE: California	
;	COUNTRY: USA	
;	ZIP: 94111	
;	COMPUTER READABLE FORM:	
;	MEDIUM TYPE: Floppy disk	
;	COMPUTER: IBM PC compatible	
;	OPERATING SYSTEM: PC-DOS/MS-DOS	
;	SOFTWARE: PatentIn Release #1.0, Version #1.25	
;	CURRENT APPLICATION DATA:	
;	APPLICATION NUMBER: US/08/464,538B	
;	FILING DATE: 05-JUN-1995	
;	CLASSIFICATION: 514	
;	PRIOR APPLICATION DATA:	
;	APPLICATION NUMBER: US 08/373,474	
;	FILING DATE: 01-FEB-1995	
;	CLASSIFICATION: 514	
;	PRIOR APPLICATION DATA:	
;	APPLICATION NUMBER: US 08/190,788	
;	FILING DATE: 02-FEB-1994	
;	CLASSIFICATION: 514	
;	ATTORNEY/AGENT INFORMATION:	
;	NAME: Smith, William M.	
;	REGISTRATION NUMBER: 30,223	
;	REFERENCE/DOCKET NUMBER: 16528A-001810	
;	TELECOMMUNICATION INFORMATION:	
;	TELEPHONE: 415-326-2400	
;	TELEFAX: 415-326-2422	
;	INFORMATION FOR SEQ ID NO: 62:	
;	SEQUENCE CHARACTERISTICS:	
;	LENGTH: 10 amino acids	
;	TYPE: amino acid	
;	STRANDEDNESS: single	
;	TOPOLOGY: linear	
;	MOLECULE TYPE: peptide	
;	US-08-464-538B-62	
Query Match	75.0%; Score 3; DB 2; Length 10;	
Best Local Similarity	100.0%; Pred. No. 1.5e+02;	
Matches	3; Conservative 0; Mismatches 0; Indels 0;	
QY	2 EQP 4	
Db	4 EQP 6	
RESULT 56	US-08-464-538B-238	
;	Sequence 238, Application US/08464538B	
;	Patent No. 5861476	
;	GENERAL INFORMATION:	
;	APPLICANT: Barrett, Ronald W.	
;	APPLICANT: Yanofsky, Stephen D.	
;	APPLICANT: Baldwin, David	
;	APPLICANT: Jacobs, Jeff W.	
;	APPLICANT: Bovy, Philippe R.	
;	APPLICANT: Leahy, Ellen M.	
;	APPLICANT: Pottorff, Richard S.	
;	TITLE OF INVENTION: Peptides and Compounds That Bind to the	
;	TITLE OF INVENTION: IL-1 Receptor	
;	NUMBER OF SEQUENCES: 402	
;	CORRESPONDENCE ADDRESS:	
;	ADDRESSEE: Townsend and Townsend and Crew LLP	
;	STREET: Two Embarcadero Center, 8th Floor	
;	CITY: San Francisco	

NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528A-001810
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-538B-238

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
DB 3 EQP 5

RESULT 57
US-08-398-628A-6
Sequence 6, Application US/08398628A
Patent No. 5863893
GENERAL INFORMATION:
APPLICANT: Robert A. Lazarus and Mark S. Dennis
TITLE OF INVENTION: FACTOR VIIA INHIBITORS FROM KUNITZ
TITLE OF INVENTION: DOMAIN PROTEINS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,628A

FILING DATE: 03-Mar-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/206310
FILING DATE: 04-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0882P1-1
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-628A-6

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
DB 6 SEQ 8

RESULT 58
US-08-932-589-1
Sequence 1, Application US/08932589
Patent No. 5874407
GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lazarus, Robert A.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVENTION: No. 5874407el Factor VIIa Inhibitors
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,589
FILING DATE: 17-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/566800
FILING DATE: 12/04/95
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0958BD1
TELEPHONE: 650/225-8228
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-932-589-1

Query Match

75.0%; Score 3; DB 2; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 1.5e+02;      0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 1 SEQ 3
   |||
Db 6 SEQ 8

RESULT 59
US-08-469-660-26
; Sequence 26, Application US/08469660
; Patent No. 5876973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 0211-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/984,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-469-660-26

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
   |||
Db 6 SEQ 8

RESULT 60
US-08-463-076E-105
; Sequence 105, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514

```

```

; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-105

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EQP 4
   |||
Db 2 EQP 4

RESULT 61
US-08-463-076E-106
; Sequence 106, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514

```



```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,115A
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/206310
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0882PI-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-399-115A-6

Query Match 75.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 6 SEQ 8

RESULT 65
US-08-461-384B-9
; Sequence 9, Application US/08461384B
; Patent No. 6025473
; GENERAL INFORMATION:
; APPLICANT: Cole, Susan P.C.
; APPLICANT: Deeley, Roger G.
; TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,384B
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: 08/407,207
; FILING DATE: 20-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
```

```
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-461-384B-9

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEQ 3
Db 8 SEQ 10

RESULT 66
US-08-159-339A-933
; Sequence 933, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 933:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-933

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 1 SEQ 3
Db |||
2 SEQ 4

RESULT 67

US-08-407-207A-6
; Sequence 6, Application US/08407207A
; Patent No. 6063621
; GENERAL INFORMATION:
; APPLICANT: Deeley, Roger G.
; APPLICANT: Cole, Susan P.C.
; TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PARTIQ RESEARCH & DEVELOPMENT INNOVATIONS
; STREET: Queen's University at Kingston
; CITY: Kingston
; STATE: Ontario
; COUNTRY: CANADA
; ZIP: K7L 3N6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/407,207A
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,923
; FILING DATE: 27-OCT-1992
; APPLICATION NUMBER: 08/029,340
; FILING DATE: 8-MAR-1993
; APPLICATION NUMBER: 08/141,893
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Steeg, Carol Miernicki
; REGISTRATION NUMBER: 39,539
; REFERENCE/DOCKET NUMBER: Q1512
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613) 545-2342
; TELEFAX: (613) 545-6853
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-407-207A-6

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db |||
8 SEQ 10

RESULT 68

US-08-890-489-3
; Sequence 3, Application US/08890489A
; Patent No. 6090917
; GENERAL INFORMATION:
; APPLICANT: UNILEVER UNITED STATES, INC.
; TITLE OF INVENTION: FROZEN FOOD PRODUCT
; FILE REFERENCE: FROZEN FOOD PRODUCT 2
; CURRENT APPLICATION NUMBER: US/08/890,489A
; CURRENT FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: MIXED GRASS
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Xaa represents any amino acid found in plant
; OTHER INFORMATION: protein
US-08-890-489-3

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db |||
2 EQP 4

RESULT 69

US-08-470-335-26
; Sequence 26, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; FILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-470-335-26

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No.1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db |||
6 SEQ 8

RESULT 70

US-09-385-135-3
; Sequence 3, Application US/09385135
; Patent No. 6162789
; GENERAL INFORMATION:
; APPLICANT: UNILEVER UNITED STATES, INC.
; TITLE OF INVENTION: FROZEN FOOD PRODUCT
; FILE REFERENCE: FROZEN FOOD PRODUCT 3
; CURRENT APPLICATION NUMBER: US/09/385,135
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 08/890,489
; EARLIER FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT

ORGANISM: MIXED GRASS
FEATURE:
NAME/KEY: UNSURE
LOCATION: (1)..
OTHER INFORMATION: Xaa represents any amino acid found in plant
US-09-385-135-3

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EQP 4
Db 2 EQP 4

RESULT 71
US-08-735-021-26
Sequence 26, Application US/08735021B
Patent No. 6194377
GENERAL INFORMATION:
APPLICANT: GOODEARL, ANDREW
APPLICANT: STROOBANT, PAUL
APPLICANT: MINGHETTI, LUISA
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: MARCHIONNI, MARK
APPLICANT: CHEN, MARIO S.
APPLICANT: CHEN, MARIO
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
FILE REFERENCE: 04585/00200L
CURRENT APPLICATION NUMBER: US/08/735,021B
CURRENT FILING DATE: 1996-10-22
EARLIER APPLICATION NUMBER: 08/472,065
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/036,555
EARLIER FILING DATE: 1993-03-24
EARLIER APPLICATION NUMBER: 07/965,173
EARLIER FILING DATE: 1992-10-23
EARLIER APPLICATION NUMBER: 07/940,389
EARLIER FILING DATE: 1992-09-03
EARLIER APPLICATION NUMBER: 07/907,138
EARLIER FILING DATE: 1992-06-30
EARLIER APPLICATION NUMBER: 07/863,703
EARLIER FILING DATE: 1992-04-03
NUMBER OF SEQ ID NOS: 192
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 10
TYPE: PRT
ORGANISM: Bos taurus
US-08-735-021-26

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 72
US-08-734-664A-26
Sequence 26, Application US/08734664A
Patent No. 6204241
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew
APPLICANT: Stroobant, Paul
APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Marchionni, Mark

APPLICANT: Chen, Mario
APPLICANT: Hiles, Ian
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
PREPARATION AND USE
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible Pentium
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA: US/08/734,664A
APPLICATION NUMBER: US/08/734,664A
FILING DATE: 22-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/249,322
FILING DATE: 26-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 91 07566.3
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200J
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-734-664A-26

Query Match 75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEQ 3
Db 6 SEQ 8

RESULT 73
US-08-470-339-26
Sequence 26, Application US/08470339C
Patent No. 623286
GENERAL INFORMATION:
APPLICANT: GOODEARL, ANDREW

```

; APPLICANT: STROSBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; EARLIER APPLICATION NUMBER: 91 07566.3 GB
; EARLIER FILING DATE: 1999-04-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-470-339-26

```

```

Query Match      75.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SEQ 3
      |||
Db      6 SEQ 8

```

```

RESULT 74
US-08-467-602-26
; Sequence 26, Application US/08467602C
; Patent No. 644642
; GENERAL INFORMATION:
; APPLICANT: Sklar, Robert
; APPLICANT: Marchionni, Mark
; APPLICANT: Gwynne, David I.
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
; FILE REFERENCE: 04585/028003
; CURRENT APPLICATION NUMBER: US/08/467,602C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/209,204
; EARLIER FILING DATE: 1994-03-08
; EARLIER APPLICATION NUMBER: 08/059,022
; EARLIER FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-467-602-26

```

```

Query Match      75.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SEQ 3
      |||
Db      6 SEQ 8

```

RESULT 75

```

US-09-106-872A-7
; Sequence 7, Application US/09106872A
; Patent No. 6486311
; GENERAL INFORMATION:
; APPLICANT: Burks Jr., A. Wesley
; APPLICANT: Stanley, J. Steven
; APPLICANT: Cockrell, Gael
; APPLICANT: King, Nina E.
; APPLICANT: Sampson, Hugh A.
; APPLICANT: Helm, Ricki M.
; APPLICANT: Rannon, Gary A.
; TITLE OF INVENTION: Peanut Allergens and Methods
; FILE REFERENCE: HS 103 CIP
; CURRENT APPLICATION NUMBER: US/09/106,872A
; CURRENT FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: PCT/US96/15222
; PRIOR FILING DATE: 1996-09-23
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Soy
US-09-106-872A-7

```

```

Query Match      75.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SEQ 3
      |||
Db      8 SEQ 10

```

```

Search completed: November 25, 2003, 20:16:07
Job time : 6.3617 secs

```